

SEARCH REQUEST FORM

Requestor's Name: GAMBEL Serial Number: 023/427551
Date: 12/17/1967 Phone: 302-3977 Art Unit: 1215

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

SEQUENCE INTERFERENCE SEARCH

SEQUENCE INTERFERENCE SEARCH

SEQ ID NOS. 1-12

11 (1) (2) (3) (4) (5) (6) (7) (8) (9) (10) (11) (12)

APR 1962 (SIF 71 154 397 351)

(1) INTERFERENCE SEARCH

(2) B7(W) 100 107(W) 2

(3) (1) + (2) PRINT FOR OFFICIAL USE ONLY

(4) (2) (4) (16 C10 OR 7 C10 OR 10 C10)

20 C10 OR 7 C10 OR 10 C10

PRINT

REQUEST INFO

REMARKS

12/17/1967

STAFF USE ONLY

Date completed: 12/17/1967
Searcher: _____
Terminal time: _____
Elapsed time: _____
CPU time: _____
Total time: _____
Number of Searches: 2
Number of Databases: 2

Search Site

____ STIC
____ CM-1
____ Pre-S

Type of Search

☒ N.A. Sequence
☒ A.A. Sequence
____ Structure
____ Bibliographic

Vendors

____ IG Suite
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ Other

US-08-487-550-Lrge

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 20:52:14 1996; MasPar time 430.89 Seconds
1243.553 Million cell updates/sec.

Tabular output not generated.

Title: >US-08-487-550-1

Description: (1-705) from US08487550.seq

Perfect Score: 705

N.A. Sequence: 1 ATGAGGTCGCCGCTCAGCT.....CCCTACAGAACTGTCATGA 705

Comp: TACTCCAGGCGCCAGTCGA.....GGGATCTTACAGTACT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 270440 seqs, 380027776 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: emb1-new3

1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PIN

9:PRI1 10:PRI2 11:PRO 12:ROD 13:SYN 14:UNC 15:VRT

16:VIR1 17:VIR2

Database: genbank92

18:BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7

25:BCT8 26:BCT9 27:INV1 28:INV2 29:INV3 30:INV4 31:INV5

32:INV6 33:MAM1 34:MAM2 35:PAT1 36:PAT2 37:PAT3 38:PHG

39:PLN1 40:PLN2 41:PLN3 42:PLN4 43:PLN5 44:PLN6 45:PLN7

46:PLN8 47:PRI1 48:PRI2 49:PRI3 50:PRI4 51:PRI5 52:PRI6

53:PRI7 54:PRI8 55:PRI9 56:PRI10 57:PRI11 58:PRI12

59:PRI13 60:ROD1 61:ROD2 62:ROD3 63:ROD4 64:ROD5 65:ROD6

66:ROD7 67:STR 68:SYN 69:UNA 70:VRL1 71:VRL2 72:VRL3

73:VRL4 74:VRL5 75:VRL6 76:VRL7 77:VRT1 78:VRT2 79:VRT3

Database: genbank-new1

80:BCT 81:INV1 82:INV2 83:MAM 84:PHG 85:PIN 86:PRI

87:ROD 88:STR 89:SYN 90:UNA 91:VRL 92:VRT

Database: u-emb145_92

93:part1

Statistics: Mean 10.856; Variance 4.427; scale 2.452

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	ID	Description	Pred. No.
1	550	78.0	803 51	HSIGVL022	Human rearranged immu	0.00e+00
2	541	76.7	747 51	HSIGVL031	Human rearranged immu	0.00e+00
3	486	68.9	725 51	HSIGVL002	Human rearranged immu	0.00e+00
4	478	67.8	839 51	HSIGVL026	Human rearranged immu	0.00e+00
5	478	67.8	872 56	HUMIGLAM2	Human Ig rearranged 1	0.00e+00
6	474	67.2	791 51	HSIGVL028	Human rearranged immu	0.00e+00
7	472	67.0	737 51	HSIGVL023	Human rearranged immu	0.00e+00
8	472	67.0	780 51	HSIGVL011	Human rearranged immu	0.00e+00
9	468	66.4	806 51	HSIGVL005	Human rearranged immu	0.00e+00
10	449	63.7	664 51	HSIGVL004	Human rearranged immu	0.00e+00
11	427	60.6	750 51	HSIGVL027	Human rearranged immu	0.00e+00
12	421	59.7	810 51	HSIGVL025	Human rearranged immu	0.00e+00
13	421	59.7	870 51	HSIGVL	Human mRNA for Ig lam	0.00e+00
14	419	59.4	802 51	HSIGVL032	Human rearranged immu	0.00e+00
15	417	59.1	747 51	HSIGVL006	Human rearranged immu	0.00e+00
16	408	57.9	827 51	HSIGVL021	Human rearranged immu	0.00e+00
17	407	57.7	642 59	S42404	Ig lambda chain=anti-	0.00e+00
18	406	57.6	600 86	HUMIGTAT7F	Homo sapiens (clone t	0.00e+00
19	406	57.6	600 56	HUMIGTAT7F	Homo sapiens (clone t	0.00e+00
20	406	57.6	600 10	HSIGTAT7F	Homo sapiens (clone t	0.00e+00
21	404	57.3	877 56	HUMIGHEPAL	Human (hybridoma H210	0.00e+00
22	403	57.2	915 51	HSIGVL009	Human rearranged immu	0.00e+00
23	402	57.0	663 9	HS07991	Human lymphoma immuno	0.00e+00
24	402	57.0	663 52	HSU07991	Human lymphoma immuno	0.00e+00
25	400	56.7	783 51	HSIGVL001	Human rearranged immu	0.00e+00
26	397	56.3	756 51	HSIGVL034	Human rearranged immu	0.00e+00
27	394	55.9	666 52	HSU07992	Human myeloma immunog	0.00e+00
28	394	55.9	666 9	HS07992	Human myeloma immunog	0.00e+00
29	391	55.5	819 51	HSIGVL029	Human rearranged immu	0.00e+00
30	381	54.0	652 56	HUMIGLVCX	Human immunoglobulin	0.00e+00
31	374	53.0	585 10	HSIGTATAB	Homo sapiens (clone t	0.00e+00
32	374	53.0	585 56	HUMIGTATAB	Homo sapiens (clone t	0.00e+00
33	374	53.0	585 86	HUMIGTATAB	Homo sapiens (clone t	0.00e+00
34	374	53.0	820 51	HSIGVL024	Human rearranged immu	0.00e+00
35	367	52.1	755 51	HSIGVL033	Human rearranged immu	0.00e+00
36	360	51.1	805 34	S66247	Ig lambda =immunoglob	0.00e+00
37	360	51.1	805 33	MVIGLAM	M.vison immunoglobuli	0.00e+00
38	350	49.6	838 51	HSIGLEV	Human mRNA for Ig lam	0.00e+00
39	339	48.1	780 51	HSIGVL030	Human rearranged immu	0.00e+00
40	339	48.1	881 56	HUMIGLYM1	Human immunoglobulin	0.00e+00
41	334	47.4	623 59	S77011	[pseudogene] Ig V lam	3.95e-302
42	331	47.0	577 59	S77601	anti-carcinoma surfac	4.91e-299
43	329	46.7	868 34	MVIGLVCJA	Mink immunoglobulin 1	5.67e-297
44	318	45.1	441 51	HSIGLCA	H.sapiens gene for Ig	1.23e-285
45	318	45.1	8381 51	HSIGU266	Human U266 rearranged	1.23e-285

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	NID	KEYWORDS	SOURCE	ORGANISM
1	HSIGVL022	Human rearranged immunoglobulin lambda light chain mRNA.	X57812	g33723	Ig lambda light chain; immunoglobulin.	human.	Homo sapiens
							Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;

Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

1 (bases 1 to 803)

Klobeck, H.G.

Direct Submission

Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.

Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany

REFERENCE

2 (bases 347 to 393)

Combrato, G. and Klobeck, H.G.

V lambda and J lambda-C lambda gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism

Eur. J. Immunol. 21 (6), 1513-1522 (1991)

JOURNAL

91257162

for overlapping sequences see: X51754-55; J00252-54; M15641-42.

FEATURES

source

NCBI gi: 33723

Location/Qualifiers

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/tissue_type="spleen"

/cell_type="B-cell"

/clone_lib="phage library cML"

/clone="cML2"

/isolate="individual ML"

/chromosome="22"

mRNA

1..803

/gene="immunoglobulin lambda light chain"

/note="cDNA"

/evidence="experimental"

sig_peptide

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/gene="immunoglobulin lambda light chain"

/note="variable region; V(lambda)III"

/gene="immunoglobulin lambda light chain"

/note="NCBI gi: 33724"

/codon_start=1

/db_xref="PDB:33724"

/translation="MAWTVLLGLLHSGTSTVYLPQPPSVSVAPKAARITCGGI

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AYCQWDSSDHVVFGGKTLVIGQPKAASVTLFPSPSEELQNKATLVCLISDF

YPAVTVAKKADSPVRAGVETTPSKSNKYAASSYLSLTPEQWKSRSYSCQVTH

EGSTVEKTVAPTECS"

67..391

/gene="immunoglobulin lambda light chain"

/note="variable region; V(lambda)III"

/gene="immunoglobulin lambda light chain"

/note="J-segment"

354..391

/gene="immunoglobulin lambda light chain"

/note="J-segment"

392..711

/gene="immunoglobulin lambda light chain"

/note="constant region"

BASE COUNT

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ORIGIN

Query Match 78.0%; Score 550; DB 51; Length 803;

Best Local Similarity 92.8%; Pred. No. 0.00e+00;

Matches 596; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Db 68 cctatgtgctgactcagccacctcgtgctcagtgcccccaggaagcgccaggatta 127

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Qy 62 CCTATCAACTCACTCAGCCACCCCTCGGTCTCAGTGTCCAGGACACAGCCGCGAGATCA 121

Db 128 cctgtgggggaatcaacattgcaagttaaagtgtgcaactggtaccagcagaagccagcc 187

Qy 122 CTTGTGGGGGACACACTAGATAATGAATATGTCCACTTGTACACGACGAGCCGCGC 181

Db 188 agccctctgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 247

Qy 182 GGGCCCTTACTTGTGTCATCTATGATGATGATGATGATGATGATGATGATGATGATGAT 241

Db 248 tctctgctcccaactctgggaacacggccaccctgaacatcagtagggtcgaagccgggg 307

Qy 242 TCTCTGGCTCCAAATCAGGAACACGCGCCCTCACCATCAACGGGGTCGAGGCGGGG 301

Db 308 atgagccgcctattatgctcaggtgtggatagtagtagtagtagtagtagtagtagtagtag 367

Qy 302 ATGAGGCTGACTATTACTTCTCAGGTCTGGGACAGGGCTAGTATCATCTCGGTCTTCGAG 361

Db 368 gagggaccaagtgcacctcctaggtcagcccaagggtgccccctcggtcactctgttcc 427

Qy 362 GAGGACCGGGGTGACCGTCTAGGTACGCCCAAGGTCGCCCTCGGTCTGTTCC 421

Db 428 cgcctctctgtgaggtctcaagccaacagggccacactggtgtgtctcataagtagt 487

Qy 422 GGGCTTCTCTGAGGAGCTTCAAGCCCAAGGCGCACACTGGTGTGTCTATAGTACT 481

Db 488 tctaccggagagcctgacagtggcctggaagccagatagcagccctcaagcgaggag 547

Qy 482 TCTACCGGGGCGCTGACAGTGGCTCGAAGCGCAGATAGCAGCCCGCTCAAGCGGGAG 541

Db 548 tggagaccacacacccctccaaacaaagcaaacagtagcagcgccagcagtagtctga 607

Qy 542 TGGAGACCAACACCCCTCCAAACAAAGCAACAAAGTACCGGGCGCAGCTACCTGA 601

Db 608 gctgacgctgagcagtggaggtcccacagaagctacagctgccaggtcacgcatgaag 667

Qy 602 GCCTGAGCGCTGAGCAGTGGAGTCCACAGAGCTACAGCTGCCAGTCCAGGTCAGGTCAGG 661

Db 668 ggaacacctggaagaagcagctggccctcacagaatgttcat 709

Qy 662 GGAGACCGCTGGAGAGACAGTGGCCCTCAGAGAATGTTCTAT 703

RESULT

2

LOCUS HSI01031 747 bp RNA PRI 04-NOV-1994

DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.

ACCESSION X57821

KEYWORDS g33741

SOURCE Ig lambda light chain; immunoglobulin.

ORGANISM human.

Eukaryotes

Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 747)

Klobeck, H.G.

Direct Submission

Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.

Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany

REFERENCE

2 (bases 347 to 386)

AUTHORS Combiato, G. and Klobeck, H. G.
TITLE V lambda and J lambda-C lambda gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism
JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE 91257162
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

FEATURES

source
NCBI gi: 33741
Location/Qualifiers
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/cell type="B-cell"
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/chromosome="22"
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/note="cDNA"
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6..704
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GSTVEKTVAPTECS"
63..384
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/note="variable region; V(lambda) III"
347..384
/gene="immunoglobulin lambda light chain"
/note="J-segment"
385..704
/gene="immunoglobulin lambda light chain"
/note="constant region"
BASE COUNT 171 a 230 c 211 g 135 t
ORIGIN
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Best Local Similarity 93.3%; Pred. No. 0.00e+00;
Matches 599; Conservative 0; Mismatches 40; Indels 3; Gaps 2;
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Qy 62 CCTATGAACCTGACTCAGCCACCCTCGGTGTGCTGCTGCCGAGACAGCGCGCAGATCA 121
Db 124 cctgtggggaaataaacattggaagtataaagtgtgactggtaccagcagaagcaggcc 183
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Qy 122 CCTGTGGGGAGACACAGTAGAATATGAATATGTCACCTGTTACGACAGAGAGCGACGCC 181
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Db 184 agggccctgtgctgtctatgatagcagccctcagggatccctgagcgat 243
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Qy 182 GGGCCCTTACTGTGCTATCTATGATGATGATGATGATGATGATGATGATGATGATGAT 241
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Db 244 tctctgctccaactctgggaacagcggccacctgacctcagcaggtctgaaagcgggg 303
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Qy 242 TCTCTGGCTCCAAATCAGGAACACACCCGCCCTGACCATCAACGGGGTCGAGCGCGGG 301
Db 304 atgagcgcagctattactgtcaggtgtgggatagtagtagtgatg-t--ggattccggcg 360
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Qy 302 ATGAGGCTGACTATTACTGTCTCAGGTGTGGGACAGGGGTAGTATCATCCGGGTCTTCGGAG 361
Db 361 gaggagcaactgaccgtcctcaggtcagcccaaggctgcccccctcggtcactctgttcc 420
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Qy 362 GAGGACCCGGGTGACCGTCTAGGTGACGCCCAAGGCTGCCCTCGGTCACTCTGTTC 421
Db 421 cgcctcctctcaggagcttcaagccaacaagccacactggtgtgtctcataagtgact 480
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Qy 422 CGCCCTCTCTCAGGAGCTTCAAGCCCAAGCCACACTCTGCTCTCATAAGTGACT 481
Db 481 tctaccggggagcgtgacagtggtcgtggaaggcagatagagccccctcaaggcgggag 540
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Qy 482 TCTACCGGGAGCGGTGACAGTGGCTTGAAGGCAGATAGCAGCCCGTCAAGGCGGGAG 541
Db 541 tggagaccaccacccctccaaacaagaacaaagtaacgagtcgagcagcagctatctga 600
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Db 601 qcctgacgctgagcagtggaagtcccacagaagctacagctgccaggtcacgcatgaag 660
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Qy 602 CCCTGACCGCTGAGCAGTGGAAAGTCCACAGAGCTACAGTGCAGGTGCGCATGAG 661
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Qy 662 GGAGCCCTGGAAGACAGCTGGCCCTTACAGATGTTTCAAT 703

RESULT

3
LOCUS HSIGVL002 725 bp RNA PRI 04-NOV-1994
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION X57802
KEYWORDS g33701
NID g33701
SOURCE Ig lambda light chain; immunoglobulin.
ORGANISM human.
Eukaryotes; Mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 725)
AUTHORS Klobeck, H.G.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G. Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany
2 (bases 355 to 401)
AUTHORS Combiato, G. and Klobeck, H.G.
TITLE V lambda and J lambda-C lambda gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism
JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE 91257162
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

FEATURES

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NCBI gi: 33701
Location/Qualifiers
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/clone="cML23"
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/chromosome="22"
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/evidence=experimental
24..719
CDS
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24..80
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81..399
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/notes="variable region, V(lambda)III"
362..399
misc_feature
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BASE COUNT 164 a 226 c 199 g 136 t
ORIGIN
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Best Local Similarity 90.2%; Pred. No. 0.00e+00;
Matches 579; Conservative 0; Mismatches 57; Indels 6; Gaps 5;

Db 82 cctatgagctgactcagccaccctcagtgccgtgtcccccagcagacagccagcatca 141
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QY 62 CCTATGAATGACTCAGCACCCCTCGGTGTGTCAGTGTCCTCCAGGACAGAGCCGCGAGTCA 121

Db 142 cctgctctgagatacattggggataaataatgcttgctgtgtatcagcagaagccagcc 201
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QY 122 CTTGTGGGGAGACACACAGTAGAATGAATATGTCACACTGGTACCAGAGAGCCAGCCG 181

Db 202 actccctctgctgtgctatctttcaagatagcaagcgccctcaggagatccctgagcgat 261
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QY 182 GGGCCCTTACTACTGTGTCATGTCATGATGATGATGATGATGATGATGATGATGATGAT 241

Db 262 tcttggctccaacttgggaacacagcactctgaccatcagcgggagaccaggtatgg 321
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QY 242 TCTCTGGGTCCTCAATCAGGGACACACCGCCCTCGTACCATCAAGGGGTCAGGCGGGG 301

Db 322 atgagctgactattactgtcaggcgtggagacag--c-agg-a-c-tgcggtattcgccg 375
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QY 302 ATCAGGCTGACTATTTACTGTGTCAGGTGTGGGACAGGGGTAGTGATCATCCGGTCTTCGGAG 361

Db 376 gaggaaccaagctgacctctcctaggtcagcgccaagctgccctcctcgtcactctgttcc 435
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QY 362 GAGGACCCGGGTGACCGCTGCTAGTACAGCCCAAGGCTGCCCTCGGTCACTCTGTTC 421

Db 436 cgccctcctctgagaggttcaagccaagccacactgggtgtctctcataagtgact 495
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QY 422 CCCTCTCTCTCTGAGGAGCTTCAAGCCCAACAGGCCACACTGCTGTGTCTCATAGTGACT 481

Db 496 tctaccggggagccgtgacagtgccgtggaaggcagatagcagcccgtaagggcgag 555
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Db 556 tggagaccacaccctccaaacaagcaacaagtacgcgcgagcagctatctga 615
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QY 542 TGGAGACACACACACCTCCAAACAAGCAACAAGTACCGCGCCAGCAGCTACTCTGA 601

Db 616 ccctgagccctgagcagtggaagtcccccagaagctacagctgcccaggtcacgcatgaag 675
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QY 602 CCCTGACGCTGACGAGTGGAGTCCACAGAGCTACAGCTGCCAGGTCCACCATGAAG 661

Db 676 ggaagccctggagaagacagctggccctccacagaattgttcat 717
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QY 662 GGAGCAGCTGCGAAGACAGCTGGCCCTTACAGAAATGTTTCAT 703

RESULT 4
LOCUS HSIQVL026 839 bp RNA PRI 04-NOV-1994
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION X57816
NID g33731
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 839)
AUTHORS Klobeck, H.G.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.
Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie
und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000
Muenchen 2, Germany
REFERENCE 2 (bases 354 to 400)
AUTHORS Combriato, G. and Klobeck, H.G.
TITLE V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism
JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE 91257162
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

NCBI gi: 33731 Location/Qualifiers
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/cell_type="B-cell"
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/gene="immunoglobulin lambda light chain"
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Best Local Similarity 89.6%; Pred. No. 0.00e+00;
Matches 575; Conservative 0; Mismatches 61; Indels 6; Gaps 4;
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Qy      62 CCTATGAACCTGACTCAGCCACCTCGGTGTACGTGTGCCAGGACAGCGCCAGGATCA 121
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Db      141 cctgtctggagataaattgggggataaatatgcttctgtatcagcagaagcagcc 200
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Qy      122 CTTGTGGGGAGACAACTAGAAATGAATGTCTCCACTGGTACAGCAGACGACGCGC 181
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Db      261 tctctggctccaattctgggaacacagccactcgaccatcagtgagaccaggtcatgg 320
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Qy      242 TCTTGGCTCCAAATCAGGGAACACGCCACCTCGACCATCAACGGSGTCAGGCCGGG 301
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Db      375 gagggaccaagttgacgctcctagtcagcccaaggtgccccctcggtcaetctgtcc 434
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QY	602	GCTTGACCGCTGAGCAGTGGAGATCCACACAGAGCTCACAGCTCCACAGCTACCGCATGAAG	661
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DEFINITION	Human Ig rearranged lambda-chain mRNA VJC-region subgroup lambda-IV		05-JAN-1995
ACCESSION	M18645		
NID	q186103		
KEYWORDS	C-region; V-region; immunoglobulin lambda;		
SOURCE	immunoglobulin light chain; variable region subgroup lambda-IV. Human hybridoma H6-3C4 (cell fusion of mouse myeloma NS1 cells and human peripheral blood lymphocytes), cDNA to mRNA, clone p3C4-lambda-4.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.		
AUTHORS	1 (bases 1 to 872) Yamaaki,N., Komori,S. and Watanabe,T.		
TITLE	Complementary DNA for a human subgroup IV immunoglobulin lambda-chain		
JOURNAL	Mol. Immunol. 24 (9), 981-985 (1987)		
MEDLINE	88013904		
COMMENT	NCBI gi: 186103		
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Query Match      67.8%; Score 478; DB 56; Length 872;
Best Local Similarity 87.5%; Pred. No. 0.00e+00;
Matches 558; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
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Qy 602 GCCTGACCGCTGAGCAGTGGAGTCCACAGACGTACAGCTGCCAGTCACGCATGAAG 661
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Db 638 ggcacacgtggaagacagtgccctacagaatgttcat 679
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Qy 662 GGAGCACCGTGGAGAGACAGTGGCCCTACAGAAATGTTTCAT 703
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RESULT 9
LOCUS HSIGVL005 806 bp RNA PRI 04-NOV-1994
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION X57805
NID g33707
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chosnata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Homnidae; Homo.
1 (bases 1 to 806)
Klobeck, H.G.
Direct Submission
Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.
Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie
und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000
Muenchen 2, Germany
2 (bases 354 to 400)
Combrinato, G. and Klobeck, H.G.
V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism
Eur. J. Immunol. 21 (6), 1513-1522 (1991)
91257162
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.
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FEATURES

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363..398
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399..718
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/notes="constant region"
BASE COUNT 191 a 255 c 208 g 152 t
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Query Match 66.4%; Score 468; DB 51; Length 806;
Best Local Similarity 86.7%; Pred. No. 0.00e+00;
Matches 553; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
Db 79 tgaagtgaactcagaccctactgtgtgtggccttgggacagagcgtcaggatcaaatg 138
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Db 199 cctacactctcatcaatggttaaagacaacgcccctcaggatcccagaccgattctc 258
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Db 259 tggctccacctcaggaacacagcttcttgaccatcaactgggactcaggcggaagatga 318
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Qy 306 GGCTGATATTACTGTCAGGTCTGGGACAGGGCTAGTATCATTCGGTCTTCGGAGGAGG 365
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Db 379 gaccacgtgaccgtccttaagtgcagcccaagctgccccctcggtcactctgttccccgc 438
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Qy 366 GACCGGGTGACCGCTCTAGGTACGCCAAGGCTGCCCGCTCGGTACTGTTCCCGCC 425
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Db 439 ctctctgagagcttcaagccaacaagccacacactggtgtgtctcataagtgcattcta 498
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Qy 426 CTCCTCTGAGGAGCTTCAAGCCAAACAAGGCCACACTGCTGCTCTATAAGTCACTTCTA 485
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Db 559 gaccacacacccctccaacaaagcaacaagtcacgagcagcagctatcttgagcct 618
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Db 679 caccgtgagagaagacagtggtggccctcacagaatgttcat 716
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RESULT 10
LOCUS HSIGVL004 664 bp RNA PRI 04-NOV-1994
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION X57804
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NID g33705
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 664)
AUTHORS Klobeck, H.G.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.
Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie
und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000
Muenchen 2, Germany
REFERENCE 2 (bases 211 to 257)
AUTHORS Combriato, G. and Klobeck, H.G.
TITLE V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism
JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE 91257162
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

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Best Local Similarity 89.2%; Pred. No. 0.00e+00;
Matches 511; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

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Qy 131 CAGACAAACAGTAGAATAATGTCCACTGGTACAGCAAGAACCCAGCGCGCCCTA 190
Db 61 tacttgtcatctatggtcaaaaaaacggccctcaggatcccaggccgattcttggct 120
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Qy 191 TACTGGTCACTATGATAGTACCGCGCCCTCAGGGATCCCTCAGCGATTCTCTGGCT 250
Db 121 ccagctcaggaaaacacagcttcttgaccatactggggcccccaggcgaagatgagctg 180
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Qy 251 CCAATCAGGGAACACGCCACCTGACCATCAAGGGGTGCGAGCGGGGGATGAGGCTG 310
Db 181 acttattactgttaactccgggacagcagtggttaaccatctggtgtcggcgaggagacca 240
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Qy 431 CTGAGGAGGCTTCAAGGCAACAGGCCACACTGGTGTCTCTATAAGTCACTTCTTACCCGG 490
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Db 541 tggagagagcagtggtgcccctacagaatgttat 573
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RESULT 11
LOCUS HSIGVL027 750 bp RNA PRI 20-JUL-1995
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION X57817
NID g33733
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 750)
AUTHORS Klobeck, H.G.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.
Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie
und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000
Muenchen 2, Germany
REFERENCE 2 (bases 338 to 384)
AUTHORS Combriato, G. and Klobeck, H.G.
TITLE V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism

/gene="immunoglobulin lambda light chain"

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CDs          6..713
/gene="immunoglobulin lambda light chain"
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misc_feature  63..393
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359..393
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/note="J-segment"
394..713
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/note="constant region"
BASE COUNT  176 a  275 c  211 g  148 t
ORIGIN
Query Match          59.7%; Score 421; DB 51; Length 810;
Best Local Similarity 87.0%; Pred. No. 0.00e+00;
Matches 495; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Db 143 caacatcgcaactaatgatgtatcgtaccagcaactcacaggaagcgcccaact 202
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Qy 135 CAACAGTAGAANTGAATATGTCCACTGCTACCAAGAGCCAGCGGGCGCCCTACTACT 194

Db 203 cctcatctataggaataatcacaggcgccctcagggtccctgacgcattctctggtccaa 262
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Qy 195 GGTCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 254

Db 263 gtcgtggtcctcagcctccctggccatcagtggtccctcagtcagagtgatgattgatta 322
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Qy 255 ATCAGGGACACGCCACCCCTGACCATCAGCGGGTCGAGGGCGGGGATGAGCTGACTA 314

Db 323 ttactgtgcagcatggatgacagcctcagtggtccggtgttcggcgaggaggaacaaagt 382
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Qy 315 TTACTGTGAGGTGTGGGACAGGGCTAGTGATCATCGGGTCTTCGGAGAGGACCGGGGT 374

Db 383 gaccgtcctcagtlcagcccaagctgccctcgttcaactctgttccgcctcctctga 442
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Qy 375 GACCGTCTAGGTACGCCCAAGGCGTCCCGCTCGGTGCTACTGTTCGCCCGCTCTCTGA 434

Db 443 ggaggttcaagcaacaaggcccaactggtgtgtcctaagtgaactctaccggagac 502
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Qy 435 GGAGCTTCAAGCCCAACAGGCCACACTGGTGTCTCATAAGTCACTTCTACCCGGGAGC 494

Db 503 cgtgacagtggtcctggaagcgagatagcagcccgctcaaggcggagtgagaccaccac 562
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Qy 555 ACCCTCCAAAACAAAGCAACAGTACCGGCGCAGCAGCTACTGAGCTGAGCGCTGA 614

Db 623 qcagtggaagtcaccacaagctacagctgacaggtcagcatgaagggagcaccgtgga 682
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Qy 615 GCAGTGGAAAGTCCCAACAGACTACAGCTGCCAGGTCAAGGATGAGGAGCAGCGTGA 674

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Qy 675 GAACACAGTGGCCCTACAGAAATGTTTCAT 703

RESULT 13
LOCUS      HSLGLV      870 bp      RNA      PRI      27-NOV-1995
DEFINITION Human mRNA for Ig lambda-chain.
ACCESSION  X14583
NID        g33394
KEYWORDS   Ig light chain; immunoglobulin; lambda-immunoglobulin.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 870)
AUTHORS    Kishimoto,T.
TITLE      Direct Submission
JOURNAL    Submitted (03-MAR-1989) Kishimoto T., Yoshitomi Pharmaceutical
            Industries Ltd, Research Labs, 7-25 Koyata 3-chome, Iruma Shi,
            Saitama, 358 Japan
REFERENCE  2 (bases 1 to 414)
AUTHORS    Kishimoto,T., Okajima,H., Okumoto,T. and Taniguchi,M.
TITLE      Nucleotide sequences of the cDNAs encoding the V-regions of H- and
            L-chains of a human monoclonal antibody with broad reactivity to
            malignant tumor cells
JOURNAL    Nucleic Acids Res. 17 (11), 4385 (1989)
MEDLINE    89296497
COMMENT    hybridoma; clones=4G12 L6
            Data kindly reviewed (03-JUL-1989) by Kishimoto T.

FEATURES             Location/Qualifiers
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                        /tissue_type="lymph node"
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     CDS                25..732
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BASE COUNT  206 a  285 c  213 g  166 t
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Query Match          59.7%; Score 421; DB 51; Length 870;
Best Local Similarity 87.0%; Pred. No. 0.00e+00;
Matches 495; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Db 162 caacattgggaataattatctcctggtaccagcagctcccaaggaacagcccaact 221
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Qy 135 CAACAGTAGAANTGAATATGTCCACTGCTACCAAGAGCCAGCGGGCGCCCTACTACT 194
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RESULT	14	
LOCUS	HSIGVL032	802 bp RNA
DEFINITION	Human rearranged immunoglobulin lambda light chain mRNA.	PRI 04-NOV-1994
ACCESSION	X57822	
NID	g33743	
KEYWORDS	Ig lambda light chain; immunoglobulin.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrarhina; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 802)	
TITLE	Klobeck, H.G. -	
JOURNAL	Direct Submission	
KEYWORDS	Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G. Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany	
REFERENCE	2 (bases 342 to 388)	
AUTHORS	Combrato, G. and Klobeck, H.G.	
TITLE	V lambda and J lambda-C lambda gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism	
JOURNAL	Eur. J. Immunol. 21 (6), 1513-1522 (1991)	

MEDLINE	91257162
COMMENT	for overlapping sequences see: X51754-55; J00252-54; M15641-42.
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source	Location/Qualifiers 1..802 /organism="Homo sapiens" /tissue type="spleen" /cell type="B-cell" /clone_lib="phage library cML" /clone="cML93" /isolate="individual ML" /chromosome="22"
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mRNA	1..802 /gene="Immunoglobulin lambda light chain" /note="cDNA" /evidence=experimental <1..707
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misc_feature	56..386 /gene="immunoglobulin lambda light chain" /note="variable region; V(lambda)I"
misc_feature	356..386 /gene="immunoglobulin lambda light chain" /note="J-segment"
misc_feature	387..706 /gene="immunoglobulin lambda light chain" /note="constant region"
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Query Match	59.4%; Score 419; DB 51; Length 802;
Best Local Similarity	86.8%; Pred. No. 0.00e+00;
Matches	494; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
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Dbb	196 cttcatctataataataatgagcgccctcagggtgcctgaoctttctctgggtcccaa 255
Qy	195 GTGCATCTATGATGATAGTAGTGACCGGCCCTCAGGGATCCCTGACGGATTCTCTGGCTCCA 254
Dbb	256 gtctggcacctcagctccctgccactcagtgggctccagtcctgacgatgaggtgatta 315
Qy	255 ATCAGGAACAACCGCCACCCCTGCACCATCAACGGGGTTCAGCGCCGGGATGAGGCTCACTA 314
Dbb	316 ttactgtgcagcagtggaatgacagctgaatggcggctctttggcgaggaggacaagtt 375
Qy	315 TTACTGTCAGGTCGGGACAGGGCTAGTCATCATCCGGCTTTCCGAGGAGGAGCCGGGT 374
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Qy . 375 GACCGTCTAGGTACGCCCAAGGTCGCCCTCGGTCACTGTGTCCCGCCCTCTCTCA 434

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Qy 435 GGAGCTTCAAGCCAACAAGGCCACACTGTGTGTCTCATAGTCACTTCTACCGGGAGC 494

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Qy 555 ACCCTCCAAACAAGCAACAAGTACGCGGCCGAGCAGCTACCTGAGCCTCAGCCCTGA 614

Db 616 gcaagtggagtcctccaaagctacagctgccaggtcaagcatgaagggagcagcgtgga 675
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Qy 615 GCAGTGGAAGTCCCAAGAGCTACAGCTGCAGCTCAGCATGACGCATGAAGGGAGCACCGTGA 674

Db 676 gaagcagctggccctacagaattgtcat 704
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Qy 675 GAAGACAGTGGCCCTACAGAACTGTTCA 703

RESULT 15

LOCUS H5IGVL006 747 bp RNA PRI 20-JUL-1995

DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.

ACCESSION X57806

NID g33709

KEYWORDS Ig lambda light chain; immunoglobulin.

SOURCE human.

ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.

REFERENCE 1 (bases 1 to 747)
Klobeck, H.G.
TITLE Direct Submission

JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.
Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie
und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000
Muenchen 2, Germany

REFERENCE 2 (bases 335 to 381)
Combiato, G. and Klobeck, H.G.
TITLE V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism

JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)

MEDLINE 91257162

COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

FEATURES
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mRNA 1..747
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/note="variable region; V(lambda)I"
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BASE COUNT 169 a 244 c 196 g 138 t

ORIGIN

Query Match 59.1%; Score 417; DB 51; Length 747;
Best local Similarity 86.6%; Pred. No. 0.00e+00;
Matches 493; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Db 129 caacattgggaataattatgtacctgtaccagcagctcccggaaggagggccccaact 188
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Qy 135 CAACAGTAGAATGAATATGTCACCTGGTACCAGCAGACGCGGGCCCTACTACT 194
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Db 189 cctcatctttgaaataataaagcagccctcagccattcctgaccgattctctggtccaa 248
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Qy 195 GGTCTATCATGATGATGACCGGCCCTCAGGGATCCCTGAGCGATTCTTGGCTCAA 254

Db 249 gtcctggcagctcagccacctgggagatcgccggctccagactgggagagcgcgat 308
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Qy 255 ATCAGGAACACCGCCACCCTCACCATCAACGGGTCGAGGCCGGGATCAGGCTGACTA 314

Db 309 ttaactcggaacatggatagcagcctgactgatgtggttttcggcggggggaccaaagt 368
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Qy 315 TTACTGTGAGGTGTGGACAGGGCTAGTATCATCCGGTCTTCGGAGGAGGACCGGGT 374

Db 369 gacgtcctagtcagcccaaggctgccctcctgctcactctgttccgcctcctctga 428
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Qy 375 GACGCTCTAGTGTACGCCAAGGCTGCCCTCGGTCACTGTGTCGCCGCTCTCTGA 434

Db 429 ggaagctcaagccaacaagccacactggtgtgtctcataaagtgaacttctaccgggagc 488
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Qy 435 GGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTATAAGTCACTTCTACCGGGAGC 494

Db 489 cgtgacagtgccctggaagcagatagcagcccgctcaaggcggagtggaagaccaccac 548
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Qy 495 CGTGACAGTGGCTGGGAAGCAGATAGCAGCCCGCTCAAGCGGGAGTGGAGACACCAC 554

Db 549 accctccaaacaagaacaagaftacgcggccagcagctatctgagcctgacgcctga 608
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Qy 555 ACCCTCCAAACAAGCAACAAGTACGCGGCCAGCAGCTACCTGAGCTCAGCCCTGA 614

Db 609 gcaagtggagtcctccaaagctacagctgccaggtcacgcattgaagggagcagcgtgga 668
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Qy 615 GCAGTGAAGTCCCAAGAGCTTACAGCTGCCAGTCAAGCATGAAGGGAGCACCGTGA 674

Dec 17 20:45

US-08-487-550-1.rge

29

Db . 669 gaagacagtggccctacagaatgttcat 697
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Qy 675 GAAGACAGTGGCCCTACAGAATGTTTCAT 703

Search completed: Tue Dec 17 20:59:32 1996
Job time : 438 secs.

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 20:59:52 1996; MasPar time 61.16 Seconds
898.374 Million cell updates/sec

Tabular output not generated.

УВАЖАЮЩИЙ

Title: >US-08-487-550-1

Description: (1-705) from US08487550.seq

Perfect Score: 705

N.A. Sequence: 1 ATGAGGGTCCCCGGCTCAGCT.....CCCCACAGAA TGTT CATGA 705

Comp: TACTCCCAGGGCGAGTCCA.....GGGGATGCTTACAAGTACT

Scoring table: TABLE default

Gap 6

STD : Dbase 0: Query 0

Searched: 102519 seqs, 38967980 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-aenesed24

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 8.751; Variance 5.406; scale 1.619

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			ID	Description	Pred. No.
		Match	Length	DB			
1	478	67.8	872	1	N81655	VDJC regions of human	0.00e+00
2	419	59.4	884	1	Q03609	Sequence encoding 4G1	1.13e-262
3	413	58.6	654	8	Q49835	Anti-HIV-1 recombinan	1.55e-258
4	404	57.3	902	6	Q35100	Antibody D lambda lig	2.46e-252
5	318	45.1	8387	3	Q22489	Human U266 lambda gen	3.05e-193
6	318	45.1	9071	3	Q23370	U266-Lambda gene and	3.05e-193
7	318	45.1	9071	3	Q22491	Human U266 lambda gen	3.05e-193
8	250	35.5	387	6	Q35904	Anti-CD4 V-lambda cod	8.24e-147

ALIGNMENTS

RESULT	1
ID	N81655 standard; DNA; 872 BP.
AC	N81655;
DT	09-NOV-1990 (first entry)
DE	VJJC regions of human sperm-immobilising monoclonal antibody..
KW	Anti-human sperm-immobilising monoclonal antibody; leader region;
KW	variable region; joining region; constant region; sterility;
KW	vaccine; contraceptive; ss.
OS	Homo sapiens.
Key	Location/Qualifiers
CDS	40..729
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FT	/product=VJC region
FT	misc_feature 91..375
FT	/tag= b
FT	/label=V region
FT	misc_feature 376..412
FT	/tag= c
FT	/label=J region
FT	misc_feature 413..729
FT	/tag= d
FT	/label=C region
PN	J63126482-A.

PD 30-MAY-1988.
PR 15-NOV-1986; 272412.
PA (TOFU) TOA NENRYO KOGYO KK.
DR WPI; 88-187839/27.
DR P-PSDB; P81260.
PT Cell strain producing human sperm-immobilising monoclonal antibody -
PT has at least V-gene in H chain coding genetic family and V gene in L
PT chain of DNA originating from antibody of sterile woman.
PS Disclosure; 14pp; Japanese.
CC A VDJC segment is inserted into pSC41ambda5 together with a
CC leader region. A cell strain, pref. a myeloma cell, can
CC produce the Ab with immobilising value (SI50) of at least 5000,
CC sperm agglutination value at least 1:1600 dilution, specifically
CC reacting against human ejaculated sperm. The product can be used
CC as a vaccine and contraceptive.
CC See also N81654-N81656.
SQ Sequence 872 BP; 211 A; 269 C; 220 G; 172 T;
Query Match 67.8%; Score 478; DB 1; Length 872;
Best Local Similarity 87.5%; Pred. No. 0.00e+00; Indels 0; Gaps 0;
Matches 558; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
Db 93 tgaactgaactcaggaacctgtgtgtctgtgacctgtggagacagacagtcaggatcaatg 152
QY 66 TGAATGACTACGCCACCTCGGTGTGCTGTCCCGAGCAGACGCGCGGATCACCTG 125
Db 153 ccaaggagacagcctcagaacctatcatgcaagtgtgtaccagcagaagcaagcagc 212
QY 126 TGGGGGAGACACAGCAGTAAATGATATCTCCACTGGTACGAGAGCGCAGCGGGC 185
Db 213 cctgtactgtcatctatgatgaaacaacccgacctcagggtatcccagaccattctc 272
QY 186 CCCTATCTGTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 245
Db 273 tggctccacctcaggaacacagcttctgtaccatcactgagctcagcggaagatga 332
QY 246 TGCGTCCAAATAGGGAACACGCCACCTGACCATCAACGGGGTGGAGCGGGGATCA 305
Db 333 ggctgaactattactgaactccgggagacagcagtggttaacgtctggtatctcgcggaag 392
QY 306 GGCTGACTATTACTGTGTCAGGTGTGGCAGAGGGCTAGTATCATCCGGTCTTCGAGGAG 365
Db 393 gaccaagctgacctgactaggtcagcccaaggtgccccctcggtcaactctgtccgcgc 452
QY 366 GACCGGGTGACCGTCTTAGTTCAGCGCCAGGCTGCGCCCTCGGTCACTCTGTCGCGCC 425
Db 453 ctctctgaggagcttcaagcacaagccacactgggtgtgtctcataagtgaactcta 512
QY 426 CTCTCTCAGGAGCTTCAAGCCCAACAGGCCACACTGGTGTGTCTATAGTGACTTCTA 485
Db 513 cccgggagccctgacagtgccctggaaggagatagcagccctcagcgagcgagtgga 572
QY 486 CCGGGAGCGCTGACAGTGGCTTGGAGGCGAGATAGCAGCCCGCTCAAGGGCGGAGTGA 545
Db 573 gaccacacacctccaaacaagaacaacaagatagcgggcgacagctatctgagcct 632
QY 546 GACCACACACCTCCAAACAAGCAACAACAGTACGCGGCGCAGCAGTACCTACGCT 605
Db 633 gacgctgagcagtggaagtccccacagaagctacagctgcccaggtcacgcattgaaggag 692
QY 606 GAGCGCTGAGCAGTGGAGTCCACAGAGCTACAGCTGCCAGGTCCACCATGAGGGAG 665
Db 693 caccgtggaagaagacagtgcccccctacagaatgttcat 730

QY 666 CACGTGGAGAGACAGACAGTGGCCCTACAGATGTTCAT 703
RESULT 2
ID Q03609 standard; cDNA; 884 BP.
AC Q03609;
DT 06-AUG-1989 (first entry)
DE Sequence encoding 4G12 monoclonal antibody (MAB) L chain .
KW 4G12 MAB; human lung cancer; oesophageal carcinoma; ss.
OS Synthetic.
FH Key Location/Qualifiers
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FT /product=4G12 L
FT misc feature 25..375
FT /*tag= b
FT /label=V region 376..414
FT misc feature 376..414
FT /*tag= c
FT /label=J region 415..729
FT misc feature 415..729
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FT /number=2
PN J02046289-A.
PD 15-FEB-1990.
PF 05-AUG-1988; 196647.
PR 05-AUG-1988; JP-196647.
PA (YOSH) Yoshitomi Pharm. Ind. KK.
DR WPI; 90-094983/13.
DR P-PSDB; R05555.
PT DNA base sequence coding for 4G12 monoclonal antibody - which reacts
PT specifically with human lung cancer and oesophageal carcinoma.
PS Disclosure; Page 549; 9pp; Japanese.
CC Sequence is cloned and synthetic DNA/RNA of human Ab L chain C regions
CC is used as probe to obtain sequences coding for 4G12 MAB.
CC See also Q03607-Q03610.
SQ Sequence 884 BP; 219 A; 286 C; 212 G; 166 T; 1 Others;
Query Match 59.4%; Score 419; DB 1; Length 884;
Best Local Similarity 86.8%; Pred. No. 1.13e-262;
Matches 494; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
Db 162 caacattgggaataatattatgtctgtaccagcagctcccaagaacagcccccaact 221
QY 135 CAACAGTAGAAATGAATATGTCCACTGGTACCAGCAAGCCGCGGGCCCTATACT 194
Db 222 cctcattatgacaataaataagcgacctcagggtattcctgaccgattctctggctccaa 281
QY 195 GGTCACTATCATATAGTAGACCGGCCCTCAGGATCCCTGAGCGGATCTCTGGCTCCA 254
Db 282 gtctgcacgtcagccacctgggcatcaccgggacctccagctgggagagcgccgatta 341
QY 255 ATACGGAACACCCACCACCCCTGACCATCAACGGGGTCGAGGCCGGGATGAGGCTGACTA 314
Db 342 ttactcgggaacatggatagcagcctgagtgctgggtatttcggcgagggagccaagct 401
QY 315 TTACTCTCAGGTGTGGCAGGGCTAGTATCATCCGGTCTTCGGAGGAGGCCCGGCT 374

Dbb 402 gaccgtctcaggtcagcccaaggctgcccctcggtcactctgttccgcctcctctga 461
|||||
Qy 375 CACCCTCTAGGTAGCCAGCAAGGCTGCCCTCGCTCACTGTTCGCCCTCCTCTGA 434
Dbb 462 ggagcttcaagcccaacaaggcccaactggtgtgtctcctaagtgaacttaccgggagc 521
|||||
Qy 435 GGAGCTTCAAGCCCAACAAGGCCACACTGCTGTGTCTCACTAAGTGACTTCTACCGGGAGC 494
Dbb 522 cgtgacagtggcctggaaggcagatgacgcccctgcaaggcgggagtgagacaccac 581
|||||
Qy 495 CGTGACAGTGGCTGAGCGGAGATGACGAGCCCGCTCAAGCGGGGAGTGGAGACACAC 554
Dbb 582 accctccaaacaagaacaaagctacgcggccagcagctatctgagcctgacgcctga 641
|||||
Qy 555 ACCCTCCAAACAAGCAACAAGTACCGGGCCAGCAGCTACCTGAGCCTCAGCGCTGA 614
Dbb 642 gcaagtggagctcccaagaagctacagctgccagctcaagcagatgaaggagacaccgtgga 701
|||||
Qy 615 GCAGTGAAGTCCCCACAGAGCTACAGCTGCGCAGGTACCGCATGAGGGAGCACCGTGA 674
Dbb 702 gaagacagtggcccctacagaattgtcat 730
Qy 675 GAAGACAGTGGCCCTACAGAATGTTTCAT 703

RESULT 3

ID Q49835 standard; cDNA; 654 BP.
AC Q49835;
DT 27-APR-1994 (first entry)
DE Anti-HIV-1 recombinant antibody 447-52D light chain coding sequence.
KW Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;
KW HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
KW acquired immune deficiency syndrome; chimeric antibody;
KW surface glycoprotein gp120; V3 loop; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..654
FT /*tag= a
FT /note= "encodes recombinantly modified 447-52D
FT light chain"
PN W09319785-A.
PD 14-OCT-1993.
PF 23-MAR-1993; U02629.
PR 01-APR-1992; US-861701.
PA (MERI) MERCK & CO INC.
PA (JOHN/) JOHNSON L S.
PA (PFAR/) PFARR D S.
PI Conley AJ, Emami EA, Johnson LS, Mark GE, Pfarr DS;
DR WPI; 93-336600/42.
DR P-PSDB; R42163.
PT New recombinant human antibody - with HIV neutralising activity
PT against at least two isolates, useful for preventing or treating
PT infection in diagnosis, etc.
PS Example 9; Fig 2B; 154pp; English.
CC EBV-transformed cell lines and mouse-human heterohybridomas
CC producing human MAbs specific for the gp120 V3 loop of HIV-1 MN
CC isolate were obtained. MAB 447-52D was found to recognise the
CC tetrapeptide motif GPGR, i.e. the Principal Neutralising
CC Determinant common to the V3 loop of different HIV isolates.
CC A recombinant Ab was produced in which the L chain V region was
CC derived from 447-52D and to which a signal sequence and a L chain
CC intronic sequence are appended, fused to a fragment contg. a short
CC intronic sequence of the human lambda 2 C region and the human

CC lambda 2 constant encoding domain.
SQ Sequence 654 BP; 156 A; 199 C; 178 G; 121 T;
Query Match 58.6%; Score 413; DB 8; Length 654;
Best Local Similarity 87.4%; Pred. No. 1.55e-258;
Matches 500; Conservative 0; Mismatches 69; Indels 3; Gaps 3;
Dbb 81 cacattgggaataattatgattggtaccagcagttcccaagaaacacgccccaaact 140
|||||
Qy 135 CAACAGTAGAATAATATGCTCACTGCTACCAAGCAAGCCAGCGCGGCCCTATACT 194
Dbb 141 cctcattatggcaataataagcagccctcagggaattcctgaccgattctctggtccaa 200
|||||
Qy 195 GGTCACTATCATGATAGTAGAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCA 254
Dbb 201 gtctggcagctcagccaccctgggcatacccgagctccagctgggagcagggccgatta 260
|||||
Qy 255 ATCAGGGACACCCGCCCTGACCAATCAACGGGTGAGCGCGGGGATGAGGCTGACTA 314
Dbb 261 ttctcgcacaatgggatagcgccctgagtgctgattgggtgttcggcgagggagacaa 320
|||||
Qy 315 TTACTGTCAAGTGTGGACAG-GGC-T-AGTGATCATCCGGTCTTCGGAGAGGGACCG 371
Dbb 321 gctgaccgtcctaagtccagcccaaggctgcccctcggtcactctgttccgcctcctc 380
|||||
Qy 372 GGTGACCGTCTAGCTCAGCCCAAGGCTGCCCTCGCTCACTCTGTTCGCCCTCCTC 431
Dbb 381 tgaggagcttcaagcccaacaaggccacactggtgtgtctcataagtgaacttaccggg 440
|||||
Qy 432 TGAGGAGCTTCAAGCCCAAGGCCACACTGCTGTCTCTATAAGTCACTTCTACCGGG 491
Dbb 441 agcgtgacagtggtcctggaaggcagatagcagccccctcaaggcgggagtgagacac 500
|||||
Qy 492 AGCGGTGACAGTGGCTGGAAGGCATAGACAGCCCCGCTCAGCGGGGAGTGGAGACCAC 551
Dbb 501 cacacctccaaacaagaacaaagtacggcgccagcagctatctgagcctgacgc 560
|||||
Qy 552 CACACCTCCAAACAAGCAACAAGTACCGGGCCAGCAGCTACCTGAGCCTGACGCC 611
Dbb 561 tgagcagtggagtcaccagagactcaagctgccaggtcacgagtcaggggagcaccgt 620
|||||
Qy 612 TGAGCAGTGGAAAGTCCACAGAGCTACAGTGCAGGTCCAGGTCCAGCATGAAGGGAGCACCGT 671
Dbb 621 ggagaagacagtggcccctacagaattgtcat 652
|||||
Qy 672 GGAGAGACAGTGGCCCTACAGAATGTTTCAT 703

RESULT 4

ID Q35100 standard; DNA; 902 BP.
AC Q35100;
DT 19-MAY-1993 (first entry)
DE Antibody D lambda light chain.
KW Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;
KW lymphocyte; hepatitis A virus; HAV; sero; positive; patient;
KW murine; B5B3; polyadenylated; cDNA library; human; kappa; lambda; H; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 32..739
FT /*tag= a
FT sig peptide 32..88
FT /*tag= b
FT misc_RNA 89..154
FT /*tag= c

Best Local Similarity 99.7%; Pred. No. 3,05e-193;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 7062 aggtcagcccaaggtgccccctcggtcactctgttcccgccctctctgagaggttca 7121
|||||
Qy 384 AGTCTAGCCAGCCAGGCTGCCCTCGGTGCTCTCTGTCCCGCCCTCTCTGAGGAGCTTCA 443
|||||
Db 7122 agccaacaagccacactggtgtctcctaagtgtacttctaccgggagccgtgacagt 7181
|||||
Qy 444 AGCCAAAGGCCACACTGGTGTCTCTATAAGTCACTTCTACCCGGGAGCGGTGACAGT 503
|||||
Db 7182 ggcctggaagccagatagcagcccccgtcaaggcggtgagtgagaccaccacccctccaa 7241
|||||
Qy 504 GGCCTGGAGGCAGATAGCAGCCCGCTCAAGGGGAGTGGAGACCAACACACCTCCAA 563
|||||
Db 7242 aaaaagcaacaagaatcacgctgcccagcagctatctgagcctgacgctgagcagtgaa 7301
|||||
Qy 564 ACAGGCAACACAGTACGGCGGCAGAGCTACTGTAGCCCTGACGAGTGGAA 623
|||||
Db 7302 gtccacagaagctacagctgccaggtcacgcatgaaggagaccgctggaagacagt 7361
|||||
Qy 624 GTCCACAGAAAGCTACAGTCCAGGTCCAGGTACGCATGAAGGGAGCCGCTGGAGACAGT 683
|||||
Db 7362 ggcctcacagaatgttcat 7381
|||||
Qy 684 GGCCTTACAGATGTTTAT 703

RESULT 6
ID Q23370 standard; DNA; 9071 BP.
AC Q23370;
DT 14-AUG-1992 (first entry)
DE U266-Lambda gene and downstream murine Ig Heavy chain enhancer.
KW Lambda-E-mu; rearranged; immunoglobulin; light chain; transgene;
KW B cell deficiency; common variable immunodeficiency; CVID;
KW ATCC # 72003; ds.
OS Chimeric Mus.
PN W09204443-A.
PD 19-MAR-1992.
PF 27-AUG-1991; U06106.
PR 29-AUG-1990; US-575006.
PA (HARD) HARVARD COLLEGE.
PI Vasicek TJ, Leder P;
DR WPI; 92-114351/14.
PT B cell deficient transgenic FVB/N mice - comprise DNA encoding
PT the lambda light chain of a non-human animal for modelling of B
PT cell deficiency
PS Disclosure; Fig 7; 41pp; English.
CC DNA from the IgE-lambda human myeloma U266 cell line was digested
CC with EcoRI and used to prepare a phage library. The clone
CC containing the active lambda gene was identified by probing the
CC library with a radiolabelled BamHI fragment of the human lambda 2
CC gene. (The complete sequence of U266-lambda gene has EMBL Acc.#
CC X51754). The lambda-E-mu construct was prepared by cutting the
CC lambda construct at the HindIII site 0.9kb downstream of
CC C(lamba)2. The fragment was blunt-ended and ligated to a 995bp
CC XbaI fragment of pTAR-7 containing the mouse Ig heavy chain
CC enhancer. The transgene construct was used to transfect mouse
CC cells for the production of B cell deficient transgenic mice. The
CC mice can be used to study e.g. X-linked agammaglobulinemia.
SQ Sequence 9071 BP; 2196 A; 2395 C; 2321 G; 2159 T;
Query Match 45.1%; Score 318; DB 3; Length 9071;

Best Local Similarity 99.7%; Pred. No. 3,05e-193;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 7061 aggtcagcccaaggtgccccctcggtcactctgttcccgccctctctgagaggttca 7120
|||||
Qy 384 AGTCTAGCCAGCCAGGCTGCCCTCGGTGCTCTCTGTCCCGCCCTCTCTGAGGAGCTTCA 443
|||||
Db 7121 agccaacaagccacactggtgtctcctaagtgtacttctaccgggagccgtgacagt 7180
|||||
Qy 444 AGCCAAAGGCCACACTGGTGTCTCTATAAGTCACTTCTACCCGGGAGCGGTGACAGT 503
|||||
Db 7181 ggcctggaagccagatagcagcccccgtcaaggcggtgagtgagaccaccacccctccaa 7240
|||||
Qy 504 GGCCTGGAGGCAGATAGCAGCCCGCTCAAGGGGAGTGGAGACCAACACACCTCCAA 563
|||||
Db 7241 aaaaagcaacaagaatcacgctgcccagcagctatctgagcctgacgctgagcagtgaa 7300
|||||
Qy 564 ACAGGCAACACAGTACGGCGGCAGAGCTACTGTAGCCCTGACGAGTGGAA 623
|||||
Db 7301 gtccacagaagctacagctgccaggtcacgcatgaaggagaccgctggaagacagt 7360
|||||
Qy 624 GTCCACAGAAAGCTACAGTCCAGGTCCAGGTACGCATGAAGGGAGCCGCTGGAGACAGT 683
|||||
Db 7361 ggcctcacagaatgttcat 7380
|||||
Qy 684 GGCCTTACAGATGTTTAT 703

RESULT 7
ID Q22491 standard; DNA; 9071 BP.
AC Q22491;
DT 31-JUL-1992 (first entry)
DE Human U266 lambda gene.
KW Human myeloma U266 cell line; rearranged lambda gene; Ig;
KW immunoglobulin light chain; pTAR-7; heavy chain enhancer;
KW humoral immunity; transgenic mouse; ATCC No. 72003; ds.
OS Chimeric Homo sapiens.
PN W09204440-A.
PD 19-MAR-1992.
PF 27-AUG-1991; 106124.
PR 29-AUG-1990; US-575005.
PA (HARD) HARVARD COLLEGE.
PI Vasicek TJ, Leder P;
DR WPI; 92-114348/14.
PT B cell deficient transgenic non-human animals - comprise DNA
PT encoding the U266 immunoglobulin light chain and an enhancer
PT region used as models of B cell deficiency
PS Disclosure; Fig 7; 41pp; English.
CC This sequence is the EcoRI/HindIII fragment of the rearranged lambda
CC gene isolated from human myeloma U266 cell line ligated to the mouse
CC heavy chain enhancer. The resulting transgene was used in the
CC production of transgenic mice in which the proportion of spleen cells
CC which are mature B cells is not more than a quarter of that in
CC wild-type animals. The animals are more susceptible to infectious
CC diseases than the wild-type and are models for severe B cell

CC deficiency. See also Q22489 for the transgene sequence.
SQ Sequence 9071 BP; 2196 A; 2395 C; 2321 G; 2159 T;
Query Match 45.1%; Score 318; DB 3; Length 9071;
Best Local Similarity 99.7%; Pred. No. 3,05e-193;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 7061 aggtcagcccaagctgccccctcgctcactctgttcccgccctctctgagagcttca 7120
QY 384 AGGTGAGCCCAAGCTGCCCCCTCGGCTCACTCTGTTCCCGCCCTCTCTCAGGAGTTCA 443
Db 7121 agcccaagcccaactggtgtgtctcataagtgaacttctaccgggagccgtgacagt 7180
QY 444 AGCCACAAGGCCACACTGGTGTCTCTAAGTGACTTCTACCCGGGAGCGCTGACAGT 503
Db 7181 ggccctggaagcagatagacccccctcaagcgggagtgagaccaccaccctccaa 7240
QY 504 GGCTTGGAGGACAGATAGACGCCCTCGAAGCGGAGTGGAGACACACACCTCCAA 563
Db 7241 acaagcaacaacaagtacgcggccagcagctatctgagcctgacgctgagcagtggaa 7300
QY 564 ACAAGCAACAACAAGTACGCGGCCAGCGCTACCTTGAGCCCTTGACGCTGACAGTGGAA 623
Db 7301 gtcccaagaagctacagctccagctcacgcagatgaagggagcaccctggaagacagt 7360
QY 624 GTCCACAGAAGCTACAGCTCCAGCTCAGCGCATGAAGGGAGCAGCGTGGAGAGACGT 683
Db 7361 ggccctacagaatgttcat 7380
QY 684 GGCCCTACAGCAATGTTCAAT 703

RESULT 8

ID Q35904 standard; DNA; 387 BP.
AC Q35904;
DT 08-JUN-1993 (first entry)
DE Anti-CD4 V-lambda coding sequence.
KW PCR; amplify; clone; heavy; light; chain; variable; region; lambda;
KW immortalised B-cell; vector; TCAE 6; human; IgG1; constant; antigen;
KW recombinant; antibody; chimpanzee; Ig; Ag; old world monkey; eczema;
KW immunoglobulin; therapeutic; rheumatoid arthritis; ss.
OS Simian sp.
PN W09302108-A.
PD 04-FEB-1993.
PF 24-JUL-1992; U06194.
PR 25-JUL-1991; US-735064.
PR 23-MAR-1992; US-856281.
PA (IDEC-) IDEC PHARM CORP.
PI Hanna N, Newman RA, Raab RW;
DR WPI; 93-058729/07.
DR P-PSDB; R31949.
PT Recombinant antibodies including Old World monkey portion and
PT human portion - used for treatment of auto-immune diseases,
PT infectious diseases, AIDS, tumours, diabetes, proliferative
PT diseases, intestinal inflammations and allergies, etc.
PS Disclosure; Page 54; 92pp; English.
CC The sequences given in Q35903-04 encode the Simian anti CD4 VH and
CC V-lambda sequences respectively. These sequences were derived using
CC the primer sequences given in Q35901-02. The amplification products
CC were sequentially cloned into the vector TCAE 6, which contains human
CC IgG1 and human lambda constant regions. The amplified sequences could
CC be used in the production of a recombinant antibody, comprising a
CC human, chimpanzee or old world monkey immunoglobulin (Ig) constant
CC region and an antigen (Ag) binding portion of an old world monkey Ig

CC variable region, where the old world monkeys may be the same or
CC different. The recombinant antibody may be used as a therapeutic
CC agent for the treatment of rheumatoid arthritis, eczema and
CC immunological disorders.
SQ Sequence 387 BP; 70 A; 117 C; 120 G; 80 T;
Query Match 35.5%; Score 250; DB 6; Length 387;
Best Local Similarity 88.3%; Pred. No. 8,24e-147;
Matches 288; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
Db 62 cctatagtgtaagtccagctcgctcagctcgctgctcccgagcagacgagccgggtca 121
QY 62 CCTATGACCTGACTCAGCCACCCTCGGCTGCTCAGTCTCCCCAGGACACGCGCCAGGATCA 121
Db 122 cctgtggggagacaactgtggaaggaagtgtacagtggtaccagcagaagccaccgc 181
QY 122 CCTGTGGGGAGACAACAGTAGAAAATGAATATGTCACCTGGTACCAGCAAGACCGCGC 181
Db 182 aggcctcgtgtgctcatctatctgtgacagcagaagccctcagggatccctgcgcgt 241
QY 182 GGGCCCTATACTGCTCATCTATCATGATGATGACCGGCCCTCAGGATCCCTGAGCGCAT 241
Db 242 tctctggttccaaactcagggacaacccgcccacccctgaccatcagcggggtcgaggccgggg 301
QY 242 TCTCTGGCTCCAAATCAGGGAAACACCCGCCCTGACCATCAACGGGGTCGAGGCCGGGG 301
Db 302 atgagcctgactattactgtcaggtgtgggacagtactgtcgtgactgattggtcttcggcg 361
QY 302 ATGAGCTGACTATTACTGTGAGGTGTGGGACAGGGGTAGTCAATCATCCGCTTTCGGAG 361
Db 362 gagggaccgctgacccctcctcaggt 387
QY 362 GAGGGACCGGGTCAGCCGTCTCTAGGT 387

RESULT 9

ID Q64054 standard; DNA; 374 BP.
AC Q64054;
DT 08-NOV-1994 (first entry)
DE Sequence of the VL region of monoclonal antibody PEI-1 against
DE hepatitis B virus surface antigen.
KW Hepatitis B virus; surface antigen; monoclonal antibody; therapy;
KW HBsAg; diagnosis; HBV; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 1..374
FT /*tag= a
PN W094111495-A.
PD 26-MAY-1994.
PF 06-NOV-1992; U09749.
PR 06-NOV-1992; WO-U09749.
PA (SANO) SANDOZ LTD.
PI Ostberg LG;
DR WPI; 94-183497/22.
DR P-PSDB; R54051.
PT Monoclonal antibodies active against Hepatitis B surface antigen
PT - for diagnosis and treatment of Hepatitis B virus
PS Example; Page 40; 53pp; English.
CC Human volunteers were immunised with hepatitis B vaccine. MD3-4, ZMI-
CC 2, ZMI-1 and PEI-1 hybridoma cell lines were derived from
CC lymphocytes of individuals immunised with Heptavax (Merck & Co).
CC Antibodies PEI-1, ZMI-1, ZMI-2 and MD3-4 belong to the IgG1 clas.
CC The cell lines producing PEI-1, ZMI-1 and ZMI-2 were deposited as
CC ATCC HB9234, 9191 and 9192 respectively. The cell lines all behave

CC as typical (mouse x human) x human hybridomas and produce their
 CC respective Abs in concs. ranging up to 25 mg/l in standard
 CC suspension culture. The heavy variable (VH) and light variable (LH)
 CC chains of Abs P21-1, ZM1-1, ZM1-2 and MD3-4 were isolated and
 CC sequenced. Total RNA was extracted from 10(7) hybridoma cells
 CC of each cell line. ss DNA was synthesized using AMV-reverse
 CC transcriptase and oligo-dT as primer. PCRs were performed and
 CC amplified DNA was size selected. ss DNA for sequencing was isolated
 CC from each positive clone after superinfection with M13K07.
 CC Sequencing was by the dideoxy chain termination method (Sanger
 CC et al.). The codon 'AAR' in Q64053 was printed in the spec. as
 CC 'AA', but since the encoded AA was Lys, 'R' was inserted as the
 CC final nucleotide.

CC Sequence 324 BP; 71 A; 86 C; 103 G; 64 T;

Query Match 31.9%; Score 225; DB 10; Length 324;
 Best Local Similarity 85.7%; Pred. No. 7.77e-130;
 Matches 270; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 10 ctgacgcagccgcctcggtgtcagtggtgccccagggcagcagccaggtatctctgtggg 69
 QY 70 CTGACTCAGCCACCCTCGGTGTGAGTGTCCCGCAGGACAGAGCCGACCTGTGGG 129
 Db 70 ggagcaacattggagtaaaagtgtgaactggttcacagcaagcagccagccct 129
 QY 130 GGAGACACAGTAGAATAATATATGTCACCTGTGTACAGCAGACCCGCGGCCCT 189
 Db 130 gtcttggtgtctatgatgataacgaagccctcaggcattcttgagcgtattctgtggc 189
 QY 190 ATACTGGTCTATCATGATCATAGTACCGCGCCCTCAGGATCCCTGAGCGATCTCTGGC 249
 Db 190 tccaactctgggaacacgcccaccctgaccatcagcaggttcgaagccgggtgagcc 249
 QY 250 TCCAAATCAGGAACACGCCACCTGACCATCAACGGGGTCGAGCGCGGGGATGAGGCT 309
 Db 250 gactattactcaggtgtggatagtagtagtgcattgtggtattcggcgagggacc 309
 QY 310 GACTATTACTGTGAGGTGCGGACAGGGCTAGTCATCATCGGCTTCGGAGGAGGACC 369
 Db 310 aagtcgacctccta 324
 QY 370 CGGGTGACCGTCTCTA 384

RESULT 10

ID Q11187 standard; cDNA to mRNA; 318 BP.
 AC Q11187;
 DT 31-MAY-1991 (first entry)
 DE Immunoglobulin lambda chain constant region.
 KW Antibody; canine distemper virus; parvovirus; hepatitis; ss.
 OS Canis familiaris.
 PN EP-419858-A.
 PD 03-APR-1991.
 PF 24-AUG-1990; 116258.
 PR 25-AUG-1989; JP-219889.
 PR 30-SEP-1989; JP-255425.
 PR 07-JUN-1990; JP-150673.
 PA (KAGA) CHERO-SERO-THERAP.
 PI Maeda H, Eda Y, Kimachi K, Ono Y, Tokiyoshi S;
 DR WPI; 91-09533/14.
 DR P-PSDB; R11366.
 PT Gene fragments coding for constant region of canine
 PT immunoglobulin(s) - used to produce mouse-dog antibodies for
 PT diagnosis, treatment and prevention of canine.

PS Claim 6; Page 15; 49pp; English.
 CC The DNA encodes the constant region of canine Ig lambda chain. It can
 CC be used to produce mouse-dog chimeric antibodies for the diagnosis,
 CC treatment and prevention of canine diseases caused by e.g. canine
 CC distemper virus, canine parvovirus and canine hepatitis virus.
 CC See also Q11188-91.

CC Sequence 318 BP; 69 A; 115 C; 91 G; 43 T;

Query Match 31.8%; Score 224; DB 2; Length 318;
 Best Local Similarity 85.7%; Pred. No. 3.70e-129;
 Matches 269; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 1 cagcccaagcctccccctcggtcacactctcccgccctctctcaggtgctcgccgc 60
 QY 388 CAGCCCAAGGCTGCCCTCGGTCTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCC 447
 Db 61 aacaagccacccctggtgctctcatcagcagcttctaccacagcgcgtgacgtggcc 120
 QY 448 AACAAAGCCACACTGGTGTCTCTAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCC 507
 Db 121 tgaaggaagcagcagcccgctcaccacagggcgtggagaccacacagccctccaagcag 180
 QY 508 TGAAGCGCATAGCAGCCCGCTCAAGGGGGAGTGGAGACCCACACCCCTCCAAACAA 567
 Db 181 agcaacaacaagtacgcggcagcagctactcagcgtgacgtgacgtgacgtgacgtgac 240
 QY 568 AGCAACAACAGTAGTACGGCCGAGCAGCTACTGAGCTGACCCCTGAGCAGTGGAGTCC 627
 Db 241 cacagcagcttcagctgctcagcagcagggagcagccgtggagagaaggtggcc 300
 QY 628 CACAGAAGCTACAGCTGCCAGGTCAACGATGAGGAGGACCCGCTGGAGAGACAGTGGCC 687
 Db 301 ccgcagcagtgctc 314
 QY 688 CCTACAGAAATGTTT 701

RESULT 11

ID Q11946 standard; DNA; 333 BP.
 AC Q11946;
 DT 15-AUG-1991 (first entry)
 DE Anti-human RHD PAG-1 MAB (VL chain).
 KW Monoclonal antibody; rhesus D; blood-typing; CDR;
 KW haemolytic disease of the newborn; HDN; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc_feature 67..99
 FT /*tag= a
 FT /label= CDR1
 FT misc_feature 145..165
 FT /*tag= b
 FT /label= CDR2
 FT misc_feature 262..300
 FT /*tag= c
 FT /label= CDR3
 PN W09107492-A.
 PD 30-MAY-1991.
 PF 13-NOV-1990; GB-025590.
 PR 13-NOV-1989; GB-025590.
 PA (BLOO-) CENT BLOOD LAB AUTH.
 PI Hughes- Jones N;
 DR WPI; 91-178104/24.
 DR P-PSDB; R12264.
 PT DNA encoding complementary determining regions - of human

PT	anti-rhesus D antibodies, useful in prodn. of monoclonal			
PT	antibodies and for passive immunisation			
PS	Disclosure; Fig 3; 32pp; English.			
CC	The DNA sequence of eleven monoclonal antibodies are			
CC	represented in Q119145-57. Synthetic genes, for both heavy and			
CC	light chains may be created by combining selected CDR 1, 2, and 3			
CC	regions, which may be selected from different antibody mols. having			
CC	varied binding specificity. The chimaeric anti-RhD antibodies can be			
CC	used for diagnosis and therapy, and are capable of providing blood-			
CC	typing reagents of high specificity and reliability. They can also			
CC	be used in passive immunisation to prevent haemolytic disease of the			
CC	newborn.			
SO	Sequence	333 BP;	67 A;	93 C; 108 G; 65 T;

Query Match 31.3%; Score 221; DB 2; Length 333;
Best Local Similarity 88.0%; Pred. No. 3.98e-127;
Matches 256; Conservative 0; Mismatches 35; Indels 0; Gaps

2	cctatgtgctga	cagccacccctcg	gtcagtggtgcccagacagcagccaggatta	61
62	cctatcaactg	actcagccacccctcg	gtgtcagtggtcccgacagcagccaggatca	121
62	cctgtgtgggg	gaacaacattgg	acgtataaagtgtgcactggtaccagcagaagccaggcc	121
122	cctgtgtgggg	gagacaacactaga	ataatgcttccactggtaccgacagacccagccg	181
122	aggccctgtg	ctgtctctatggt	gtcagcagccggccctcagggaatccttgagcat	181
182	ggcgccctt	atctactgtcatct	atgcatgtagcagccgcccctcagggaatccttgagcat	241
182	tctctggct	ccaactctggg	aaacagccaccctgaacctcagcagaggtcgagccgggg	241
242	tctctggct	ccaaatcag	ggagacaccgccacctgcacatcaacgggtgcagccgggg	301
242	atgagccagc	actatcactg	caggtgtgggatagtatgactgctcatcagg	292
302	atcagcctg	catctatctcag	gtgtggcagcagggctagtcatctccgg	352

RESULT	12	
ID	Q10674	standard; DNA; 318 BP.
AC	Q10674;	
DT	24-MAY-1991	(first entry)
DE	Feline immunoglobulin lambda chain constant region TI-62 gene.	
KW	Feline immunoglobulin; fIg; lambda chain; chimaera; antibody; ss.	
OS	Felis catus.	
PN	EP-417486-A.	
PD	20-MAR-1991.	
PF	10-AUG-1990; 115426.	
PR	10-AUG-1989; JP-208822.	
PR	30-SEP-1989; JP-255424.	
PR	28-DEC-1989; JP-344465.	
PT	(KAGA) CHEMA-SERO-THERAPEU.	
PI	Maeda H, Eda Y, Kimachi K, Ono Y, Tokiyoshi S;	
DR	WPI; 91-081793/12.	
DR	P-PSDB; R11012.	
PT	New DNA sequences encoding constant regions of feline	
PT	immunoglobulin - and new chimeric DNA expressing mouse-cat	
PT	antibodies, useful in prevention, treatment and diagnosis of	
PT	feline disease	
PS	Claim 7; Page 15; 35pp; English.	
CC	The cDNA library of cat-mouse heterohybridoma FM-T1 cells was used	
CC	to isolate the fIg gene.	
CC	The sequence is used to produce recombinant DNA encoding the L-chain	

CC of a mouse-cat chimaeric antibody having a mouse variable
CC region linked at its 3'-site to a feline constant region.
CC The antibody expressed by cells transformed with the recombinant
CC DNA is useful in diagnosis, treatment and prevention of feline
CC disease, without showing side effects.
CC See also Q10674-75 and Q10945-46.

Query Match 29.1%; Score 205; DB 2; Length 318;
Best Local Similarity 83.0%; Pred. No. 2.63e-116;
Matches 258; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

1	Db	1	cagcccaagtcggcccccctcaggtcaacactcttccacacctcagtcgaggagctcagcgca	60
388	Qy	388	CAGCCCAAGGTCGCCCTCGGTCACTCTGTTCCGCCCTCTCTGAGGAGCTTCAAGCC	447
61	Db	61	aacaagccaccctggtgtctctgtcagtgactcttaccaccagcggctgacggtggcc	120
448	Qy	448	AACAAGGCCACACTGGTGTGTCTCATAACTGACTTCTACCGGGAGCCGTGACACTGGCC	507
121	Db	121	tggaaaggaaagtggcaccaccatcacaaagggcgtggagaccaccaagccctccagacag	180
508	Qy	508	TGAGGAGCATAGTAGAGCCCGCTCAAGCGGGAGTGGAGACACACACCTTCCAAACA	567
181	Db	181	agcaacacaagtacggcgccagcagctacctgagcgtgtcacqgaacagtggaatact	240
568	Qy	568	AGCAACAAGTACCGGCCGACAGCTTACTTGAGCCTGACCGCTGACAGTGGAAAGTCC	627
241	Db	241	cacagcatatcacctgccaggtcacgcacagagggagcactgtggagaagagtgtgttc	300
628	Qy	628	CACAGAAGCTACAGCTGCCGGTTCAGCGATGAAGGGACACCGCTGGAGACAGACTGGCC	687
301	Db	301	cctgcagagtg	311
688	Qy	688	CCTACAGAATG	698

RESULT	13	
ID	Q64170 standard; cDNA to mRNA; 318 BP.	
AC	Q64170;	
DC	29-DEC-1994 (first entry)	
DE	Sequence of feline herpes virus (FHV-1) cDNA.	
KW	Feline herpes virus; FHV-1; monoclonal antibody; ss.	
OS	Felis catus.	
Key	Location/Qualifiers	
FH	1..318	
FT	CDS	
FT	/*tag= a	
PN	W09412661-A.	
PD	09-JUN-1994.	
PF	25-NOV-1993; J01724.	
PP	28-NOV-1992; JP-S401255.	
PR	(KAGA) CHEMO SERO THERAPEUTIC RES INST.	
PI	Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;	
PI	WPI; 94-200288/74.	
DR	P-PSDB; R54096.	
PT	Feline monoclonal antibody and recombinant antibodies specific	
PT	for FHV-1 - for detection, treatment and prevention of FHV-1	
PT	infection.	
PS	Claim 20; Page 23-24; 53pp; Japanese.	
CC	The inventors claim a monoclonal antibody against feline herpes	
CC	virus (FHV-1), the sequence of which is given in Q64168, Q64169	
CC	and Q64170. They also claim a recombinant antibody against FHV-1	
CC	and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are	
CC	used in the detection, treatment and prevention of FHV-1. The	

CC sequences of the CDRs in the VH of the recombinant anti-FHV-1
CC antibody are given in R54092. The sequences of the CDRs in the VL of
CC the recombinant anti-FHV-1 antibody are given in R54093. These CDR
CC sequences are claimed.

Query Match	29.1%;	Score 205;	DB 11;	Length 318;
Best Local Similarity	83.0%;	Pred. No. 2,63e-116;		
Matches	258;	Conservative 0;	Mismatches 53;	Indels 0; Gaps 0;
Db	1	cagcccaagtgcggccctcgggtcacactcttcccacacctccagtgaggaagtcacgcga	60	
Qy	388	CAGCCCAAGGTGCCCTCGGTCACTCTGTTCGGCCCTCCCTCTCAGAGAGTTCAGGCC	447	
Db	61	aacaaggccacctgggtgtctcgtcagtgactctaccaccagcggctgacggtggcc	120	
Qy	448	AACAGGCCACACTGTTGTCTCTATATGATCTTACCCGGGAGCCCTGCACATGGGCC	507	
Db	121	tggaaagaaagtggccccccatcaccaaagggcgtggagaccaccacgaacctccagacag	180	
Qy	508	TGGAGGCAGATACGACGCCCGCTCAGCGCGGAGTGGAGACACACACCTCCAAACAA	567	
Db	181	agcaacaagaatagcggccagcagctacctgagcctgtcaccgaacagatggaatct	240	
Qy	568	AGCAACAAGTACGCGGCCAGCAGTCACTTGACGCTGACGCTCAGCAGTGGAAAGTCC	627	
Db	241	cacagcagatcacactgccaggtcacgcacgaggggagacactgtggagaagagtgtgtc	300	
Qy	628	CACAAGCTTACAGCTCCGAGTCCAGCTCAGCCATGAAGGAGACACCTGTGACAGACATGGCC	687	

Db 301 cctgcagagtg 311
||| ||| ||
Qv 688 CCTACAGAATG 698

RESULT	14	
AD	Q33036 standard; cDNA; 324 BP.	
IC	Q33036;	
DT	06-MAY-1993 (first entry)	
DE	MAB 1-3-1 variable region of heavy chain.	
KW	Monoclonal antibody; hybridoma; PCR; variable region;	
KW	constant region; heavy chain; light chain; ss.	
OS	Synthetic.	
PN	EP-520499-A.	
PD	30-DEC-1992.	
PF	26-JUN-1992; 110841.	
PR	28-JUN-1991; JP-158859.	
PR	28-JUN-1991; JP-158860.	
PR	28-JUN-1991; JP-158861.	
PA	(MITU) MITSUBISHI KASEI CORP.	
PI	Hirakawa Y, Hosokawa S, Ito N, Nagaike K, Tagawa T;	
WPI	93-001328/01.	
DR	P-PSDB; R30146.	
PT	Human monoclonal antibody specific for a cancer cell	
PT	surface antigen - prep'd. from a hybridoma obtd. by cell	
PT	fusion of myeloma cells derived from cancer patient	
PT	myeloma cells	
PS	Claim 17; Page 31 + 18; 37pp; English.	
CC	A human Mab specifically binding to a surface antigen	
CC	cell membrane comprises variable regions of the heavy	
CC	chains having the amino acid sequences of R30145-46 r	
CC	encoded by DNA sequences Q33035-36 respectively.	
SC	Sequence 324 BP; 82 A; 84 C; 93 G; 65 T	

Query Match	25.8%;	Score 182;	DB 5;	Length 324;
Best local Similarity	78.1%;	Pred. No. 8.15e-101;		
Matches	253;	Conservative 0;	Mismatches 71;	Indels 0; Gaps 0;
Db	1	tatgagctgacacagcaccctcggtgtcagtgctccacgacagacgcccaggtacc	60	
Qy	64	TATGAACTGACTAGCACCCTCGGTGTGCTGCTCCGACGACACAGGCCACGATCACC	123	
Db	61	tgctctggagatgattgcaaaagcaatatgcttattgtttaccacagaaagccagccag	120	
Qy	124	TGTGGGGGAGACAACAGTAGAANAATATGTCCATGTGGTACGACAGACGCGCGG	183	
Db	121	gccccctgctgctggtgatatatatagacagtgagagccctcaaggatccctgagcgattc	180	
Qy	184	GCCCTTACTAGTGGTCATCTATGATGATAGTAGCGGCCCTCAGGGATCCCTGAGCGATT	243	
Db	181	tctggctccagctcaggggacaacagctcacgttgaccatcagtggtcagcgacgaagac	240	
Qy	244	TC7GGGCTCCNAATCAGGGACACGCCACCCCTGCACATCAACGGGGTCAGCGCGGGGAT	303	
Db	241	gaggctgactattactgtcaatcagcagcagcagctggtacttatgagttatcgcgga	300	
Qy	304	GAGGCTGACTATTACTGTCCAGGTGTGGGACAGGGCTAGTGATCATCCGCTCTTCGAGGA	363	
Db	301	gggaccaagctgacctctcaggt	324	
Qy	364	GGACCCGGGTGACCGCTCTAGGT	387	

RESULT 15
ID N80473 standard; DNA; 701 BP.
AC N80473;
DT 07-DEC-1990 (first entry)
DE Insert of clone pZ183-1.
KW Pre-B cells; non-T acute lymphoblast leukaemia; ss;
PN EP-269127-A.

01-JUN-1988.
 PF 27-NOV-1987; 117619.
 PR 27-NOV-1986; GB-028433.
 PR 14-JUL-1987; GB-016497.
 PR 14-OCT-1987; GB-024100.
 PA (HOFF) HOFFMANN-LA ROCHE AG.
 PI Bauer SB, Kudo A, Melchers GF, Sakaguchi N;
 DI WPI; 88-148947/22.
 PT Nucleotide sequence selectively expressed in pre-B cells - used
 PT in probes for determining non-T acute lymphoblast leukaemia and
 PT for prepn. of polypeptide(s)
 PS Disclosure; p; English.
 CC This is the 0.7 kb insert of transcript pZ 183 which is select-
 CC ively expressed in all pre-B cell lines. Bases 240-554 show a
 CC strong homology to the constant (C) region of lambda-1 light (L)
 CC chains. A strong homology is also seen between posns 201-239 and
 CC the joining (J) segment sequence of the lambda-1 L-chain.
 CC See also N80470-72, N80474-77 and N82411-42.
 SQ Sequence 701 BP; 163 A; 188 G; 165 G; 185 T;

Query Match 25.7%; Score 181; DB 1; Length 701;
 Best Local Similarity 77.2%; Pred. No. 3.82e-100;
 Matches 271; Conservative 0; Mismatches 78; Indels 2; Gaps 2;

Db 202 gtcttgggtggtggagccagctcacaaatctaggtcagcccaagtctgacccttggtc 261
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 352 gtcttcgagagagaccggtgacgcgtctctaggtcagcccgagccggtcgccctcggtc 411

ID H5777270 standard; RNA; EST; 570 BP.
 *AC N32777;
 DT 13-JAN-1996 (Rel. 46, Created)
 DT 13-JAN-1996 (Rel. 46, Last updated, Version 1)
 DE yw91f04.s1 Homo sapiens cDNA clone 259615 3' similar to gb:X57809
 DE IG LAMBDA CHAIN C REGIONS (HUMAN);.
 KW EST.
 OS Homo sapiens (human)
 OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.
 RN [1]
 RP 1-570
 RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
 RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
 RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
 RA Trevasakis E., Waterston R., Williamson A., Wohlmann P., Wilson R.;
 RT *The WashU-Merck EST Project*;
 RL Unpublished.
 CC Contact: Wilson RK WashU-Merck EST Project Washington University
 CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
 CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
 CC est@wustl.edu High quality sequence stops: 356 Source: IMAGE
 CC Consortium, LINL This clone is available royalty-free through LINL
 CC ; contact the IMAGE Consortium (info@image.llnl.gov) for further
 CC information. NCBI gi: 1153176
 FH Key Location/Qualifiers
 FH source 1..570
 FT /organism="Homo sapiens"
 FT /clone="259615"
 FT /note="human"
 FT mRNA
 FT <1..>570
 SQ Sequence 570 BP; 103 A; 140 C; 180 G; 145 T; 2 other;
 Query Match 45.2%; Score 319; DB 136; Length 570;
 Best Local Similarity 96.4%; Pred. No. 0.00e+00;
 Matches 345; Conservative 0; Mismatches 10; Indels 3; Gaps 3;
 Db 141 atgaacattctgtaggccactgtctctccacggtgctcccttcacgtgacctggc 200
 Cp 703 ATGACATTCTGTAGGGGCCACTGTCTTCCACGGTCTCCCTTCATGCGTGACCTGGC 644
 Db 201 agctgaacctctgtggagctccactgtcaggctcaggctcaggctgctggccg 260
 Cp 643 AGCTGTAGCTTCTGTGGGACTTCCACTGCTCAGGCTCAGGCTCAGTGTGCTGGCG 584
 Db 261 cgtacttgctgtgctgtgtgttgagggtgtgtgtgtccactcccgcttgacgggc 320
 Cp 583 CSTACTTGTCTGCTTTGTTGGAGGGTGTGTGTCTCCACTCCGGCTTGACGGGGC 524
 Db 321 tgcattctgcttccagnc-actgtcacggtcccggttagaagtcacttatgagacaca 379
 Cp 523 TGTATCTGCTTCCAGGCGACTGTACGGTCCCGGTAGAGTCACTTATGACACACA 464
 Db 380 ccagtgtgcttctgttggcttgaactcctcagagagggcggaacagagtgcaggagg 439
 Cp 463 CCAGTGTGGCTTGTGTGCTTGAAGTCTCTCAGAGAGGGGGGGAACAGAGTGACCGAG 404
 Db 440 gggcanccttgggtgactttagcagggtcaacttggctccctccgcgaacatcaga 497
 Cp 403 GGCACGCTTGGGCTGA3CT-AGGACGG-TCACCGGGTCCCTCTCCGAAGACCGGA 348

RESULT 2

LOCUS N32777 570 bp mRNA EST 10-JAN-1996
 DEFINITION yw91f04.s1 Homo sapiens cDNA clone 259615 3' similar to gb:X57809
 IG LAMBDA CHAIN C REGIONS (HUMAN);.
 ACCESSION N32777
 NID g1153176
 KEYWORDS EST.
 SOURCE human clones=259615 primer=m13 -40 forward library=Soares placenta
 8to9weeks 2NbpP8to9M vector=pT7f3D (Pharmacia) with a modified
 polylinker host=DHI0B (ampicillin resistant) Rsite1=Not I
 Rsite2=Eco RI two placentae: one from 8 weeks and another from 9
 weeks post conception. 1st strand cDNA was primed with a Not I -
 oligo(dT) primer
 [5'-TGTTACCAATCTCAAGTGGGAGCGCGCGATTTTTTTTTTTTTTTT-3'],
 double-stranded cDNA was size selected, ligated to Eco RI adapters
 (Pharmacia), digested with Not I and cloned into the Not I and Eco
 RI sites of a modified pT7f3 vector (Pharmacia). Library
 constructed by Bento Soares and M. Fatima Bonaldo.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 570)
 AUTHORS Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
 Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
 Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
 Trevasakis E., Waterston R., Williamson A., Wohlmann P. and
 Wilson R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT
 Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 High quality sequence stops: 356
 Source: IMAGE Consortium, LINL
 This clone is available royalty-free through LINL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 FEATURES
 source
 NCBI gi: 1153176 Location/Qualifiers
 1..570
 /organism="Homo sapiens"
 /clone="259615"
 /note="human"
 mRNA
 103 a 140 c 180 g 145 t 2 others
 ORIGIN
 Query Match 45.2%; Score 319; DB 116; Length 570;
 Best Local Similarity 96.4%; Pred. No. 0.00e+00;
 Matches 345; Conservative 0; Mismatches 10; Indels 3; Gaps 3;
 Db 141 atgaacattctgtaggccactgtctctccacggtgctcccttcacgtgacctggc 200
 Cp 703 ATGACATTCTGTAGGGGCCACTGTCTTCCACGGTCTCCCTTCATGCGTGACCTGGC 644
 Db 201 agctgaacctctgtggagctccactgtcaggctcaggctcaggctgctggccg 260
 Cp 643 AGCTGTAGCTTCTGTGGGACTTCCACTGCTCAGGCTCAGGCTCAGTGTGCTGGCG 584

Db	261	cgtacttgctgctgtctgtttggaaggtgtggtggtcctcaactccgccttgacggggc	320
Cp	583	CGTACTTGTCTGCTTCTTTGAGGGTGTGGTGGCTCTCCACTCCCGCTTGACGGGCG	524
Db	321	tgtatctgacctccagnc-actgtcacggctccgggtgaaagtcaattatgagacaa	379
Cp	523	TGCTATCTGCTGCTTCAGAGCCACTGTCCGGCTCCCGGTGAAAGTCACTTATGAGACACA	464
Db	380	ccagtggtgacctgttgcttgaacctctcagagggcgagggaacagagtaccgagg	439
Cp	463	CCAGTGTGGCCTTTGCTTGAAGCTCTCTCAGAGAGGGCGGGAACAGACTGACCGAGG	404
Db	440	gggcanccttgggtgaccttagcaggggtcaacttggtccctccgcgaacatcaga	497
Cp	403	GGGCAGCTTGGGCTGACCT-AGGACGG-TCACCGGGTCCCTCTCGAAGACCGGA	348
RESULT	3		
LOCUS	R73382	469 bp	mRNA
DEFINITION	vJ92all.s1 Homo sapiens cDNA clone 156188 3' similar to gb:X57809		EST 02-JUN-1995
	IG LAMBDA CHAIN C REGIONS (HUMAN);		
ACCESSION	R73382		
NID	q847414		
KEYWORDS	EST.		
SOURCE	human clone=156188 library=Soares breast 2NblBst vector=p7T73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=Promega -2lm13 Rsite1=Not I Rsite2=Eco RI Adult female. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACCAATCTGAAGTCGGAGCGCGCCCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p7T73 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento Soares and M.Fatima Bonaldo.		
ORGANISM	Homo sapiens Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 469)		
REFERENCE			
AUTHORS	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaske, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.		
TITLE	The Washo-Merck EST Project		
JOURNAL	Unpublished (1995)		
COMMENT	Contact: Wilson RK Washo-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu High quality sequence steps: 265 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.		
FEATURES	NCBI gi: 847414		
source	Location/Qualifiers 1..469		

BASE COUNT		81 a		115 c		150 g		117 t		6 others		
ORIGIN												
<p>Query Match 42.4%; Score 299; DB 66; Length 469; Best Local Similarity 93.1%; Pred. No. 0.00e+00; Matches 323; Conservative 0; Mismatches 23; Indels 1; Gaps 1;</p>												
Db	120	atgaacattctgagggccactgtctctccacggtgtcccttcacatgcgtgacctggc	179									
Cp	703	ATGAACATTCTGATGGGCCACTGTCTCTCCACAGGTCTCCCTTCATGCGTCACTGGC	644									
Db	180	agctgtagcttttgggacctccactgctcaggcgtcaggctcaggtagctgctggccg	239									
Cp	643	AGCTGTAGCTTTGTGGACATTCCACTGCTCAGGCGTCAGGTCAGGTAGCTGTGGCGC	584									
Db	240	cgtactgttgcttctgtttggagggtggtggtctccactccgcttcacgagggc	299									
Cp	583	CGTACTGTGTGTTGTTTGTGGAGGCTGTGGTCTCCACTCCGCCCTTGACGGGGC	524									
Db	300	tgtatctgccttcagggaactgtcacggtcccggttagaagtcacttatgagacac	359									
Cp	523	TGCTATCTGCCTTCACGGCCA-CTGTACCGGCTCCGGGTAGAAGTCACATTATGACAC	465									
Db	360	accagtggccttggcttgaagctctccanaggaggtnggaacaaataaacmag	419									
Cp	464	ACCAAGTGTGGCCTTTGTGGCTTGAAGCTCTCAGAGGAGGGGGGACACAGATGACCGAG	405									
Db	420	ggggcaaccttgggttaacctaaaggacggttnaaccttggmctccgcc	466									
Cp	404	GGGGCAGCCTTGGCGTCACTAGGACGGTCACCGGGTCCCTCTCTCC	358									
RESULT	4											
LOCUS	R73492	471 bp	mRNA	EST	02-JUN-1995							
DEFINITION	v-j93d09.s1 Homo sapiens cDNA clone 156305 3' similar to gb:X57809 IG LAMBDA CHAIN C REGIONS (HUMAN);											
ACCESSION	R73492											
NUM	9847524											
KEYWORDS	EST.											
SOURCE	human clone=156305 library=Soares breast 2NbHBst vector=p7T73D (Pharmacla) with a modified polylinker host=DH10B (ampicillin resistant) primer=Promega -21m13 Reitel=Not I Rsite2=Eco RI Adult female. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' GTTACCACTTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTT 3', double-stranded cDNA was ligated to Eco RI adaptors (Pharmacla), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacla). Library went through one round of normalization to a Cot = 230. Library constructed by Bento Soares and M.Fatima Bonaldo.											
ORGANISM	Homo sapiens											
Eukaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Deuterostomia; Chordata; Tetrapoda; Amniota; Mammalia; Theria; Sarcoterygii; Chonata; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 471)												
REFERENCE	Hillier,L., Clark,N., Duboue,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaks,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.											
AUTHORS	The WashU-Merck EST Project											
TITLE												

Db 440 gggcagccttnggttaacnagga 463
|||||
Cp 403 GGGCAGCCTTGGCGTGACCTAGGA 380

6	RESULT	H26070	376 bp	mRNA	EST	10-JUL-1995
	LOCUS	y152h1.r1	Homo sapiens	cDNA clone 161925	5'	similar to gb:X57809
	DEFINITION	IG LAMEDA CHAIN C REGIONS (HUMAN);.				
	ACCESSION	H26070				
	NID	g895193				
	KEYWORDS	EST.				
	SOURCE	human clone=161925 library=Soares breast 3NBHst vector=pt7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13Rev Rsite1=Not I Rsite2=Eco RI Adulr human. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAGTGGGAGCGGCCCTTTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo.				

ORGANISM Homo sapiens
and other tetrapod Donaco.

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcropterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 376)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, C., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

The WashU-Merck EST Project
Unpublished (1995)

TITLE
JOURNAL

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 257
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

[illegible]

Db	71	gnoactctgttcccgccctcctctgaggagcttcaagccaagaagccacactggtgtg	130
Qy	410	-TCACTCTGTTCCGCGCCTCTCTGAGGAGCTTCAAGCAACAAGGCCACACTGGTGCT	468
Db	131	ctcataagtgacttctacccgggagccgtgacagtgcctgggaagcagcatagtcagc	190
Qy	469	CTCATAAGTGACTTCTCCCGGAGCCGTGCAGCTGGCTGG-AAGCGAG-ATAG-CAGC	525
Db	191	cnngtcaagntcgggagtnagaccacacaccctccataaagaacaacaagtaagc	250
Qy	526	CCGCTCAAGG-CGGGAGTGGAGACCACACACCCCTCAACAACAAAGCAACAGTACGC	584
Db	251	ggccagcagctatctgagctgagcctgagcgtggaagtcaccacagaagctncagctg	310
Qy	585	GGCCAGCAGCTACCTGAGCTGACGCTGACGAGTGGAAGTCCCCACAGAGCTACAGCTG	644
Db	311	ccaggtncagcatgaaggagaccgctggagaagacatngccctncagaatntt	366
Qy	645	CCAGTTCACGCATGAAGGGAGACCTGGAGAACAGACTGGCCCTTACAGAAGTGT	700

7
RESULT
LOCUS R55314 436 bp mRNA EST 22-MAY-1995
DEFINITION yj7tho5.sl Homo sapiens cDNA clone 154809 3', similar to gb:X57809 IG LAMBDA CHAIN C REGIONS (HUMAN);.
ACCESSION R55314
NID g824609
KEYWORDS EST.
SOURCE human clone=154809 library=Soares breast 2NBHst vector=pTT73D (Pharmacia) with a modified polylinker host=DHI0B (ampicillin resistant) primer=Promega -2lm13 Rsitel!=Not I Rsite2=Eco RI Adult female. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACAATCTGAAGCGGCGGCCGGCCCCCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization at a Cot = 230. Library constructed by Bento Soares and M.Fatima Bonaldo

ORGANISM

Homio sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcoteriygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archontes; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 436)

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubouche, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, I., Soares, M., Tan, F., Treaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 361
Source: IMAGE Consortium, LMLL

This clone is available royalty-free through LMLL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 824609

Location/Qualifiers

1..436

/organism="Homo sapiens"

/clone="154809"

/note="human"

BASE COUNT 74 a 101 c 142 g 111 t 8 others

ORIGIN

Query Match

41.1%; Score 290; DB 61; Length 436;

Best Local Similarity 97.0%; Pred. No. 0.00e+00;

Matches 292; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 136 atgaacattctgtagggccactgtcttccacaggtgctcccttcattgacgtgacctggc 195

|||||

Cp 703 ATGAACATTCTGTAGGGCCACTGTCTTCTCCACGGTGTCCCTTCATCGCTGACCTGGC 644

|||||

Db 196 agctgagcttttgggaacttccactgctcaggcgtcaggctcaggtagctgctggccg 255

|||||

Cp 643 AGCTGAGCTTCTGTGGCACTTCCACTGCTCAGCGCTCAGGCTCAGTAGCTGTGGCG 584

|||||

Db 256 cgtactgtgtgttctgtttggagggtgtggtgtctccantcccgccttgacgggc 315

|||||

Cp 583 CGTACTGTGTGTGTGTGGAGGGTGTGGTGTCTCCACTCCCGCTTGACGGGC 524

|||||

Db 316 tgcctatcgtctcagncactcactcagntcccggttagaagtcacttatgagacaca 375

|||||

Cp 523 TGCTATCTGCTTCCAGGCCACTGTCCAGGCTCCCGGTGAGAGTCACTTATGAGACACA 464

|||||

Db 376 ccagtggtgcttctgttgaagctcctcagagangtnggacagatnaccgagg 435

|||||

Cp 463 CCAGTGTGGCTTGTGGCTTGAAGCTCTCAGAGGAGGGGGACAGTGCACCGAGG 404

|||||

Db 436 g 436

Cp 403 G 403

RESULT 8

LOCUS

DEFINITION

ACCESSION

NID

KEYWORDS

SOURCE

R83196 491 bp mRNA EST 04-AUG-1995

yp87h10.s1 Homo sapiens cDNA clone 194467 3' similar to gb:X57809

IG LAMBDA CHAIN C REGIONS (HUMAN);

R83196

g928073

EST.

human clone=194467 library=Soares fetal liver spleen INFILS

vector=pT73D (Pharmacia) with a modified polylinker host=DH10B

(ampicillin resistant) primer=Promega -21ml3 Reitel=Pac I

Rs1te2=Eco RI Liver and spleen from a 20 week-post conception male

fetus. 1st strand cDNA was primed with a Pac I - oligo (dT) primer

[5' RACTGGAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),

digested with Pac I and cloned into the Pac I and Eco RI sites of

the modified pT73 vector. Library went through one round of

normalization. Library constructed by Bento Soares and M.Fatima

Bonaldo.

Homo sapiens

ORGANISM

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Choeanata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 491)

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaakis, E., Waterston, R., Williamson, A., Mohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 229

Source: IMAGE Consortium, LIND

This clone is available royalty-free through LIND; contact the

IMAGE Consortium (info@image.lind.gov) for further information.

NCBI gi: 928073

Location/Qualifiers

1..491

/organism="Homo sapiens"

/clone="194467"

/note="human"

BASE COUNT 82 a 118 c 147 g 132 t 12 others

ORIGIN

Query Match

39.7%; Score 280; DB 69; Length 491;

Best Local Similarity 91.9%; Pred. No. 0.00e+00;

Matches 318; Conservative 0; Mismatches 24; Indels 4; Gaps 4;

Db 147 atgaacattctgtagggccactgtcttccacaggtgctcccttcattgacgtgacctggc 206

|||||

Cp 703 ATGAACATTCTGTAGGGCCACTGTCTTCTCCACGGTGTCCCTTCATCGCTGACCTGGC 644

|||||

Db 207 agctntagcttctgtgggaacttccactgctcaggcgtcaggctcaggtagctgctggccg 266

|||||

Cp 643 AGCTGAGCTTCTGTGGCACTTCCACTGCTCAGGCTCAGGCTCAGTAGCTGTGGCGC 584

|||||

Db 267 cgtactgtgtgtgtgttggagggtntggtgtctccantcccgccttgacgggc 326

|||||

Cp 583 CGTACTGTGTGTGTGTGGAGGGTGTGGTGTCTCCACTCCCGCTTGACGGGC 524

|||||

Db 327 tgcctatcgtctcaggcgttccacgttccnggttagaagtcacttntgagacaca 386

|||||

Cp 523 TGCTATCTGCTTCCAGGCCACTGTCTCAGGCTCCCGGTGAGAGTCACTTATGAGACACA 464

|||||

Db 387 ccagntnagcctgttggctttaagntcccaagagaggcgggaacagatt-accag 445

|||||

Cp 463 CCAGTGTGGCTTGTGGCTTGA-CTCTCTCAGAGAGGGGGAACAGTGCACCGAG 405

|||||

Db 446 ggggcagc-ttnggttancatgaagcagctcagttng-tccctctc 489

|||||

Cp 404 GGGGAGGCTTGGGCTGACCTAGGACGGTCCACCGGGTCCCTCTC 359

|||||

RESULT 9

LOCUS

DEFINITION

ACCESSION

NID

KEYWORDS

H60966 329 bp mRNA EST

Yr22c08.r1 Homo sapiens cDNA clone 206030 5' similar to gb:X57809

IG LAMBDA CHAIN C REGIONS (HUMAN);

H60966

g1013798

EST.

Db 182 agaccacaaacacctccaaacagagcaacaagaatacgcggccagcagctacctgagcc 241

Query Match
39.4%; Score 278; DB 71; Length 435;

309 acgcattgaaggagcacccgtggaagaacagcagtcgcccctgacagaatggt 360
|||||
652 accgat-gaaggagacccgtgg-agaagacagctggccctt-acagatctgt 700

RESULT	14				
LOCUS	R83348	487 bp	mRNA	EST	04-AUG-1995
DEFINITION	yp06b01.s1 Homo sapiens cDNA clone 186601 3' similar to gb:X57809 IG LAMBDA CHAIN C REGIONS (HUMAN);				
ACCESSION	R83348				
NID	9928225				
KEYWORDS	EST.				
SOURCE	human clone=186601 library=Soares breast 3NH8et vector=pf7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=Promega -2lm13 Rsite1=Not I Rsite2=Eco RI Adult human. 1st strand cDNA was primed with a Not I - oligo(dT) primer 15' TGTACCAATCTGAAGTGGAGCGGCCCGCCCCCTTTTTTTTTTTTTT 3', double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo.				

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 487)

REFERENCE Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Woldmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)

NCBI gi: 928225	Location/Qualifiers			
source	1..487			
	/organism="Homo sapiens"			
	/clone="186601"			
	/note="human"			
BASE COUNT	85 a	123 c	159 g	113 t
ORIGIN				7 others
Query Match	38.74;	Score 273;	DB 69;	Length 487;
Best Local Similarity	95.04;	Pred. No. 0.00e+00;		
Matches 305;	Conservative	0;	Mismatches 12;	Indels 4;
Gaps	4;			
Db	116	atgaacattctgtagggccactgtctctccacgtgtcccttcattgcgtgaactggc	175	

[illegible]

RESULT	15
LOCUS	H26023 431 bp mRNA EST 10-JUL-1995
DEFINITION	Y152h1.1.s1 Homo sapiens cDNA clone 161925 3' similar to gb:X57809 IG LAMBDA CHAIN C REGIONS (HUMAN);.
ACCESSION	H26023
NID	g895146
KEYWORDS	EST.
SOURCE	human cDNA=161925 library=Soares breast 3NbHBst vector=p7T73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=Pronega -21ml3 Rsite1-Not I Rsite2=Eco RI Adult human. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'- TGTTACCATCTGAAGTCGGAGCGGCCGCTTTTTTTTTTTT 3', double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 431)

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubucq, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfs, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 313
 Source: IMAGE Consortium, LIND
 This clone is available royalty-free through LIND ; contact the

Dec 17 20:52

US-08-487-550-1.rst

21

IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 895146

Location/Qualifiers

1..431

/organism="Homo sapiens"

/clone="161925"

/note="human"

BASE COUNT 71 a 107 c 133 g 109 t 11 others

ORIGIN

Query Match 38.6%; Score 272; DB 11; Length 431;
Best Local Similarity 94.2%; Pred. No. 0.00e+00;
Matches 291; Conservative 0; Mismatches 16; Indels 2; Gaps 2;

Db 124 atgaacattctgtaggccactgtcttctccacggtgctcccttcattgctgacctggn 183
|||||
Cp 703 ATGAACATTCTGTAGGGCCACTGTCTCTCCACGGGTGCTCCCTTCATGCGTACCTGG- 645
|||||

Db 184 cagctnagcttctgtgggacttccactgctcaggcgtcaggtcanaatagctgctggcc 243
|||||
Cp 644 CAGCTGTAGCTTCTGTGGGACTTCACACTGCTCAGGGGTGAGGCTCAGGTGCTGTGGCC 585
|||||

Db 244 gctactgtgtgtgcttgtttgttgagggtntggtgtctccactccgccttgacgggg 303
|||||
Cp 584 GCTACTTGTGTGCTTGTGTTGGAGGGTGTGTTGTTCCACTCCCGCCTTGACGGGG 525
|||||

Db 304 ctgctatctgcctccagncactntccaggtcccggtccgggtagaagtcacttatgagacac 363
|||||
Cp 524 CTGCTATCTGCTTCCAGGCCACTGTCTACGGCTCCGGGTAGAAGTCACTTATGAGACAC 465
|||||

Db 364 accagtggtgcttntgtgcttnaagctcctcagaggangcggaacaaagt-accnag 422
|||||
Cp 464 ACCAGTGTGGCCTTGTGCTTGAAGCTTCTCAGAGGGGGGGGACAGAGTCACTGACCGAG 405
|||||

Db 423 ggggcaacc 431
|||||

Cp 404 GGGGACGCC 396

Search completed: Tue Dec 17 21:06:01 1996
Job time : 280 secs.

NAMES

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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Distribution rights by IntelliGenetics, Inc.

MPerch_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 21:26:22 1996; MasPar time 117.91 Seconds
Tabular output not generated. 945.851 Million cell updates/sec

Title: >US-08-487-550-3

Description: (1-1431) from US08487550.seq

Perfect Score: 1431

N.A. Sequence: 1 ATGAACACCTGCTGTTCTT.....CCCTGTCCTCCGGTAATGA 1431

Comp: TACTTTTGTCACCAAGAA.....GGACAGAGGCCCATTTACT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 102519 seqs, 38967980 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-genseq24

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 9.407; Variance 6.204; scale 1.516

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1201	83.9	1431	19	T18059 Monoclonal antibody D	0.00e+00
2	1032	72.1	1617	6	Q35099 Antibody D heavy chai	0.00e+00
3	1028	71.8	1135	1	N90736 DNA encoding linker	0.00e+00
4	1027	71.8	1136	1	N90779 Sequence of the linke	0.00e+00
5	1023	71.5	1549	3	Q20066 Encodes heavy chain o	0.00e+00
6	1012	70.7	9208	11	Q65629 Vector contg. TCAE 8	0.00e+00
7	1007	70.4	1576	8	Q49944 Human anti-HBs heavy	0.00e+00
8	1001	70.0	1458	4	Q23571 Reshaped CD4 antibody	0.00e+00

9	1002	70.0	1467	4	Q23570 Reshaped CAMPATH-1 an	0.00e+00
10	999	69.8	1458	4	Q23581 Reshaped CD4 antibody	0.00e+00
11	998	69.7	6557	18	T15932 Anti-IgE VH expressio	0.00e+00
12	996	69.6	1386	8	Q49834 Anti-HIV-1 recombinan	0.00e+00
13	995	69.5	1641	9	Q54655 chiT84.12 H3 heavy ch	0.00e+00
14	987	69.0	8540	11	Q65628 Vector contg. TCAE 8	0.00e+00
15	983	68.7	1412	4	Q25692 Sequence of the chime	0.00e+00
16	981	68.6	1174	9	Q51547 Human kappa immunoglo	0.00e+00
17	824	57.6	1006	17	T12663 Synthetic IgG4 cDNA.	0.00e+00
18	692	48.4	768	17	Q96101 IgG1 hinge, CH2, CH3	0.00e+00
19	689	48.1	693	15	Q87592 Human IgG1 antibody F	0.00e+00
20	689	48.1	1164	17	T12658 IL4.Y124D/IgG1 gene f	0.00e+00
21	689	48.1	6367	17	T12661 Vector COSfclink.	0.00e+00
22	689	48.1	6926	17	T12662 IL-4.Y124D/IgG1 fusio	0.00e+00
23	687	48.0	1231	15	Q87593 Human Fas/Fc fused OR	0.00e+00
24	685	47.9	699	9	Q53539 cDNA sequence for a h	0.00e+00
25	685	47.9	705	18	Q74083 Immunoglobulin G1 Fc	0.00e+00
26	686	47.9	745	9	Q55943 Polylinker/Fc fragmen	0.00e+00
27	686	47.9	745	15	Q92273 Fc cDNA.	0.00e+00
28	686	47.9	745	13	Q75425 Antibody Fc mutein co	0.00e+00
29	686	47.9	745	9	Q58428 Human IgG1 Fc-polylin	0.00e+00
30	684	47.8	740	6	Q41508 Human IgG1 Fc.	0.00e+00
31	683	47.7	705	7	Q42589 Human Fc polypeptide	0.00e+00
32	682	47.7	1050	5	Q28684 LFA-3-Ig fusion gene	0.00e+00
33	682	47.7	1347	12	Q67347 VCAM 2D-IgG.	0.00e+00
34	682	47.7	2043	9	Q55340 tICAM(453) IgG immuno	0.00e+00
35	681	47.6	1317	17	T00829 Plasmid pDC406/OX40/F	0.00e+00
36	680	47.5	1050	6	Q40423 DNA sequence of LFA3T	0.00e+00
37	675	47.2	1557	10	Q45225 Sequence encoding a r	0.00e+00
38	675	47.2	1587	10	Q63958 P-selectin ligand-IgG	0.00e+00
39	675	47.2	1587	16	T02490 P-selectin ligand/Fc	0.00e+00
40	662	46.3	884	2	N70398 Portion of plasmid pP	0.00e+00
41	658	46.0	765	2	N70257 Part of the nucleotid	0.00e+00
42	658	46.0	765	1	N82142 Immunoglobulin G Fc d	0.00e+00
43	645	45.1	6889	18	T15931 DHFR/intron (WTrasSD)	0.00e+00
44	631	44.1	1425	6	Q41516 Human CD40-L/Fc fusio	0.00e+00
45	631	44.1	1765	10	Q71873 Sequence coding human	0.00e+00

ALIGNMENTS

RESULT 1
ID T18059 standard; DNA; 1431 BP.
AC T18059;
DT 16-AUG-1996 (first entry)
DE Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.
KW Polymerase chain reaction; primer; amplify; PCR; light chain; MAb;
KW 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 1..1428
FT /*tag= a
FT sig_peptide 1..57
FT /*tag= b
FT mat_peptide 58..1425
FT /*tag= c
FT 3'UTR 1426..1431
FT /*tag= d
PN J08038178-A.
PD 13-FEB-1996.
PF 20-FEB-1995; 030742.
PR 18-FEB-1994; JP-021628.
PA (NISN) NISSHINO IND INC.
PA (TANAKA) TANAKA H.

Qy 1388 ACCACTACACGACGAGAGACCTCTCCCTGCTCCGGGTAA 1428
|||||

RESULT 5

ID Q20066 standard; DNA; 1549 BP.
AC Q20066;
DT 25-MAR-1992 (first entry)
DE Encodes heavy chain of 3D6 antibody.
KW Plasmid pUC3D6HC; human immunodeficiency virus; AIDS; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT sig_peptide 101..157
FT /*tag= a
FT mat_peptide 158..1528
FT /*tag= b
FT 5'UTR 1..100
FT /*tag= c
FT misc_feature 158..535
FT /*tag= d
FT /label= variable_region
FT misc_feature 158..247
FT /*tag= e
FT /label= Framework 1
FT misc_feature 248..262
FT /*tag= f
FT /label= CDR 1
FT misc_feature 263..304
FT /*tag= g
FT /label= Framework 2
FT misc_feature 305..355
FT /*tag= h
FT /label= CDR 2
FT misc_feature 356..431
FT /*tag= i
FT /label= Framework 3
FT misc_feature 452..502
FT /*tag= j
FT /label= CDR 3
FT misc_feature 503..535
FT /*tag= k
FT /label= Framework 4
FT misc_feature 536..1528
FT /*tag= l
FT /label= Constant_region
PN W09118983-A.
PD 12-DEC-1991.
PF 28-MAY-1991; 100067.
PR 29-MAY-1990; AT-001178.
PA (JUNG/) JUNGHAUER A.
PI Felgenhauer M, Himmeler G, Kohl J, Steindl F;
DR WPI; 92-007468/01.
DR P-PSDB; R20057.
PT Recombinant protein which binds to complex viral antigen and
PT HIV-1 - contains variable region of antibody derived from 3D6
PT cell line, used for detecting HIV-1 antigen
PS Claim 2; Page 24; 52pp; German.
CC The 5'-UTR is 100 bases long although the specification numbers it
CC at 98 bases. It is possible that two extra bases have been inserted
CC as a typographical error in the specification (i.e. that the 5'-UTR
CC sequence is incorrect as printed in the specification and reproduced
CC here). The sequence comprises a human cDNA insert encoding the 3D6
CC heavy chain flanked by short stretches of pUC19 DNA. The variable
CC region of the heavy chain is used in a recombinant protein with the

CC variable region from the kappa light chain of 3D6, the two V regions
CC being joined by a linker. The recombinant protein binds to HIV gp160.
CC See also Q20067 and Q20068.
SQ Sequence 1549 BP; 362 A; 464 C; 416 G; 307 T;

Query Match 71.5%; Score 1023; DB 3; Length 1549;
Best Local Similarity 86.9%; Pred. No. 0.00e+00;
Matches 1222; Conservative 0; Mismatches 181; Indels 3; Gaps 3;

Db 126 tccttttggtattttaaaagtgctcagtggaagtcagctggtggagtcgtggggag 185
|||||

Qy 26 TCCTGCTGGCAGCTCCACATGGGTCTCTCCAGGTGAAGCTCCAGCAGTGGGCGCAG 85
|||||

Db 186 gcttggtacagctggcaggtccctgagactctctgtcagcctctgattccacttta 245
|||||

Qy 86 GACTTCTGCAGCCTTCGGAGACCTGTCCCGCACCTCGCTTCTGTGGTGGCTCCATCA 145
|||||

Db 246 atgatta-tgcca-tgcac-tgggtccggcaagctccagggaaggcctggagtggtct 302
|||||

Qy 146 GCGGTTACTACTGTGACCTGGATCCGCCAGACCCAGGAGGGGAGCTGGAGTGGATTG 205
|||||

Db 303 caggtataagttggatagtagtataggtctatgagctctgtgaaggccgattca 362
|||||

Qy 206 GCCATATTATGTAATGTGCGACCAACCACTAGAAATCCCTCCCTCAAGAGTGGAGTCA 265
|||||

Db 363 ccatctccagagacaacgccgaactccctgtatctgcaaatgaacagctctgagagctg 422
|||||

Qy 266 CCATTTCAAAAGACAGCTCCAAAGACAGTTCTTCTGTGAATTTGATTTGTGACCGAGC 325
|||||

Db 423 agaacatgaccttattactgtgtaaaaggcagagattactatgatagtggtgttatt 482
|||||

Qy 326 CGGACGCGCGCTTATTACTGTGCGAGAGCGCTCGCCCTGATTGCAACCACTTTGTT 385
|||||

Db 483 tcacggttgctttgatctggtgggccaagggaacaatggtcacogtctcttcacgtcca 542
|||||

Qy 386 ATGGCGCTGGGTGATGTCTGGGGCGCGGAGACCTGGTCACCGTCTCTCAGCTAGCA 445
|||||

Db 543 ccaaggccccatcggtcttccccctggacacctctccaagagcaactctggggccacag 602
|||||

Qy 446 CCAAGGGCCCATCGGCTTCGCCCTGGCACCTCTCTCAAGAGCACTCTGTGGGGGCACAG 505
|||||

Db 603 cagcctgggtgctgctcaaggactacttccccgaaccggtgacggtgctggtgaact 662
|||||

Qy 506 CGGCGCTGGGCTGCTGTGAAGGACTACTTCCCGGACCGGTGACGGTGTGCTGGAAT 565
|||||

Db 663 caggcgccctgaccagcgctgcacaccttcccggctgctctacagctctcagagctct 722
|||||

Qy 566 CAGGCGCCTTCACCGCGCGCTGCACACCTCCCGGCTGTCTTACAGTCTCTCAGGACTCT 625
|||||

Db 723 actcctcagcagcggtggtgacctgacctccagcagcttggtggccaccagacctcaact 782
|||||

Qy 626 ACTCCCTCAGCAGCGTGTGACCTGCTCCCTCAGCAGCTTGGGACCCAGACCTACATCT 685
|||||

Db 783 gcaacgtgaatcacagccccagcaacacacaggtcgacaagaagttagccccaatctt 842
|||||

Qy 686 GCAACGTGAATCAGACGCCAGCAACACAGGTGGACAAAGAGAGAGAGCCCAATCTT 745
|||||

Db 843 gtgacaaaactcacatgccatgccacctgcccagcaactgaactcctgggggagccgtcag 902
|||||

Qy 746 GTGCAAAACTCAGATGCCCCACCGTGGCCAGCAGCTGAACTCCTGGGGGGAGCCGTCAG 805
|||||

Db 903 tcttctctctcccccccaaaacccaaggacacctctcatgctctccggacctctaggtca 962
|||||

Qy 806 TCTTCTCTCTTCCCCCCCCAAACCCAAAGGACACCTCATGTATCTCCCCGAGCCCTGAGGTCA 865
|||||

Db 963 catcgctggtggtgacgtgagccacgaagaccctgaggtcaactggtacgtg 1022
|||||
Qy 866 CATCGCTGCTGCTGACGTGAGCCAGGACCTGAGGTCAAGTTCMACTGCTACGTGG 925
Db 1023 acgcgctgaggtgcaatgaaacgaagccgagggagagcagtaacactccagct 1082
|||||
Qy 926 ACGCGCTGAGGTGCAATATCCCAAGCAAGCCGCGGAGGAGCAGTACACAGCACGT 985
Db 1083 accgtggtgacgtcctcaccgtcctgcaccaggaactgggtgaatggcaaggagtaca 1142
|||||
Qy 986 ACCGTGTGGTCAGCTGCTCCTGACCGTCTGACACGAGCTGGCTGAATGGCAAGAGTACA 1045
Db 1143 agtgaaggtctccaaagaacctccagcccccacgaagaacacatctccaaagcca 1202
|||||
Qy 1046 AGTGAAGGTCTCCAAAGACCTCCAGGCCCATCGAGAAAAACATCTCCAAAGCCA 1105
Db 1203 aagggcagcccccagaaacacaggtgtacacacctgcccccatcccgggatgagctgacca 1262
|||||
Qy 1106 AAGGCAGCCCCGAGAAACACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCA 1165
Db 1263 agaaccaggtcagctgacctgctgtgctaaaggcttctatcccagcgatcgccgtgg 1322
|||||
Qy 1166 AGAACCGAGTCAGCTGACCTGCTGCTGTAAGGCTTCTATCCCGGACATCCGCGTGG 1225
Db 1323 agtggaggaacaaatggcgagcggagaaacactacaagaccagcctcccgtgctggaact 1382
|||||
Qy 1226 AGTGGGAGGCAATGGCGAGCCGGAGAACTACAAAGACACCGCTTCCCTGCTGCACT 1285
Db 1383 ccgagagctcctcttctctctacagcaagctcaccgtggacaagcagcaggtggcagcagg 1442
|||||
Qy 1286 CCGAGCGCTCTTCTTCTTACAGCAAGCTCACCGTGGACAAGCAGGTGGCAGCAGG 1345
Db 1443 ggaacgtctctcatgctcgtgatgatgaggtctgtgcaacacactacacacagaaga 1502
|||||
Qy 1346 GGAAGCTCTTCTCATGCTCGTGTATGATGAGGCTGTGCACACCACTACACGAGAGA 1405
Db 1503 gacctcctcgtctccgggttaaatga 1528
|||||
Qy 1406 GCCTCTCCTGCTCGGGTAAATGA 1431

RESULT 6

ID Q65629 standard; DNA; 9208 BP.
AC Q65629;
DT 01-FEB-1995 (first entry)
DE Vector contg. TCAE 8 DNA.
KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;
KW cell lysis; ss.
OS Synthetic.
PN W09411026-A.
PD 26-MAY-1994.
PF 12-NOV-1993; U10953.
PR 13-NOV-1992; US-978891.
PR -03-NOV-1993; US-149099.
PA (IDEC-) IDEC PHARM CORP.
PI Anderson DR, Hanna N, Leonard JE, Newman RA, Rastetter WH;
PI Refine;
DR WPI; 94-183162/22.
PT Treating B cell lymphoma with chimeric antibody - against CD20,
PT causing rapid depletion of peripheral B cells, also new
PT antibodies and hybridomas
PS Disclosure; Fig 3; 101pp; English.
CC The sequence shows a vector contg. TCAE8, a gene encoding a chimeric

CC anti-CD20 antibody for treatment of B cell lymphomas. TCAE8
CC contains 4 transcriptional cassettes, human Ig light and heavy chain
CC constant regions, dihydrofolate reductase, neomycin phosphotransferase
CC and murine variable regions. The vector can be used to produce
CC antibodies which cause depletion of peripheral blood B cells,
CC including those associated with lymphoma. They mediate complement-
CC dependent lysis and lyse target cells by antibody-dependent cellular
CC cytotoxicity.
CC See also Q65629-35.
SQ Sequence 9208 BP; 2237 A; 2399 C; 2388 G; 2182 T;
Query Match 70.7%; Score 1012; DB 11; Length 9208;
Best Local Similarity 98.9%; Pred. No. 0.00e+00;
Matches 1023; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Db 2779 tcaatgtctggggcgagggaccacggtcacccgtctctcagctagcaccgaaggcccat 2838
|||
Qy 398 TCGATGTCTGGGGCGGGAGACCTGCTACCGCTCTCTCAGCTAGACCAAGGGCCCAT 457
Db 2839 cggctctcccccctggcacccctctccaagagcacctctgggggcacagcgccctggct 2898
|||||
Qy 458 CGGTCTTCCCTTGGCACCCCTCTCCAAAGCAGCCTCTGGGGGACAGCGCGCTGGGCT 517
Db 2899 gctcgtcaaggactactccccgaacccggtgacggtgtcgtggaactcagggccctga 2958
|||||
Qy 518 GCCTGGTCAAGGACTACTTCCCGCAACCGGTGAGGTGCTGGAACTCAGCGCCCTGA 577
Db 2959 ccagcggtgcaacacctcccggctgtcctacagtcctcaggactctactccctcagca 3018
|||||
Qy 578 CCAGCGGCTGCACACTTCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCA 637
Db 3019 gctggtgacgtgacctccagcagcttgggcaaccagacctacatctgcaacgtgaate 3078
|||||
Qy 638 CGGTGTGACCTGCGCTTCCAGCAGCTTGGGCAACCAGACCTACATCTGCAACGTGAATC 697
Db 3079 acaagccagcaacacccaaggtggacaagaagcagagcccaaatcttgtacaaaacte 3138
|||||
Qy 698 ACAAGCCAGCAACACCAAGGTGGAACAAGCAGAGCCCAATCTTGTGACAAAATC 757
Db 3139 acacatgccaccgtgccacgaacctgaaactcctggggggaccctcagctcttctcttcc 3198
|||||
Qy 758 ACATATGCCACCGTGCACGACCTGAACCTCTGGGGGACCGTCACTTCTCTCTCC 817
Db 3199 ccccaaaacccaaggacacctctcatgatctcccggaccctgaggtcacatgcgtgg 3258
|||||
Qy 818 CCCCAAAACCCAGGACACCTCATATCTCCCGGACCCCTGAGGTACATCGCTGGTGG 877
Db 3259 tggacgtgagccacgaagacctgaggtcaacttcaactggtacgtggagcgctggagg 3318
|||||
Qy 878 TGCAGCTGAGCCACGAAGACCTCTGAGCTCAAGTCAACTGGTGTGAGACGGCGTGGAG 937
Db 3319 tgcaaatgccaaagacgaagcgggagagcagctacaacagcagctaccgtgtggtca 3378
|||||
Qy 938 TGCATAATGCCAAGCAAGCCGGGAGGAGCAGTACAACAGCAGCAGTACCGTGTGTGCA 997
Db 3379 gctcctcaccgtcctgcaccaggaactggctgaatggcaacgagtaacaagtgcaggtct 3438
|||||
Qy 998 CGCTCTCAGCGTCTGCACAGCACTGGCTGAATGGCAAGGAGTACAAAGTCAAGGTCT 1057
Db 3439 ccaacaagacctcccagcccccatcgagaaacacatctccaaagccaaaggcagcccc 3498
|||||
Qy 1058 CCACAAAGCCCTCCCGCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCC 1117
Db 3499 gagaaccacaggtgtacacctgccccatcccgggatgagctgaccaagaaccaggtca 3558

1118 GAGAACACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAACACAGGTCA 1177
3559 gcttgactgctgtgtaaggtcttatcccagcgacatcccggtgagtgaggagagca 3618
1178 GCCTGACCTGCTGTGCTCAAGGCTTCTATCCACGGACATCCGCGTGGAGTGGGAGACA 1237
3619 atgggcagcggagagaactacaagacaacgctcccggtgctggactccgacggtcct 3678
1238 ATGGCAGCGCGAGAACAACTACAAAGACACCGCTCCCGTGTGACTCCGACGGCTCCT 1297
3679 tcttcctctacagaagctcaccgtggacaagagcaggtggcagcaggggaagctctct 3738
1298 TCCTTCTCTACAGCAAGCTCACCGTGGACAGACAGCAGGTGGCAGCAGGGAGCTTCT 1357
3739 catgtccggtgatgatgaggtctgcacaaccactacacgacagaagagcctctccctgt 3798
1358 CATGCTCCGTGATGCTAGGCTCTGCAACACCACTACACGCGACAGAGGCTCTCCCTGT 1417
3799 ctccgggttaataga 3812
1418 CTCGGGTAAATGA 1431

RESULT 7

ID Q49944 standard; cDNA; 1576 BP.
AC Q49944;
DT 29-APR-1994 (first entry)
DE Human anti-HBs heavy chain.
KW Antibody; Ab; light; heavy; chain; hepatitis B;
KW HB; surface antigen; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 15..1394
FT /*tag= a 15..41
FT sig peptide
FT /*tag= b 42..1391
FT mat peptide
FT /*tag= c
FT /*notes= "claim 2, page 27"
PN W09320205-A.
PD 14-OCT-1993.
PE 30-MAR-1993; J00396.
PR 30-MAR-1992; JP-074678.
PA (SUNR) SUNTORY LTD.
PI Arima K, Kurihara T, Matsukura S, Nishihara T, Tsuruoka N;
DR WPI; 93-336913/42.
DR P-PSDB; R42066.
PT Human anti-hepatitis B surface antigen antibody gene - can be
PT used to produce L and H chains of the antibody in large quantity
PS Disclosure; Fig 6-8; 46pp; Japanese.
CC Polynucleotides encoding the L and H chains of human anti-HBs
CC Ab are given in Q49943-Q49944. The Ab can be easily produced in
CC large quantities for therapeutic use.
SQ Sequence 1576 BP; 394 A; 483 C; 426 G; 273 T;
Query Match 70.4%; Score 1007; DB 8; Length 1576;
Best Local Similarity 99.0%; Pred. No. 0.00e+00;
Matches 1017; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Db 368 ctggggcagggaacccctgttcacgctctctcagcctccacgaaggcccatcggtctt 427
405 CTGGGGCCGGGAGACCTGGTGACCGTCTCTCTACAGTACGACCAAGGGCCCATCGGTCTT 464

428 cccctggcacctctcccagagacactctgggggcacagcgccctggctgctggt 487
465 CCCCCTGGCACCCCTCTCCAAAGACACCTCTGGGGGCACAGCGCCCTGGCTGGT 524
488 caaggactactccccgaaccggtgacggtgtcgtggaactcaggcgccctggccagcgg 547
525 CAAGGACTACTTCCCGCAACCGGTGACGGTGTCTGGAACCTCAAGCGCCCTGACACGGG 584
548 qgtgcaacactccccggtgtcctacagtcctcaggactctactccctcagcagcgtggt 607
585 CTGCACACTTCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCTGGT 644
608 gacgtgacctccagcagcttgggcaaccagacctacatctgcaaacgtgaatcacaagcc 667
645 GACGTGCCCTCGACAGCTTGGGCAACCCAGACCTACATCTGCAACGTGAATCACAGCC 704
668 cagcaacacaaggtggacaagaagttagcccaaatctgtgacaaaactcacacatg 727
705 CAGCAACACCAAGGTGGACAGAAAGCAGAGCCCAATCTTGTGCAAAAATCACACATG 764
728 cccacggtgccacgacctgaactcctgggggaccgtcagttcttctctcccccaaa 787
765 CCCACGCTGCCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCTTCCGCCCAA 824
788 acccaaggacacctcatgatctcccggaccctgaggtcacatgctggtggtgagct 847
825 ACCCAAGGACACCTCATATCTCCCGGACCCCTGAGTGCATCATCTGCTGGTGGAGCT 884
848 gagccacgaagacctgaggtcaagttcaactggtacgtggagcgtggagtgcataa 907
885 GAGCCAGGAAGACCTGAGGTCAAGTTCAACTGTGCTGAGCGCGCTGGAAGTGCATAA 944
908 tgccaagacaaagccgggagagcagtlacaacagcagctaccgggtggtcagcgtcct 967
945 TGCCAAGACAAAGCCGGGGAGGAGCAGTACAACAGCACGTACCGTGTGTCAGCGTCT 1004
968 caccgtctgcaccaggactggtgaatggcaaggagtacaagtgaagggtctccaacaa 1027
1005 CACCGTCTCGACAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGTCTCCAACA 1064
1028 agcctccagcccccatcgagaaaccatctccaaagccaaagggcagccccgagaacc 1087
1065 AGCCTTCCCGACGCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGACC 1124
1088 acaggtgtacacctgcccccatcccggtgagctgaccaagaaccaggtcagcgtgac 1147
1125 ACAGGTGTACACCTTGCCCCCATCCCGGATGAGTGCACAAAGAACACAGGTGAGCTGAC 1184
1148 ctgctggtcgaaggttctatcccagcacatcccggtggagtggagagcaatgggca 1207
1185 CTGCTGTGTTAAAGGCTTCTATCCAGCGACATCCCGTGTGAGGAGCAATGGGCA 1244
1208 gccggagacaactacaagacaacgctcccggtgctggactccgaaggtctcttctct 1267
1245 GCGGAGAAACAAAGTACAAGACCGCGCTCCGCTGTGAGTCCGACGGCTCTTCTTCTCT 1304
1268 ctacagaagctcacogtggacaagagcaggtggcagggggaacgtcttctcatgctc 1327
1305 CTACAGCAAGCTCACCGTGGACAGACGAGTGGCAGCAGGGGAACGTCTTCTCATGCTC 1364
1328 cgtgatgatgaggtctgtcacaaccactacacgacaagaagacctctccgtgtctccggg 1387
1365 CGTGATGATGAGGCTGTGCACAAACCACTACACGACGAAGACGCTCTCTCTCTCCGGG 1424

KW Antigen; CDR; complementarity determining region; graft rejection;
KW autoimmune diseases; rheumatoid arthritis; allergy; ss.
OS Rattus rattus.

FH Key Location/Qualifiers

FT CDS 36..1448

FT /*tag= a

FT misc feature 183..197

FT /*tag= b

FT /note= "Complementarity determining region 1"

FT misc feature 240..296

FT /*tag= c

FT /note= "Complementarity determining region 2"

FT misc feature 392..422

FT /*tag= f

FT /note= "Complementarity determining region 3"

PN W09205274-A.

PD 02-APR-1992.

PF 16-SEP-1991; G01578.

PR 17-SEP-1990; GB-020282.

PA (GORM/) GORMAN S D.

PI Clark M R, Cobbold S P, Gorman S D, Waldmann H.

DR WPI; 92-132139/16.

DR P-PSDB; R22757.

PT Humanisation of antibodies binding to human CD4 antigen - by

PT mutation of framework-encoding regions of DNA encoding variable

PT domain of rat or mouse antibody chain

PS Disclosure; Fig 5; 74pp; English.

CC The sequence is that of the reshaped CAMPATH-1 heavy chain cDNA.

CC Reshaped CD4 antibody can be used to induce tolerance against an

CC antigen. It can also be used to alleviate autoimmune diseases such

CC as rheumatoid arthritis, and to prevent graft rejection. Tolerance

CC to a graft, e.g. an organ graft or a bone marrow transplantation can

CC also be useful to alleviate allergies. Tolerance to allergens could

CC also be achieved. See also Q23566-Q23581.

SQ Sequence 1467 BP; 352 A; 467 C; 384 G; 264 T;

Query Match 70.0%; Score 1002; DB 4; Length 1467;

Best Local Similarity 98.5%; Pred. No. 0.00e+00;

Matches 1017; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Db 417 gattactgggggcaaggcagcctcgtcacagtctcctcagctccaccaggcccatcg 476

Qy 400 GATGCTGGGGCCCGGGAGACCTGGTCACCGCTCTCTCAGCTAGCACGAGGCGCCATCG 459

Db 477 gtcttccccctggcaccctcctccaagagcacctctgggggacagcgccctgggctgc 536

Qy 460 GTCTTCCCCCTGGCACCCCTCTCCAGACGACCTCTGGGGGACAGCGGCCCTGGGCTGC 519

Db 537 ctggtcaaggactacttccccgaaccggtgacggtgtcgtggaactcagcgccctgacc 596

Qy 520 CTGGTCAAGGACTACTTCCCGCAACCGGTGACGGGTCTGGGAACCTCAGSGCCCTGACC 579

Db 597 agcgcggtgcacacttccccgggtgtcctacagtcctcaggaactctactccctcagcgc 656

Qy 580 AGCGGCGTGCACACTTTCGGGCTCTCTACAGTCTCTCAGGACTCTACTCTCAGCAGC 639

Db 657 gtggtgacctgacctccagcagctgggacccagacacctatctgcaacgtgaatcac 716

Qy 640 GTGGTGACCGTGGCTTCAGCAGCTTGGGACCCAGACCTAGATCTGCAACGTGAATCAC 699

Db 717 aagcccaagcaaccagggtgacaaagaagtgtgagcccaatcttgtgacaaactcac 776

Qy 700 AAGCCCGACACACCAAGGTGGAGAAAGAGCAGAGCCCAAAATCTTGTGACAAACCTCAC 759

Db 777 acatgccaccgtgccacacactgaactcctgggggagaccgtcagttcctctctccccc 836

Qy 760 ACATGCCACCCTGCCACGACCTGAACCTCTGGGGGACCCGCTTCCTCTTCCCTTCCCC 819

Db 837 ccaaaacccaaggacacacctcatgatctcccagccacctgaggtcacatgcgtggtggtg 896

Qy 820 CCAAAACCCAGGACACCCCTCATGATCTCCGACCCCTGAGGTACATCGCTGCTGCTG 879

Db 897 gacgtgagccacgaagacctgaggtcaagttaactggtacgtggagcgctggaggtg 956

Qy 880 GACGTGAGCCAGCAGACCCCTCAGGTCAAGTTCAACTGTTAGCTGGAGCGGCTGGAGGTG 939

Db 957 cataatgccaaagcagcgaggagagcagctacacacagcagcagctaccgtgtggtcagc 1016

Qy 940 CATATGTCACAGCAAGCCGCGGAGAGGAGCGAGTACAAACAGCAGCTACCGTGTGTCAGC 999

Db 1017 gtccctcacccgtcctgacccaggaactggctgaatggcaaggagtacaagtgcgaaggtctcc 1076

Qy 1000 GTCTCTACCGCTCTGACACGAGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCC 1059

Db 1077 acaaaagccctcccagcccccatcgagaaaaaccatctccaaagccaaaggcagcccgga 1136

Qy 1060 AACAAAGCCCTCCACGCCCCCATGAGAAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA 1119

Db 1137 gaaccacaggtgtacacacctgcccccacccccggatgagctgacccaagaaccaggtcagc 1196

Qy 1120 GAACACAGGTGTACACCTTCCGCCCATCTCCCGGATGAGTGCACCAAGAACCCAGGTGAGC 1179

Db 1197 ctgacctgctgggtcaaaaggtcttctatcccagcagacatcgccgtggagtgaggagcaat 1256

Qy 1180 CTGACCTGCTGGTTCANAGGCTTCTATCCACGACGACATCGCCGTGGAGTGGGAGAGCAAT 1239

Db 1257 gggcagcgagagaacaactacaagacacgctcccgctgctgactccgacggtccttc 1316

Qy 1240 GGGCAGCGGAGAACAACTACANAAGACACGCTCCCGTCCGACTCCGACGGGTCTCTTC 1299

Db 1317 ttccctacagcaagctcaccgtggacaaagagcaggtggcagcaggggaaacgtctctca 1376

Qy 1300 TTCCTCTACGAAGCTCACCGCTGGCAAGAGCAGTGGCAGCAGGGGAACGCTCTTCTCA 1359

Db 1377 tgetccggtgatgcagtgaggtctctgccaaccaactacacgagaagagcctctccctgtct 1436

Qy 1360 TGCTCCGCTGATGCAATGAGGCTCTGCACACCACTACACGCGAGAGGCCTCTCCCTGTCT 1419

Db 1437 ccgggttaaatga 1448

Qy 1420 CCGGGTAAATGA 1431

RESULT 10

ID Q23581 standard; DNA; 1458 BP.

AC Q23581;

DT 20-OCT-1992 (first entry)

DE Reshaped CD4 antibody heavy chain cDNA CD4VH9EM-Ser30

KW Antigen; CDR; complementarity determining region; graft rejection;

KW autoimmune diseases; rheumatoid arthritis; allergy; ss.

OS Rattus rattus.

FH Key Location/Qualifiers

FT CDS 36..1439

FT /*tag= a

FT misc feature 183..197

FT /*tag= b

FT /note= "Complementarity determining region 1"

FT misc feature 240..290

D	355	gaagctttggggcaaaaggacacacggttcacccgtgagctcagctccaccaggggcccatcg	414
Q	400	GATGTCGTGGGCGCCGGGAGACCTGGTCACCGCTCTCTCAGCTAGCAACCAAGGGCCCATCG	459
D	415	gtcttccccctggcacccctcctccaagagacacctctgggggacacagcgccctgggtgc	474
Q	460	GTCTTCCCTCCCTGGCACCCTCTCCAGAGAGACACTCTGTGGGGGCACAGGGGCGCTGGGTCG	519
D	475	ctgggtcaaggactaettccccgaaccggtgacggtgctggtggaactcagggcgccctgaac	534
Q	520	CTGGTCAGAGACTACTTTCCTCCGGAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACC	579
D	535	agcggcgtgcacaccttcccggctgtcctacagtctctcaggactctactccctcagcagc	594
Q	580	AGCGCGTGCACACCTTCCCGGTGTCTCAGACTCTCAGAGACTACTCTCTCAGCAGC	639
D	595	gtgggtgaacctggccctccagcagcttggggaaccagacctacatctgaaagtgaaatac	654
Q	640	GTGGTCACCTGGCCTCCAGCAGCTTGGGCAACCGACACTATCTGCAACGTGAATCAC	699
D	655	aagcccgacgaacacaaagtggaagaanaagttgagcccaaatcttgtgacaaacatcac	714
Q	700	AAGCCCGACACACCAAGGTGGACAAGAAACGACAGCCCAAACTTTGTGACAAAATCAC	759
D	715	acatgcccaacctggccagcagacctgaacctcctgggggagcagctcagttctctctcccc	774
Q	760	ACATGCCCACCGTGGCCAGCAGCTGAATCTCTGGGGGAGCGCTCAGTCTCTCTTCCCC	819
D	775	ccaaaacccaaggacacctcatgatctcccggaccctcagggtcacatcggtgggtggtg	834
Q	820	CGAAACCCAGGACACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCTGGTGGTG	879
D	835	gacgtgagccagcaagaacctgaggtgcaagttcaactggtacgtggacggcggtggaggtg	894
Q	880	GAGCTGACCCACACAGA-3CTGAGGTCAAGTTCACTGGTACGTGACGGGTGGAGGTG	939
D	895	cataatgccaaagaaacccggagagagcagttacaacagcagctaccgltggtgcagc	954
Q	940	CATAATGCCAAGACAAAGCCGGGGAGGAGCAGTACACACGACCTACCGCTGTGGTCAGC	999
D	955	gtctcaccgtcctgcacacagactgggtgaaatggcaagagagtacaagtgcaaggtctccc	1014
Q	1000	GTCTCAGCGTCTGCACGAGACTGGCTGAATGGCAAGAGGTACAAGTGCAAGGTCTCC	1059
D	1015	aacaaagccctcccagcccccatctgagaaataccatctccaaagccaaaggcgaccocga	1074
Q	1060	AACAAAGCCCTCCAGCCCCCATCGAGAAACCACTCTCCAAAGCAAAAGGCGCCCGCA	1119
D	1075	gaaccacaggtgtacacactgcccccactcccgggatgagctgaccaagaacacaggtcagc	1134
Q	1120	GAACACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACAGGTTCAGC	1179
D	1135	ctgaacctcctggtcaaaaggcttctatcccagcgacatcgccgtggagtgaggagagcaat	1194
Q	1180	CTGACTCCTGTGTAAGGGTTCTATCCGACGACATCGCCGTGAGTGGAGAGAGAAAT	1239
D	1195	ggcgagcggagacaacctacaagacacgacctccggtgctggactccgagcgctctctc	1254
Q	1240	GGCGAGCGGAGAACAA-TACAAGACCAACGCTCCGCTGTGGACTCCGAGGGCTCTTCT	1299
D	1255	ttcctctacagcaagctcacctggagcaagagcaggtggcagcaggggagcagctctctca	1314
Q	1300	TTCTCTTACAGCAAGCT-ACCGTGGCAAGACAGAGGTGGCAGAGGGGAAGCTCTTCTCA	1359

Db	1315	tgctccgtgatgcgtgagctctgcacaaacctacacagcagaagagcctctccctgtct	1374
Qy	1360	TCGTCGCGTGCATGAGGCTCTGCACACCACTACGACGAGAGGCTCTCCCTCTCT	1419
Db	1375	ccgggtaaatga	1386
Qy	1420	CCGGGTAAATGA	1431
RESULT	13		
ID	Q54655	standard; cDNA; 1641 BP.	
AC	Q54655;		
DT	24-JUN-1994	(first entry)	
DE	chiT84.12 H3 heavy chain.		
KW	Chimeric; carcinoembryonic antigen; CCA; murine; mouse; constant;		
KS	region; transform; myeloma cell; light chain; tumour; ss.		
OW	Synthetic.		
FH	Key	Location/Qualifiers	
FT	CDS	52..1486	
FT	/*tag= a		
FT	/product= chiT84.12 H3 heavy_chain		
PN	W09325237-A.		
PD	23-DEC-1993.		
PF	15-JUN-1993; U05709.		
PR	15-JUN-1992; US-904074.		
PA	(CITY) CITY OF HOPE.		
PA	(YANG/) YANG Y.		
PI	Fischer R, Paxton R, Shively JE, Wu A, Yang YHJ;		
PI	Yang YH;		
DR	WPI; 94-007204/01.		
DR	P-PSDB; R47453.		
PT	New chimeric T84.12 antibody active against carcinoembryonic		
PT	antigen - has murine variable and human constant regions, also		
PT	DNA encoding it and transformed myeloma cells		
PS	Claim 1; Page 22-23; 27pp; English.		
CC	The sequences (054651-52) show the light and heavy chain cDNAs		
CC	of murine T84.12. The T84.12 antibody is directed against the		
CC	tumour marker carcinoma embryonic antigen, and is useful for		
CC	tumour imaging and immunotherapy.		
SQ	Sequence 1641 BP; 370 A; 516 C; 444 G; 311 T;		
Query Match	69.5%;	Score 995; DB 9; Length 1641;	
Best Local Similarity	98.4%;	Pred. No. 0.00e+00;	
Matches 1011; Conservative	0; Mismatches 16; Indels	0; Gaps	0;
Db	459	ctggggcgcaaggactctggccactgtctctgcagctccaccaaggccatcggtctt	518
Qy	405	CTGGGGCGCCGGAGACCTGGTCCGCTCTCTCAGCTAGCACCAAGGCCCATCGGTCTT	464
Db	519	ccccctggcacctctctccaagagcacctctgggggcacagcgccctgggtcctggt	578
Qy	465	CCCCCTGGCAACCCCTCTCCAAAGGACCTCTGGGGGCACAGCGGCCCTGGGCTGGT	524
Db	579	caagactactccccgaaccggtgacggtgtcgtggaactcaggcgccctgaccagcg	638
Qy	525	CAMGGACTACTTCCCGCAACCCGGTCAGGGTGTCTGTGGAACTCAGCGGCCCTGACCA	584
Db	639	ggtgcacacctcccgctgtctactagtcctcaggactctactccctcagcagcggt	698
Qy	585	CGTGCACACCTTCGCGGCTGCTCTACAGTCTCTCAGGACTCTATCTCCCTCAGCAG	644
Db	699	gacgctgcctccagcagcttgggcacccagacctacatctgcaacgtgaatcacaagc	758

QY 645 GACCGTGGCCCTCCAGCAGCGTTGGCGACCCAGACCTACATCTGCAACGTAATCAACAGCC 704

Db 759 gacgaacacaaagtgagcaaaaagtgtgcccacaaatctgtgacaaaactcacacatg 818
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QY 705 CAGCAACACAAAGGTGGCAGAGAAACGAGCCCAATCTTGTCAGAAACTCAGACATG 764
|||||

Db 819 cccacagtgcccagcaacctgaactctctgggggacccgtcagttcttctcttcccccccaaa 878
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QY 765 CCCACGTCGCCAGCACTGAACCTCTGGGGGACCGTCAGTCTCTTCCGCCCAAA 824
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Db 879 acccaagacacccctcatgatctcccgagccctgaggtcacatgggtgtgtggaacgc 938
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QY 825 ACCAAGGACACCTCATGATCTCCGGGACCCCTGAGGTCATGCGTGGTGGACGT 884
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Db 939 gaccacgaagacccctgaggtcaagttcaactggtacgtgagccggtggaagtgataa 998
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QY 885 GAGCCACGAAGACCTGAGGTCAAGTTCAACTGTGTAGCTGGACGGCTGGAGTGCATTA 944
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Db 999 tgcaagaaaaagccgaggagagcagttacaacagcacgtaccgtgtgtgagcgtctct 1058
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QY 945 TGGCAGAGCAAAAGCCCGCGGAGGAGCAGTACACAGCAGTACCGCTGTGTGTCAGCGTCT 1004
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Db 1059 caccgtctgcacagagtggtggtgaatgcaagagtagacaagtgaaggtctcaacaa 1118
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QY 1005 CACCGTCTGCACAGAGCTGGTGAATGGCAAGGAGTACAAGTGCAGAGTCTCAACAA 1064
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Db 1119 agccctccagcccccatcgagaaaaccatctccaaagccaaaggaaccccgagaacc 1178
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QY 1125 ACAGGTGTACAGCTGCCCCATCCCGGATCCCGGATGAGCTGACCAAGAAACAGGTGAC 1184
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Db 1239 ctgctgtgcaaaaggtctctccccagagacatgcgctggagtggaagagaatggca 1298
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QY 1185 CTGCTGTCAAGGCTTCTATCCAGCCACATCCCGGTGAGTGGAGAGCATGGGCA 1244
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Db 1299 gccggagaaacact acaagacacgctcccggtgctggactccgacggtctcttctct 1358
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QY 1245 GCGGAGAAACACTACAAGACCAAGCTCCGCTCTGGACTCCGACGGCTCTCTTCTCT 1304
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Db 1359 ctacagaagctcacgtggacaagagagtggtgacagaggggaacgtctctcatgctc 1418
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QY 1305 CTACAGCAAGCTCACGCTGGCAAGAGCAGGTGGCAGCAGGGGAAACGTCTTCTCATCTC 1364
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Db 1419 cgtgatgatgaggtctgcacaaacctacacgagagaagacctctccctgtctccggg 1478
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QY 1365 GGTGATGATGAGGCTCTGCACAAACCACTACACGCAAGAGGCTCTGCCCTCTCTCGGG 1424
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Db 1479 taaatga 1485
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QY 1425 TAAATGA 1431
|||||

RESULT 14

ID Q65628 standard; DNA; 8540 BP.

AC Q65628;

DT 01-FEB-1995 (first entry)

DE Vector contg. TCAE 8 DNA.

KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;

KW cell lysis; as.

OS Homo sapiens.

PN W09411026-A.

PD 26-MAY-1994.

PF 12-NOV-1993; U10953.

PR 13-NOV-1992; US-978891.

PR 03-NOV-1993; US-149099.

PA (IDEC-) IDEC PHARM CORP.

PI Anderson DR, Hanna N, Leonard JE, Newman RA, Raetletter WH;

PI Refime;

DR WPI; 94-183162/22.

PT Treating B cell lymphoma with chimeric antibody - against CD20,

PT causing rapid depletion of peripheral B cells, also new

PT antibodies and hybridomas

PS Disclosure; Fig 2; 101pp; English.

CC The sequence shows a vector contg. TCAE8, a gene encoding a chimeric

CC anti-CD20 antibody for treatment of B cell lymphomas. TCAE8

CC contains 4 transcriptional cassettes, human Ig light and heavy chain

CC constant regions, dihydrofolate reductase and neomycin

CC phosphotransferase. The vector can be used to produce antibodies

CC which cause depletion of peripheral blood B cells, including those

CC associated with lymphoma. They mediate complement-dependent lysis

CC and lyse target cells by antibody-dependent cellular cytotoxicity.

CC See also Q65629-35.

SQ Sequence 8540 BP; 2069 A; 2221 C; 2226 G; 2023 T;

Query Match 69.0%; Score 987; DB 11; Length 8540;

Best Local Similarity 99.7%; Pred. No. 0.00e+00;

Matches 990; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 2152 gctagacacaaagggcccatcggtcttccccctggcaccctctccaagagacacctggg 2211
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QY 439 GCTAGACCAAGGGCCATCGCTTCCCGCTGGCACCTCTCTCAAGAGACCTCTGGG 498
|||||

Db 2212 ggcacagcgccctgggtgctggtcaaggaactctccccgaacccgtgacgtgtcg 2271
|||||

QY 499 GGCACAGCGGCCCTGGGCTGGCTGCTCAAGACACTACTTCCCGAACCGGTGAGGTG 558
|||||

Db 2272 tggaaactcagcgccctgacagcggtgcacaccttcccggctgtcctacagtcctca 2331
|||||

QY 559 TGGAACTCAGAGCGCGCTGACAGCGCGTGACACCTTCCGGGCTGCTACAGTCTCA 618
|||||

Db 2332 ggaactctactccctcagcaggtgtggtgacctgacctccagcagcttcggcaccagacc 2391
|||||

QY 619 GGACTCTACTCCCTCAGCAGCGCTGCTGACCTGCTCCAGCAGCTTGGGCAACCCAG 678
|||||

Db 2392 tacatctgcaagtgatcaacaagccacgacacacacaaaggtggacaagaagcagagccc 2451
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QY 679 TACATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGCAAGAAAGCAGAGCC 738
|||||

Db 2452 aaatcttggacaaaactcacatgccaccgtgcccagcactgaactcctgggggga 2511
|||||

QY 739 AAATCTTGTGCAAAACTCACATGCCACCGTGGCCAGCAGCTGAATCTCTGGGGGA 798
|||||

Db 2512 ccgtcagttcttctcttcccccaaaacccaaggaacacctgatctccccgacccct 2571
|||||

QY 799 CCGTCAGTCTTCTCTTCCCGCCCAAAACCCAGGACACCTCATGATCTCCCGACCCCT 858
|||||

Db 2572 gaggtcacatcggtggtggaactgagccacgaagaccctgaggtcaagttcaactgg 2631
|||||

QY 859 GAGTCACATGCTGCTGGTGGAGCTGAGCGTACGACCAAGACCCCTGAGGTCAAGTTCACTG 918
|||||

Db 2632 taogtggacgggtgaggtgcataatgccaaagaacgcgcggggagagcagtaaac 2691
|||||

QY 919 TACGTGGAGCGGCTGGAGGTGCATATATGCAAGACAAACCGCGGGAGGAGCAGTACAAC 978
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Db 2692 agcagctaccgtgtggtcagcgtctcaccgtctgcaaccagagactggtggaatggcaag 2751
|||||

Qy 979 AGCAGCTACCTGTGTGCTAGGCTCTCACCGCTCTGACACGAGCTGGCTGAATGGCAAG 1038
Db 2752 gactacaagtgaaggtctccaacaagccctccagcccccatcgaaaaaccatctcc 2811
Qy 1039 GAGTACAGTGCAGAGTCTCCACAAAGCCCTCCAGCCCCCATCGAAGAACCATCTCC 1098
Db 2812 aaagccaaagggcagcccgagaaacacaggtgtacacccctgcccccatcccgagatgag 2871
Qy 1099 AAAGCCAAAGGGCAGCCCGAGAACACAGGTGTACACCTGCCCCCATCCCGGGATGAG 1158
Db 2872 ctgaccagaacacaggtcagctgacctgctggtcaaggtctctatcccaaggaatc 2931
Qy 1159 CTGACCAAGAACCGCTCAGCTGACCTGCCTGCTCAAGGCTTCTATCCAGGCACATC 1218
Db 2932 gccgtggagtggagagcaatgggcagccggagagacaactacaagaccacgctccgtg 2991
Qy 1219 GCCGTGGAGTGGAGAGCAATGGCGAGCGGAGACACTACAGACACGCGCTCCCGTG 1278
Db 2992 ctgactccagcgctcctctctctctacagcaagctcacccgtggagagagcaggtgg 3051
Qy 1279 CTGGACTCCGACGGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAGACAGGTGG 1338
Db 3052 cagcaggggaacgtctctcatgctccgtgatgatgaggtcttgacacaccactacag 3111
Qy 1339 CAGCAGGGGAACGCTCTCTCATGCTCCGTGATGATGAGGGCTCTGCAACACCACTACAG 1398
Db 3112 cagaagagctctcctgtctccgggtaaatga 3144
Qy 1399 CAGCAGAGCTCTCCCTGCTCTCCGGTAAATGA 1431

RESULT 15

ID Q25692 standard; cDNA; 1412 BP.

AC Q25692;

DE 28-DEC-1992 (first entry)

KW Sequence of the chimeric H chain cDNA contained in pTB1373

KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;

KW antithrombotic agent; myocardial infarction therapy; ss.

OS Synthetic.

FH Key Location/Qualifiers

FT sig peptide 13..69

FT /*tag= a

FT /product= Leader

FT CDS 70..414

FT /*tag= b

FT /product= VH

FT CDS 415..708

FT /*tag= c

FT /product= CH1

FT CDS 709..753

FT /*tag= d

FT /product= hinge

FT CDS 754..1083

FT /*tag= e

FT /product= CH2

FT CDS 1084..1407

FT /*tag= f

FT /product= CH3

FN EP-491351-A.

PD 24-JUN-1992.

PF 17-DEC-1991; 121591.

PR 18-DEC-1990; JP-413829.

PR 11-NOV-1991; JP-294464.

PA (TAKE) TAKEDA CHEM IND LTD.
PI Iwasa S, Taka H, Matanabe T, Tada H;
DR WPI; 92-209528/26.
DR P-PSDB; R24812.
PT Chimeric monoclonal antibodies - contain anti-human fibrin
PT antibody light and heavy chain variable and constant for treating
PT thrombotic conditions e.g. myocardial infarction
PS Example; Figure 11; 87pp; English.
CC Plasmid pTB1373 contains the whole length of a mouse-human
CC chimeric anti-human fibrin heavy chain cDNA open reading
CC frame. It was prep'd. using Poly(A)+ RNA from the anti-fibrin
CC chimeric Ab-producing transformant FIB1-H01/X63 as a template
CC to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as
CC a primer for first strand cDNA synthesis and the 5'C2H and 3'EH
CC primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding
CC cDNA was amplified. Similarly a human gamma-1 chain CH1 domain
CC encoding cDNA and an anti-fibrin antibody VH cDNA and a leader
CC peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'CIH
CC respectively as a primer for first strand cDNA synthesis and the
CC primer combination of 5'CIH and 3'C2H, of 5'LIH and 3'CIH and of
CC 5'SH and 3'LIH respectively as primers for PCR. The amplified gene
CC products were isolated and used to produce plasmids. After
CC confirmation of the cDNA sequence of each plasmid, the cDNA
CC encoding LH, VH, CH1 and CH2CH3 were joined together to give
CC plasmid pTB1373 contg. the whole length chimeric H chain
CC (LH, VH, CH1, CH2CH3), also abbreviated as IgH-F1B,
SQ Sequence 1412 BP; 325 A; 433 C; 381 G; 273 T;

Query Match 68.7%; Score 983; DB 4; Length 1412;
Best Local Similarity 97.9%; Pred. No. 0.00e+00;
Matches 1005; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Db 381 ctggggccaaggaccctgtgctcaccgtctcaggtctagcaccaggccctcggtctt 440

Qy 405 CTGGGGCCCGGGAGACCTGTGTCACCGCTCTCTCAGCTAGCACCAGGGCCCATCGGCTTT 464

Db 441 cccctctggcaccctctccaagagcactctgggggcacagcgccctggctgctggt 500

Qy 465 CCCCTCGCACCTCTCTCCAAAGACACCTCTGGGGGCACAGGGCCCTGGGCTGCCTGCT 524

Db 501 caagactactctcccgcaaccggtgacggtgtcgtggaaactcaggcgccctgaccagcg 560

Qy 525 CAAGGACTACTTCCCGGAACCGGTGACGGTGTCTGGAACTCAGGGCCCTGACGACGG 584

Db 561 cgtgcacacttcccggtgtctacagtcctcaggactctactccctcagcagctggt 620

Qy 585 CGTGCACACTTCCCGGCTCTCTACAGTCTCTCAGGACTCTACTCTCCCTCAGCAGGCTGT 644

Db 621 gaccgtgccctccagcagcttgggcacccagacctacatctgcacgctgaatcacaagcc 680

Qy 645 GACCGTGCCCTCCAGCAGCGCTTGGGACCCACGACCTACATCTGCACGCTGAATCAAGCC 704

Db 681 cagcaacaccaaggtggacaagagagtgagcccaaatcttgtgacaaaactcacagtg 740

Qy 705 CAGCAACACCAAGGTGGACAAAGAAACAGAGCCCAAAATCTTGTGACAAAATCACATG 764

Db 741 tcaacgctgcccggtcgaactcctcctggggggaccgtcagctctctctctcccccaaa 800

Qy 765 CCCAGCGTCCCGACGACCTCTCCAGTCTCTGGGGGACCGTCACTCTCTCTCCGCCCAA 824

Db 801 acccaaggacacctcatgatctcccgagccctcaggtcacatgcgtggtggtggagct 860

Qy 825 ACCCAGGAGACCCCTCATCTCTCCGGGACCCCTGAGGTACATGCGTGTGTGTGGACGT 884

Db' 861 gaccacgaagaccctgaggtcaagttcaactggtacgtgacggcgtgaggtgcataa 920
|||||
QY 885 GAGCCACGAAGACCCCTGAGGTCGAAGTCAAGTGGTACGTGGACGGCGTGGAGTGCATAA 944

Db 921 tgccaagacaaagccgcggaggagcagtgacaacagcacgtaccgtgtggtcagcgtcct 980
|||||
QY 945 TGCCAAGACAAAGCCGCGGAGGAGGACGTACAAACAGCAGTACCGTGTGTCAGCGTCCT 1004

Db 981 caccgtcctgcaccaggactggtgaaatggcaaggagtacaagtgaaggtctccaacaa 1040
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QY 1005 CACCGTCTCGACCCAGGACTGGCTGGAATGGCAAGGAGTACAAGTGCAAGGTCTCCACAA 1064

Db 1041 agccctccagcccccatcgagaaaccatctccaaagccaaaggcgagccccgagaacc 1100
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QY 1065 AGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAGCCAAAGGGAGGCCGCCGAGAAC 1124

Db 1101 acaggtgtacacccctgcccccatccggaggagagatgaccaagaaccaggtcagcctgac 1160
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QY 1125 ACAGGTGTACACCCCTGCCCCCATCCCGGGATGAGCTACCAAGAAACAGGTCAGCCTGAC 1184

Db 1161 ctgcctggtcaaggtttctatcccagcgacatcgccgtggagtgaggagacaatgggca 1220
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QY 1185 CTGCTGTCAAGGCTTCTATCCAGCCACATCGCCGTGGAGTGGGAGAGCAATGGGCA 1244

Db 1221 gccgagagaacaactacaagaccacgctcccggtgctggactccgaoggtcctcttct 1280
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QY 1245 GCCGAGAGACAACCTACAAGACACGGCTCCCGTGTGGACTCCGACGGGTCTTCTTCT 1304

Db 1281 ctatagaagctcacccgtggacaagcaggtggcagcagggggaacgtctctcatgctc 1340
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QY 1305 CTACAGCAAGCTCACCGTGGACAGAGAGGTTGGCAGCAGGGGAACGTCTTCTCATGCTC 1364

Db 1341 cgtgatcatgaggtctctgcacaaccactacacgcagagagacctctccctgtccccggg 1400
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QY 1365 CGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAGAGCCCTCTCCCTGTCTCCGGG 1424

Db 1401 taaatga 1407
|||||
QY 1425 TAAATGA 1431

Search completed: Tue Dec 17 21:28:27 1996
Job time : 125 secs.

Dec 17 21:23

US-08-487-550-3.rst

1

AVAILABILITY (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 21:28:50 1996; MasPar time 514.89 Seconds
999.205 Million cell updates/sec

Tabular output not generated.

Title: >US-08-487-550-3

Description: (1-1431) from US08487550.seq

Perfect Score: 1431

N.A. Sequence: 1 ATCAACACCTGTGGTCTT.....CCCTGTCCGGGTAATGA 1431
Comp: TACTTTGTGACACCAAGAA.....GGACACAGGCCCAATTACT

Scoring table:

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 514334 seqs, 179763086 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

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LOCUS	H00346	468 bp	mRNA	EST	19-JUN-1995				
DEFINITION	YJ23C05.r1 Homo sapiens cDNA clone 149576 5' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);.								
ACCESSION	H00346								
KEYWORDS	g863279								
SOURCE	EST.								
human clone=149576 library=Soares placenta Nb2HP vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13Rp1 Rsite1=Not I Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(GT) primer [5' AACTCGAAGAAATCCGCCGCGAGGATTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. .									
ORGANISM	Homo sapiens								
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 468)									
REFERENCE	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Travaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.								
AUTHORS	The WashU-Merck EST Project								
TITLE	Unpublished (1995)								
JOURNAL									

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 272
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

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NCBI gi: 863279
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Matches 440; Conservative 0; Mismatches 24; Indels 4; Gaps 4;

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RESULT	2	384 bp	mRNA	EST	18-SEP-1995
LOCUS	YU3605.r1				
DEFINITION	Homo sapiens CDNA clone 235928 5' similar to gb:M8789 IG GAMMA-1 CHAIN C REGION (HUMAN);.				

NID
KEYWORDS

992191
EST.
clone=235928 primer=M13RP1 library=Soares ovary tumor NbHOT vector=pTTT3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Roitel=Not I Roite2=Eco RI Female, 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACCAATCTCAAGTCGGAGCGGCGGGTTTTTTTTTTT 3', double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTT3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens

1 (bases 1 to 384)

REFERENCE

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.

TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	<p>Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 304 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL ; contact the</p>

IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 992191
FEATURES
Location/Qualifiers
1..384
source

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ORIGIN			64 t
			5 others

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[illegible]

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RESULT	3	T93165	415	h0	MBNA	EST	22 MAR-1005
LOOTS							

DEFINITION
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ACCESSION T93165
NID c725079

KEYWORDS EST. SOURCE human clone-118668 library-Stratagene lung (#937210) vector=pBluescript SK- host=SOLR cells (kanamycin resistant)

[illegible]

ORGANISM	Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia	
Eutheria; Primates; Catarrhini; Hominoidea; Homo.	

AUTHORS
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

TITLE
JOURNAL
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,
Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
WashU-Merck EST Project
Unpublished (1995)

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 9501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
 High quality sequence stops: 299
 Source: IMAGE Consortium, LINL
 This clone is available royalty-free through LINL ; contact the
 IMAGE Consortium (info@image.linnl.gov) for further information.

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Db 181 ggcgtagggtgcataatgccaaagacaaagccgaggagggagcagtagcacacgacgtac 240
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Ov 928 ggctggaggtgcataatgccaaacaaagccgaggagggagcagtagcacacgtac 987
|||||

Db 241 cgtgtggtcagcgtcctcaccgtcctgcaccagggaacttgacctgaatggcaaggagtagc 300
|||||
988 CCTGTGGTCAGCTCTTCACTCTCTGACCAAGG-ACT-GGCT-GAATGCCAAGGCACTAC 1044
|||||

Db 301 agttgcaggtcttcaacaagccctcccaggcccccttcgaaggaaaccatctcca 360
||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Ou 1045 acgtcgacgctttcacaacagccctccaccatccca--gaaacattctcca 1099

Db 361 agccaaaggcagcccgaggaaccacag 390
|||||
Ou 1100 agccaaagcccgaggaaccacag 1128

RESULT	4	502750	494 b2	rDNA	EST	14-ITN-1095
LOCUS						

DEF-IN11110N	Y125C07.11 Homo sapiens CUNA crone 1497123 similar to gp:n81
ACCESSION	IG GAMMA-1 CHAIN C REGION (HUMAN); R82750

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NID 9862141
 KEYWORDS EST.
 SOURCE human clone-149772 library-Soares placenta Nb2HP vector-p7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RPI Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5']
 AACTGGAGAAATTCGGCGCGCAGGAATTTTTTTTTTTTTTTT 3', double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
 Homo sapiens
 ORGANISM
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 484)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
 TITLE
 The WashU-Merck EST Project
 JOURNAL
 Unpublished (1995)
 COMMENT

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 290
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 862141
 Location/Qualifiers
 source 1..484
 /organism="Homo sapiens"
 /clone="149772"
 /note="human"
 BASE COUNT 122 a 143 c 129 g 88 t 2 others
 ORIGIN
 Query Match 21.7%; Score 310; DB 69; Length 484;
 Best Local Similarity 91.9%; Pred. No. 0.00e+00;
 Matches 442; Conservative 0; Mismatches 20; Indels 19; Gaps 19;

Db 1 cacaagccagcaacacgaagtgagagagtgagcccaaatcttgacaaaact 60
 |||||
 Qy 697 CACAAGCCCAACACACCAAGGTGAGGAAGACGAGCCCAATTTGTGACAAAAC 756
 Db 61 cacacatcccacgtgccagacactgaactcctgggggacgcgtcagcttctcttc 120
 |||||
 Qy 757 CACACATCCCAACCCGTCGCCAGCACCTGAATCTCTGGGGGACCGTCAGTCTCCTTC 816
 Db 121 cccccaaacccaaggaacacctgatctcccgagcccttgaggtcacatgggtg 180
 |||||
 Qy 817 CCCCCAAACCAAGCAGACACCTCATGATCTCCGGGACCCCTGAGGTCACATGGCGTGC 876
 Db 181 gtggacgtgagccacgaagacccctgaggtcaagttcaactggtacgtggacggtggag 240

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8

Qy 877 GTGCAGCTGAGCCAGCAACCCCTGAGCTCAAGTTCAGTGTGAGCGCGTGAG 936
 |||||
 Db 241 gtgcataatgccaaagccgagagagcagtcacacagcagcagtcacgtgtgtgt 300
 |||||
 Qy 937 GTGCATAATGCCAAGCAAAAGCCGCGGAGGAGCAGTACACAGCAGCAGTACCGTGTGT- 995
 |||||
 Db 301 cagcgtctccacgttctctgcacagcagattgggttgatgggcaaggaggtacaagt 360
 |||||
 Qy 996 CAGCGT-CCTCACCCT-CCTG-CACCAGGACTGGCT-GAATGG-CAAGG-AGT-ACAAGT 1048
 |||||
 Db 361 tgaagtgattcccaaaagccttccagggcccttttttagaagaaaccttttccaaa 420
 |||||
 Qy 1049 -GCAAGGTCT-CCAACAAAGCCCT-CCAG-CCCCCATCG-AG-AAAACCATCT-CCAAA 1101
 |||||
 Db 421 gccaaagggcagcccccagagacacacagtcgttacaacttggtcccttcccggagga 480
 |||||
 Qy 1102 GCCAAGGG-CAG-CCCCGAG-AACCACAGGTGTACACCTGCCCCAT-CCCGGGATGA 1157
 |||||
 Db 481 g 481
 Qy 1158 g 1158

RESULT 5
 LOCUS H67250 364 bp mRNA EST 27-OCT-1995
 DEFINITION yu65h03.r1 Homo sapiens cDNA clone 238709 5' similar to gb:H87789
 IG GAMMA-1 CHAIN C REGION (HUMAN);
 ACCESSION H67250
 NID gi1025990
 KEYWORDS EST.
 SOURCE

human clone=238709 primer=M13RPI library=Weizmann Olfactory Epithelium vector=pBluescript SK- host=SO1R cells (kanamycin resistant) Rsite1=EcoRI Rsite2=XhoI From 35 year old female. The cDNA was oligo (dT) primed with an XhoI restriction enzyme recognition site and an 18 base poly dT sequence. For the 5' end, the synthesized cDNA termini were treated with T4 DNA polymerase and EcoRI adaptors were ligated to the blunt ends.

ORGANISM Homo sapiens
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 364)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
 TITLE WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 241
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 1025990

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[5' TGTTACCAATCGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 363)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality.

NCBI gi: 927913

Location/Qualifiers

1..363

/organism="Homo sapiens"

/clone="187156"

/note="human"

BASE COUNT 54 a 99 c 115 g 82 t 13 others

ORIGIN

Query Match 20.6%; Score 295; DB 69; Length 363;
Best Local Similarity 92.3%; Pred. No. 0.00e+00;
Matches 308; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Db 31 tcattaccgggagacaggagagctcttctggtgtagttgtgagagcctcatg 90

Cp 1431 TCATTATCCGGACACAGAGGAGGCTCTTCGCGCTGCTAGTGGTTCGACAGCCTCATG 1372

Db 91 catcaggagcatgagaagcgtccctgctgccaactgctcttctgtccacggtgagctt 150

Cp 1371 CATCAGGAGCATGAGAGCTTCCTCCCTGCTGCGACCTCTCTTGTGCGACGCTGAGCTT 1312

Db 151 nctatagagaagaagagcctcgggtccacagcagcgagcggtggtctttagttgtt 210

Cp 1311 CCTGTAGAGGAAGAAGAGCGCTCGGAGTCCACACGGAGCGGCTGTGTGTTGTTT 1252

Db 211 ctccgctgccattgctctcccactccacggcgatgtcgctgggatatagagcctttgac 270

Cp 1251 CTCGGCTGCCCATGTCTCCACTCCAGCGCATGTCTGCTGGGATAGAGCCTTTGAC 1192

Db 271 cagggaggtcaggctnaccgggntcttgggcanetcccccnnggatgggggcaagggttna 330

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Cp 1191 CAGGCAGGTGAGCTGACCTGGTCTTGGTCAGCTATCCCGGATGGGGCAGGCTGA 1132

Db 331 cacccttggttttcnqggtmnccttgcctt 363

Cp 1131 CACCTGTGTTCTCGGGGCTGCCCTTTGGGCTTT 1099

RESULT

8

LOCUS

H62381

473 bp

mRNA

EST

06-OCT-1995

DEFINITION

IG GAMMA-1 CHAIN C REGION (HUMAN);

ACCESSION

H62381

NID

g1015213

KEYWORDS

EST.

SOURCE

clone=236330 primer=Promega -2ml3 library=Soares ovary tumor

NbHOT vector=pT7T3D (Pharmacia) with a modified polylinker

host=DH10B (ampicillin resistant) Reitel=Not I Rsite2=Eco RI

Female. 1st strand cDNA was primed with a Not I - oligo(dT) primer

[5' TGTTACCAATCTGAAGTGGAGCGCGGCTTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I and Eco

RI sites of a modified pT7T3 vector (Pharmacia). Library

constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 473)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and

Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 284

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LML; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 1015213

Location/Qualifiers

1..473

/organism="Homo sapiens"

/clone="236330"

<1..>473

BASE COUNT 77 a 114 c 158 g 116 t 8 others

ORIGIN

Query Match 20.0%; Score 286; DB 22; Length 473;

Best Local Similarity 91.0%; Pred. No. 0.00e+00;

Matches 332; Conservative 0; Mismatches 29; Indels 4; Gaps 4;

Db 100 tcattaccggagacaggagagctcttctgtgtagttgtgagagcctcatg 159

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Cp 1431 TCATTTACCCGACGACGAGGAGGCTTCTTCGCGTGTAGTGGTTGTCGACAGCCTCATG 1372
|||||
Db 160 catcaggagcatgagaacggtccctctgctgccacctgctcttctgcccacggtgagctt 219
|||||
Cp 1371 CATCAGGAGCATGAGAGACGTTCCCTGCTGCGCACCTGCTCTTGTGCGACGGTGAGCTT 1312
|||||
Db 220 gctgtagaggaagagccgctcgagtcacagcatggaggtggtcttctgtagttt 279
|||||
Cp 1311 GCTGTAGAGGAGAGAGCGCTCGGAGTCCAGACGCGGAGCGGTGGTCTGTAGTGTCT 1252
|||||
Db 280 ctccggtcccatgctctccactccagggcgagtgctgctgggtgagagcctttna 339
|||||
Cp 1251 CTCGGCTGCCATGCTCTCCACTCCACGG-CGATGTCGCTGGATAGACGCTTTGA 1193
|||||
Db 340 ccaggaggtcaggtgancgttcttctggtcatctctcccgaggtggtggcgaggt 399
|||||
Cp 1192 CCAGGAGGTGAGTCACTGG-TTCTTGTGACGCTCATCCCGGATGGGGCGAGGTG 1134
|||||
Db 400 taaaccgtngtctcggtgtgcttngt-ttngaaangtttt-tcgtatgggntt 457
|||||
Cp 1133 TACACTGTGTCTCGGGGTGCGCTTTGGCTTTGGAGATGTTTCTCATGGGGCT 1074
|||||
Db 458 ggaag 462
|| ||
Cp 1073 GCGAG 1069

RESULT 9
LOCUS R66507 358 bp mRNA EST 30-MAY-1995
DEFINITION y132f05.r1 Homo sapiens cDNA clone 140961 5' similar to gb:M87789
IG GAMMA-1 CHAIN C REGION (HUMAN);
ACCESSION R66507
NID g839145
KEYWORDS EST.
SOURCE human clones=140961 library=Soares placenta NB2HP vector=pT7T3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta
obtained at birth (full term). 1st strand cDNA was primed with a
Not I - oligo(dT) primer [5']
AACTGGAGAAATCCCGCGCGAGGATTTTTTTTTTTTTTTT 3', double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified pT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 358)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F.,
Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE

The WashU-Merck EST Project
Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

Dec 17 21:23

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14

Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 219
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 839145

FEATURES
source Location/Qualifiers
1..358
/organism="Homo sapiens"
/clone="140961"
/note="human"

BASE COUNT 90 a 109 c 92 g 63 t 4 others
ORIGIN

Query Match 19.9%; Score 285; DB 64; Length 358;
Best Local Similarity 97.8%; Pred. No. 0.00e+00;
Matches 310; Conservative 0; Mismatches 3; Indels 4; Gaps 4;
Db 2 acaagtccaaggtctccaacaagccctccagcccccatcgagaaacacattctccaaag 61
|||||
Qy 1043 ACAAGTCAAGGTCTCCACAAGCCCTCCAGCCCCCATCCAGAAACCATCTCCAAG 1102
|||||
Db 62 ccaaggagggcccgagaaacacaggtgtacacctgcccccatccccgggatgagctga 121
|||||
Qy 1103 CCAAGAGGCGAGCCCGAGAACCAAGGTGTACACCTGCCGCCATCCGGGATGAGCTGA 1162
|||||
Db 122 ccaagaaccaggtcagctgacctgctggtcaaaaggcttctatccccagcgacatcgcg 181
|||||
Qy 1163 CCAGAACACAGGTGAGCTGACCTGCTGCTCAAGGCTTCTATCCAGCGACATCGCGG 1222
|||||
Db 182 tggagtggagagcaatggcgagccgagagacaactacaagaccagcctcccggtgctgg 241
|||||
Qy 1223 TGGAGTGGGAGAGCAATGGCGAGCCGAGAACAACTACAAGACACCGCTCCCGTCTGG 1282
|||||
Db 242 gattccagagctcttctctcttcttaccagagtcacccgtgggacagagcaggtgg 301
|||||
Qy 1283 -ACTCCAGCGGCTCTCTTCTCTCT-ACAGCAAGCTCACCGCTGG-ACAAGAGAGGT-GG 1338
|||||
Db 302 cagcaggggaagcgtntt 318
|||||
Qy 1339 CAGCAGGGGAGCGTCTT 1355
|||||

RESULT 10

LOCUS H28084 421 bp mRNA EST 13-JUL-1995
DEFINITION y156d10.s1 Homo sapiens cDNA clone 162259 3' similar to gb:M87789
IG GAMMA-1 CHAIN C REGION (HUMAN);

ACCESSION

H28084
g98437

NID

g98437

KEYWORDS

EST.

SOURCE

human clone=162259 library=Soares breast 3NBH8st vector=pT7T3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=Promega -21ml3 Rsite1=Not I Rsite2=Eco RI Adult
human. 1st strand cDNA was primed with a Not I - oligo(dT) primer
[5'] TGTACCAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTT 3',
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT7T3 vector (Pharmacia). Library went through one round
of normalization to a Cot = 20. Library constructed by Bento Soares
and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

317 ctccggctgccattgctctcccantccacggcgatntcgctgggatagaagcctttgac 376
1251 CTCGGCTGCCATTGCTCTCCCACTCAACGGCCGATGCTCGTGGGATAGAGCCTTTGAC 11928

Db 377 caggcagtcagctgactggtcttctgtcagctcatcccggtatggggcagggt 434
|||||
Cp 1191 CAGGAGGTGAGGTCACCTGG-TTCTTGGTCAGCTCATCCGGGATGGGGCAGGCT 1135
|||||

RESULT 12
LOCUS T65937 436 bp mRNA EST 20-FEB-1995
DEFINITION yc24f06.s1 Homo sapiens cDNA clone 81635 3' similar to gb:M87789 IG
GAMMA-1 CHAIN C REGION (HUMAN);
ACCESSION T65937
NID 9674982
KEYWORDS EST.
SOURCE human clone=81635 library=Stratagene lung (#937210)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=21ml3 Rsite1-EcoRI Rsite2-XhoI Normal lung tissue from a 72
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCCGCACGAG-3'; 3' adaptor sequence:
5'-CTCGAGTTTTTTTTTTTTTTT-3'.
Homo sapiens
ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 436)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLE WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 241
Source: IMAGE Consortium, L1NL
This clone is available royalty-free through L1NL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 674982
FEATURES
source
Location/Qualifiers
1..436
/organism="Homo sapiens"
/clone="81635"
/note="human"
BASE COUNT 74 a 113 c 140 g 104 t 5 others
ORIGIN
Query Match 19.2%; Score 275; DB 99; Length 436;
Best Local Similarity 94.2%; Pred. No. 0.00e+00;
Matches 310; Conservative 0; Mismatches 15; Indels 4; Gaps 4;
Db 112 tttcccgagacaggagagctcttctgctgtagtgtgtgcaganc-tcatgcac 170
|||
Cp 1427 TTACCCGAGACAGGAGGAGGCTTTCTCGCTGTACTGTGTGCAGAGCCTCATGCATC 1368
|||||
Db 171 acggagcatgagagacgttccctctgctgccacctgctcttgtccacggtgagctt-ctg 229
|||||
Cp 1367 ACGGAGCATGAGAGAGAC-CTTCCCTGCTGCCACCTGCTCTTGTCTCCAGGTCAGCTTCTG 1308
|||||
Db 230 tagaggaagaaggagcctcgcggagtcacgacggaggcgtggtctttagttgtctcc 289

Cp 1307 TAGAGGAGAGGAGCGCTCGAGTCCAGCGGAGCGGCTGTGTGTAGTGTCTCC 1248
|||||
Db 290 ggtgcccactgtctcccacttcaacgcatcgcctgggataagaagc-ttnaccagg 348
|||||
Cp 1247 GCGTGGCCCATTCCTCTCCACCATCCACGGCGATGTCGCTGGGATAGAGCCCTTGACCA 1188
|||||
Db 349 nagtgaagctgactgggtctctgttaa-ctcatcccccgatggggcgaagtataaac 407
|||||
Cp 1187 CAGTCAAGCTCACTGGTCTTGGTCAGCTCATCCGGGATGGGGCAGGCTGTACAC 1128
|||||
Db 408 tgtggtctcgggctccctcttggcttt 436
|||||
Cp 1127 TGTGTTCTCGGGGCTGCCCTTTGGCTTT 1099
|||||

RESULT 13
LOCUS T65912 479 bp mRNA EST 20-FEB-1995
DEFINITION ycl1h01.r1 Homo sapiens cDNA clone 80401 5' similar to gb:M87789 IG
GAMMA-1 CHAIN C REGION (HUMAN);
ACCESSION T65912
NID 9674957
KEYWORDS EST.
SOURCE human clone=80401 library=Stratagene lung (#937210)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=M13RP1 Rsite1-EcoRI Rsite2=XhoI Normal lung tissue from a 72
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCAGAG-3'; 3' adaptor sequence:
5'-CTCGAGTTTTTTTTTTTTTTT-3'.
Homo sapiens
ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 479)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLE WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 273
Source: IMAGE Consortium, L1NL
This clone is available royalty-free through L1NL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 674957
FEATURES
source
Location/Qualifiers
1..479
/organism="Homo sapiens"
/clone="80401"
/note="human"
BASE COUNT 104 a 140 c 130 g 98 t 7 others
ORIGIN
Query Match 19.1%; Score 273; DB 99; Length 479;
Best Local Similarity 96.7%; Pred. No. 0.00e+00;

Matches 323; Conservative 0; Mismatches 3; Indels 8; Gaps 8;

Db 1 cagcccccacgagaaacaccatctcaagcaaaagcagccccgagacacaggtgt 60
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Qy 1073 CAGCCCCCATCGAAGAACCATCTCAAGCCAAAGGCGAGCCCCGAGACACAGTGT 1132
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Db 61 ataccctgcccccatcccgagatgagctgaccaagaacacaggtcagcctgacctg 120
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Qy 1133 ACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACACAGGTGACCTGCGCTGG 1192
|||||
Db 121 tcaaggtctctatccagagacatcgctggagtgaggagagcaatggcagcggaga 180
|||||
Qy 1193 TCAAGAGCTTATCCAGGACATCGCGTGGAGTGGGAGAGCAATGGCGAGCGGAGA 1252
|||||
Db 181 acaactacaagacacgcctccgctgctggactccagcagcgtctctctctacagca 240
|||||
Qy 1253 ACACCTAGACACACGCGCTCCGCTGGACTCCGAGCGGCTCTTCTCTCTACAGCA 1312
|||||
Db 241 agctcaccgtgggacaagcaggtggcgagcaggggaaacgtcttctctctgctcgt 300
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Qy 1313 AGCTCAGCTGG-ACAGACGAGCTGG-CACAGCGGAGAGCTCTT-CT-CATGCT-CCGT 1367
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Db 301 tgatcatggaggtcttgcaacacattacaag 334
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Qy 1368 -GATCATG-AGGCTCT-GCAACACCATACACG 1398
|||||

RESULT 14

LOCUS H61373 297 bp mRNA EST 06-OCT-1995
DEFINITION yu41d01.r1 Homo sapiens cDNA clone 236353 5' similar to gb:M87789
IG GAMMA-1 CHAIN C REGION (HUMAN);.

ACCESSION

H61373

NID

g1014205

KEYWORDS

EST.

SOURCE

clone=236353 primer=M13Rpl library=Soares ovary tumor NBR07
vector=pf7T3D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) Rsitel=Not I Rsite2=Eco RI Female. 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified pT73 vector (Pharmacia). Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 297)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaaskie, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, L1NL
This clone is available royalty-free through L1NL; contact the
IMAGE Consortium (info@image.l1nl.gov) for further information.
Trace considered overall poor quality.

NCBI gi: 1014205

Location/Qualifiers

1..297

/organism="Homo sapiens"

/clone="236353"

<1..>297

BASE COUNT 81 a 92 c 75 g 41 t 8 others

ORIGIN

Query Match 18.9%; Score 271; DB 22; Length 297;
Best Local Similarity 94.3%; Pred. No. 0.00e+00;
Matches 280; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Db 1 caggactngcgaatggcaaggaacaaagtgcgaagtctccaacaagaagccctccagcc 60
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Qy 1018 CAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGCTCTCCAACAAGCCCTCCAGCC 1077
|||||
Db 61 ccgatcgagaaacacatctccaaagcgaagggcgagccccgagacacacaggtgtacacc 120
|||||
Qy 1078 CCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACC 1137
|||||
Db 121 ctgccccctccggagagatgacaaagacacaggtcagcctgacctgcctgggtcaaa 180
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Qy 1138 CTGCCCCCATCCCGGATGAGCTGACCAAGAACACAGGTGAGCTGAGCTGCTGCTCAA 1197
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Db 181 ggtctctatccagcagcatcgctgagtgagagcaatggcgagcgagagcanc 240
|||||
Qy 1198 GCTTCTATCCCGCAGCATCGCGTGGAGGAGCAATGGCGAGCGGAGCAAC 1257
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Db 241 tacaagacacagctccgctgctgagctcagcagcgtctctatttactatagaag 297
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Qy 1258 TACAAGACCGAGCTCCGCTGCTGAGCTCCGAGCGGCTCTTCTCTCTACAGCAAG 1314
|||||

RESULT 15

LOCUS

T59950 418 bp mRNA EST 09-FEB-1995

DEFINITION y001g07.s1 Homo sapiens cDNA clone 79452 3' similar to gb:M87789 IG

GAMMA-1 CHAIN C REGION (HUMAN);.

ACCESSION

T59950

NID

9661787

KEYWORDS

EST.

SOURCE

human clones=79452 library=Stratagene lung (#937210)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=21m13 Rsitel=EcoRI Rsite2=XhoI Normal lung tissue from a 72
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCAGAG-3'; 3' adaptor sequence:
5'-CTCAGTTTTTTTTTTTTTTT-3'.

ORGANISM

Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 418)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaaskie, E.,
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
WashU-Merck EST Project

JOURNAL
COMMENT

Unpublished (1995)

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 339
Source: IMAGE Consortium, L1NL
This clone is available royalty-free through L1NL ; contact the
IMAGE Consortium (info@image.l1nl.gov) for further information.

NCBI gi: 661787

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/clone="79452"
/note="human"

BASE COUNT 70 a 110 c 136 g 93 t 9 others
ORIGIN

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Best Local Similarity 96.5%; Pred. No. 0.00e+00;
Matches 277; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

Db 132 tcattaccggagacagaggaggtcttctgtgtagtgttntgcagacctcatg 191
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Cp 1431 TCATTACCCCGACACGGAGAGCTCTCTCGCTGTAGTGGTTGGCAGAGCCTCATG 1372
|||||
Db 192 catcacggagcatgagaagacgttccctgctgccactgctctntccacggtgagctt 251
|||||
Cp 1371 CATCAGGAGCATGAGAGAGCTTCCCTGCTGCCACCTCTCTTGTCCACGGTGAGCTT 1312
|||||
Db 252 gctntagagaagaagagcctcggagtcacagcagggagggcgtgctctgtagtgtt 311
|||||
Cp 1311 GCTGTAGAGAGAGAGAGAGCGCTCGGAGTCCAGCAGGAGCGCTGGTCTTGTAGTTGTT 1252
|||||
Db 312 ctccgggtgccattgtctctccactccacggcgatntcgtgggataagaacctttgac 371
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Cp 1251 CTCGGCTGCCCATTGCCTCCCACTCCAGGGCGATGCTGCTGGGATAGAGCCTTTGAC 1192
|||||
Db 372 caggcaggtcaggtgacctgggtcttgggtcancctcatcccnnga 418
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Cp 1191 CAGGAGGTAGGCTGACCTGG-TTCTTGG-TCAGCTCATCCCGGA 1147
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Search completed: Tue Dec 17 21:37:35 1996
Job time : 525 secs.

BASE COUNT	212 a	208°c	183 g	140 t
ORIGIN				

Query Match 54.4%; Score 392; DB 59; Length 743;
Best Local Similarity 85.3%; Pred. No. 0.00e+00;
Matches 474; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Db 180 gacaataacttaactggtaccagcagaagccaggtaaggctccaagctgctgatctac 239
 ||||| | | | | | | | | | | | | | | | | | | | | |
Ov 163 GACAGCTTCTGATCGTGGTAFCAGCAGAAGCCAGGCCAACCTCCAAGGCTCCTGATTAT 222

240 aatacaacaatttgcaaacgggtgtgccaacgagattcagcgttagcggtagcggtagc 299
223 AAGGTTTCAACCGGGAAGCTCTGGGGTCCCAACAGATTACCGGGCACTGGGCGAGGACA 282

Db 300 gacttcaccttcaccatcagcagcctccgcccagagacatcgccacctactactgcttg 359
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Ov 283 GATTTCACACTGAATAATCAGCGCCACTGGAGCTGCACATGTTGGGTTTTATTCTGCCGG 342

Db 360 cagcatataagttaggcgcgacgttcggccaagggaaccaagtgaaatcaaacgtact 419
|| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
343 CACGCTCACCAACCGTCCTCCGCAGTCCCCCCCACCCACGACGCTCACAATGACAACTCC 402

[illegible]

Db 480 gcctctgttgtgcctgctgaataaacttctatcccagagagccaaagtacagtggag 539

Db 540 gtgataacgcccctccaatcggtgaactcccaggagagtgtcacagagcaggacagcaag 599

Db 600 gacagcacctacagcctcagcagcaccctgacgctgagcaagcagcactcagagaacac 659

Db 660 aaagtctacgcctgcgaagtcacccatcagggcctgagctgcgcctcacaaagagcttc 719

Db 720 aacaggggagagtgtt 735
|||||

xy	703	nnnnnnnnnnnnnnnn	719
RESULT	q		

LOCUS	042 bp	mRNA	FBI	19-00L-1993
DEFINITION	Homo sapiens Ig rearranged kappa L-chain (IGKV) mRNA subgroup VK-1 hybridoma, partial cds.			

KEYWORDS immunoglobulin light chain subgroup VK-I; immunoglobulin-kappa processed gene.

SOURCE	ORGANISM
homo sapiens lymphocyte cdna to mknva.	Homo sapiens
	Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
	Eutheria; Primates; Haplorhini; Catarrhini. Homiidae

REFERENCE 1 (pages 1 to 642)

AUTHORS Takeda, S., Dorfman, N.A., Robert-Guroff, M., Notkins, A.L. and Rando, R.F.

anti-human immunodeficiency virus immunoglobulin Fab domains in
Escherichia coli
Hybridoma 14 (1), 9-18 (1995)
JOURNAL
METINF 95286185

COMMENT	NCBI gi: 163926
FEATURES	Location/Qualifiers
source	1..642

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/organism="Homo sapiens"
/cell_line="hybridoma T15G1"
/cell_type="B"
/sequenced_mol="cDNA to mRNA"

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CDS
<1..>642
/issue_type= lymphocyte
/gene="IGKV"
/man="2a1?"
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/note="NCBI gi: 18592/"
/codon_start=1
/db_xref="GDB:G00-119-341"

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KLLIYKASTLESQVPSRFGSGSGTFFAL

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ESTEQDSKDSTYLSSTILSKADYEKIH	BASE COUNT	ORIGIN
166 a 186 c 161 g 129 t		

Query Match 54.2%; Score 390; DB 56; Length 642;
Best Local Similarity 86.1%; Pred. No. 0.00e+00;
Matches 465; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Db 103 tggtatcaacaaaaaacagggaagccccctaaactcctgatctataagggtctacctta 162

Qy 1/8 TGGTATCAGCAGAGCCAGGCCAACCTCCAAGGCTCCTGATTATAAGGTTTCTAACCGG 231

[illegible]

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0₉ 298 ATCAGCGCATGTGGAGGCTCAAGATGCTTGGGGTTATTTCTCGGGGCAAGGTACAGGACT 357

Db 283 tcgtccacttttggccaggggaccaaactggagatcaaaagaactgtggctgcaccatct 342

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Db 343 gtcttcattccggccatctgatgagcagttgaaatctggaactgcctctgttgtgc 402

410 GTCCTCATTCCCGGCATCTGATGAGCAGTGGAAATCTGGAACTGCCCCTGTTGTGTGTC 417

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b 463 caatcgggttaactcccaggaggaattctcacatagcaggatcagcagaagacagcacctacagc 522

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Qy 598 CTCAGCAGCACCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCTGC 657

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Dec 17 21:40

US-08-487-550-5.rge

15

Qy 658 GAAGTACCCATCAGGGCTGAGCTGCGCCCTCACAAAGCTTCACAGGCGGAGACTGT 717

RESULT 10
LOCUS A27396 4163 bp DNA PAT 23-MAY-1995
DEFINITION Template clone sequence Aab N010.12.5.
ACCESSION A27396
NID 9905200
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 4163)
AUTHORS .
TITLE METHODS FOR PRODUCING MEMBERS OF SPECIFIC BINDING PAIRS
JOURNAL Patent: WO 9220791-A 92 26-NOV-1992;

COMMENT NCBI gi: 905200
FEATURES Location/Qualifiers
source 1..4163
/organism="Artificial sequences"
BASE COUNT 1034 a 1104 c 1057 g 968 t
ORIGIN

Query Match 53.2%; Score 383; DB:36; Length 4163;
Best Local Similarity 85.3%; Pred. No. 0.00e+00;
Matches 463; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
Db 967 tgaactgtctccaaagaagtcaggcaactcccccaaaagatgattatgacacatcca 1026
Qy 173 TGAGTTGGTATACAGAGAAGCCAGCCAACTCCAAAGGCTCCTATTATAAGTTTCTA 232
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Qy 233 ACCGGGACTCTGGGCTCCACACAGATTTCAGCGCAGTGGCGCAGGACAGATTTCACAC 292
Db 1087 tcacaatcagcagcagtgaggatgagatgctgccattattactgccagcagtgagta 1146
Qy 293 TGAATAATCAGCGAGTGGAGGCTGAAGATCTTGGGCTTTATTCTCGCGGCAAGGTACAA 352
Db 1147 gtaatccactcagcttcggtgctgggacaaagctcgagatcaaacggaactgtggctgcac 1206
Qy 353 GGAATCTCTCCACTTTCCGGGAGGACCAAGTGGAAATCAAACTACGCTGGCTGCAC 412
Db 1207 cactgtcttcacttcccgccactgagcagcagtggaactctggaactgcctctgttg 1266
Qy 413 CATCTGTCTTCATCTTCCCGCCATCTGATGACAGTTGAAATCTGGAATCGCCTGTG 472
Db 1267 tgtgctgctggaataaactctatccagagagggccaaagtcacagtggaggtggataaag 1326
Qy 473 TGTGCTCTGTAATAACTTCTATCCAGAGAGGCCAAAGTACATGGAAGTGGATAAGC 532
Db 1327 cctccaatcgggttaactccccaggagtgctacagagcaggacgaagcagcaacct 1386
Qy 533 CCTCCAAATCGGTAACTCCAGGAGAGTGTACAGAGCAGGACGAAGGACAGCACT 592
Db 1387 acagcctcagcagcactgacgctgagcaagcagactacgagaacaacaagtctaac 1446
Qy 593 ACAGGCTCAGCACACCTTGACGCTGAGGAAGCAGACTAGCAGAAACACAAAGTCTAGC 652
Db 1447 cctgcgaagtccaccatcagggctgagttcgcccgctcacaagagcttcacacgcggag 1506
Qy 653 CTGCGAAGTCAACCATCAGGGCTCAGCTCGCCGCTCACAAAGCTTCAACAGGGAG 712

Dec 17 21:40

US-08-487-550-5.rge

16

Db 1507 agt 1509
Qy 713 AGT 715

RESULT 11
LOCUS A21386 945 bp RNA PAT 12-JUL-1994
DEFINITION Plasmid DNA with human cDNA insert.
ACCESSION A21386
NID g583509
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 945)
AUTHORS .
TITLE RECOMBINANT PROTEIN WHICH BINDS TO A COMPLEX VIRAL ANTIGEN OF HIV-1
JOURNAL Patent: WO 9118983-A 2 12-DEC-1991;

COMMENT NCBI gi: 583509
FEATURES Location/Qualifiers
source 1..945
/organism="Artificial sequences"
CDS 28..732
/note="NCBI gi: 583510"
/codon_start=1
/product="3D6 antibody light chain"
/db_xref="PID:g583510"
/translation="MDMRVPAQLGLLLLPKCAKDIOMTQSPSTLSASVGRVTIT
CRASQISRLAWYQKRPCKVPKLLIYKASLESQVPSRSGSGSTFTLTSSLP
DFATYQYQYNSYFSGPGTKVDIKRTVAAPSVFIPFSDQLKSGTASVWLLNNFY
PREAKVQKVDNALQSGNSQESVTEQDSKSTYSLSLTLSKADYKHRYACEVTH
QGLSSPVTKSFNRGEC"
BASE COUNT 229 a 274 c 226 g 216 t
ORIGIN

Query Match 52.6%; Score 379; DB:36; Length 945;
Best Local Similarity 87.8%; Pred. No. 0.00e+00;
Matches 475; Conservative 0; Mismatches 60; Indels 6; Gaps 3;
Db 196 tggatcagcagaacacaggaaagtcctcaagctcctgactctataagcactatagttta 255
Qy 178 TGTATACAGAGAAGCCAGGCCAACCTCCAGGCTCCTGATTTATTAAGGTTTCTAACCGG 237
Db 256 gaaagtgggtcccatcaagctcagcagcagtgagatcgggacagaatcactctcacc 315
Qy 238 GACTCTGGGGTCCACAGACAGATTTCAGCGCAGTGGGGCAGGACAGATTTCACACTCAAA 297
Db 316 atcagcagcctgagcctgagctgatttgcaacttattactgccaaca--gtataat-agt 372
Qy 298 ATCAGCGCAGTGGAGGCTGAAGATGTTGGGTTTATTCTCGGGCAAGGTACAAAGACT 357
Db 373 tatte----ttcggccctgggacaaagtgagatatacaacgaactggctgcacact 429
Qy 358 CCTCCCACTTTTCGGCGGAGGCCAAGGTGGAAATCAAACTACGCTGGCTGCACACTCT 417
Db 430 gtcttcacttcccgcactctgagcagcagtggaactggaactgcctctgtgtgtgc 489
Qy 418 GTTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTC 477
Db 490 ctgctgaataactctatcccaagagggccaaagtcacagtggaggtggataacgcctc 549
Qy 478 CTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACGTGGAAGTGGATTAAGCGCCTC 537

Db	550	caatcgggttaactccacgagagagtgtccagagcagcagcagcagcagcagcactacagc	609
Qy	538	CAATCGGTTAACTCCACGGAGAGTGTACACAGCAGCAGCAGCAAGCAGCAGCTACGC	597
Db	610	ctcagcagcaccctgacgtgagcaaaagcagactacgagaacacacaaagtctacgcctgc	669
Qy	598	CTCAGCAGCAGCCCTGACCTGACGAACGACACTACGAGAAACACAAAGCTTACGCCTGC	657
Db	670	gaagtccaccatcagggcctgagctgcgccgtcacaagaagcttcaacaggggagagtggt	729
Qy	658	GAGTCAACCATCAGGGCCTGACCTGCCCTCACAAGAGCTTCAACAGCGGAGAGTGT	717
Db	730	t 730	
Qy	718	T 718	
RESULT	12		
LOCUS	MAC1GRKVDG	499 bp mRNA	PRI 13-MAY-1994
DEFINITION	Macaca fascicularis immunoglobulin kappa light chain variable region, constant region mRNA.		
ACCESSION	L13314		
NID	g293132		
KEYWORDS	constant region; immunoglobulin kappa-chain; variable region.		
SOURCE	Macaca fascicularis cDNA to mRNA.		
ORGANISM	Macaca fascicularis		
REFERENCE	Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Cercopithecoidea; Cercopithecinae; Papionini.		
AUTHORS	Lewis, A.P., Barber, K.A., Cooper, H.J., Sims, M.J., Worden, J. and Crowe, J.S.		
TITLE	Cloning and sequence analysis of kappa and gamma cynomolgus monkey immunoglobulin cDNAs		
JOURNAL	Dev. Comp. Immunol. 17 (6), 549-560 (1993)		
MEDLINE	94131152		
COMMENT	NCBI gi: 293132		
FEATURES	Location/Qualifiers		
source	1..499		
CDS	/organism="Macaca fascicularis"		
	<1..>499		
	/note="putative; NCBI gi: 293132"		
	/codon start=1		
	/product="immunoglobulin kappa-chain"		
	/db_xref="PID:g293132"		
	/translation="QPLIYEVSNRACVDFRSGSGSDFTFIKISRVEADVGYYTC MQYTHPIFFFGTGKLDIKRAVAQSVFIFFPSEDQVKSGTGVVCLIANEYPREASV KWKVDGALKATDNRSESVTEQDSKUNFTYLSLSTFLSTSYQSHNVYACEVTHQGLGSP VKYSFN"		
BASE COUNT	129 a 136 c 127 g 107 t		
ORIGIN			
Query Match	51.8%;	Score 373;	DB 56; Length 499;
Best Local Similarity	87.5%;	Pred. No. 0.00e+00;	
Matches	435;	Conservative 0;	Mismatches 62; Indels 0; Gaps 0;
Db	3	gcccttgattatgaggtttcaacacggcctctgaggtccagacaggttcagtgccag	62
Qy	210	GCTCTGATTATAGGTTTCTAAACCGGACTCTGGGTGCCAGACAGATTTCAGCGGCAG	269
Db	63	tggttcgacactgatttcacactcaaatcacagagatggagctgagagatgttgggt	122
Qy	270	TGGGCGAGGACAGATTTTCACATGAAATCAGCGACTGGAGCGGTGAAGATCTTGGGT	329

Db	123	ttattactgcatgaataacacacattccattcacttctggcccgaggaccacaaactgga	182
Qy	330	TTATTTCTGGGCAAGGTACRAGGACTCTCCACTTTCCGGGAGGACCAAGGTGCA	389
Db	183	latcaaacagagctgtggctgcacacatctgtcttcatcttcccgcacatctgaggatcaggt	242
Qy	390	RATCAACGCTAGCTGGCTGCGACCATGTCTTCACTTCCCGCCATCTGATGAGCAGTT	449
Db	243	gaaatctgaaactgtctctgtgtgcttgcctgaataactctatccacagagagccag	302
Qy	450	GAATACTGGAACCTGCCTCTGTTGCTGCCTGCTGAATAACTTCTATCCACAGAGGCCAA	509
Db	303	cgtaaagtggaagtgagtggtgccctcaaaacggataaactcccagagagagtgacacaga	362
Qy	510	AGTACAGTGGAAAGGTGGATAAGCGCCTCCAAATCGGGTAACCTCCACGAGAGCTGTACAGA	569
Db	363	gcaggacagaagggacacacacctacagctcgagcagcagccctgacgctgagcagcacaga	422
Qy	570	GCAGCAGCAGGACAGACACTACAGCTCAGCAGACCCCTGACGCTGACGAAAGCA	629
Db	423	ctaccagagtcaaatgtctatgctgcgaggtcacccatcaggcgctgagctcgccgt	482
Qy	630	CTACGAGAACACAAAGTCTACGCCTCGGAAGTCAACCATCAGGGCCTGAGCTGCGCCGT	689
Db	483	caccaagagcttcaaga	499
Qy	690	CACMAAGAGCTTCAACA	706
RESULT	13		
LOCUS	107074	468 bp	PAT 14-NOV-1994
DEFINITION	Sequence 18 from patent EP 0314317.		
ACCESSION	107074		
NID	g590385		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 468)		
AUTHORS	Capon, D.J. and Gregory, T.J.		
TITLE	Adhesion variants, nucleic acid encoding them and compositions comprising them		
JOURNAL	Patent: EP 0314317-A1 18 03-MAY-1989;		-
COMMENT	NCBI gi: 590385		
FEATURES	Location/Qualifiers		
source	1..468		
BASE COUNT	126 a 131 c 118 g		93 t
ORIGIN			
Query Match	51.1%;	Score 368;	DB 37; Length 468;
Best Local Similarity	92.2%;	Pred. No. 0.00e+00;	
Matches	402; Conservative	0; Mismatches 34; Indels	0; Gaps 0;
Db	1	gaattcaactctcacatcatcagcgctgcagctgaagcttttgcaactttattactgccaa	60
Qy	283	GATTCACTGAAATFACGCGAGCTGGAGCTGAAGATGTTGGGGTTTATTCTCGGG	342
Db	61	cagtatagaagtttgtcgctcacttctcgcgaggagaccaggtggagatcaaacgaact	120
Qy	343	CAAGGTGTAAGGACTCTCCCACTTTTCGGCGAGGACCAAGCTGGAATCAAACTACG	402

Db 121 gtggctgcaccatctgtctctcatctcccgccatctgtgagcagttgaaatctggaact 180
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Qy 403 GTGGCTGCACCATCTGTCTTCTCTCCCGCATCTGTATGAGAGTTGAAATCTGGAAC 462
Db 181 gctctgtgtgtgctctgaaataactctatccagagagggccaaagtacagtgaag 240
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Qy 463 GCCTCTGTGTGTGCTCTCAATAACTTTCTATCCAGAGAGGCCAAAGTACAGTGAAG 522
Db 241 gtgataaacgccctccaatcgggttaactcccagagaggtgtcacagagcagcagcaag 300
|||||
Qy 523 GTGATAAACGCCCTCCAATCGGTTAACTCCAGGAGAGTGTACAGAGCAGCAGCAAG 582
Db 301 gacagcaactacagcctcagcagcaccctgacgtgagcaagcagactacagagaacac 360
|||||
Qy 583 GACAGCACTACAGCCTCAGCGACCCCTGACGCTGAGCAAGCAGACTACAGAAACAC 642
Db 361 aaagtctacgctgcgaagtcacccatcagggcctgagctgcgccgtcacaaagagcttc 420
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Qy 643 AAAGTCTACGCCCTGCGAAGTCCCATCAGGGCCTGAGCTGCGCCGTACAAAGAGCTTC 702
Db 421 aacagggaagagtggt 436
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Qy 703 AACAGGGGAGAGTGTT 718

RESULT 14
LOCUS I09304 468 bp PAT 14-NOV-1994
DEFINITION Sequence 7 from patent WO 8902922.
ACCESSION I09304
NID g587990
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 468)
AUTHORS Capon,D.J. and Gregory,T.J.
TITLE ADHESON VARIANTS
JOURNAL Patent: WO 8902922-A 7 06-APR-1989;

COMMENT NCBI gi: 587990
FEATURES
source
1..468
/organism="unknown"
BASE COUNT 126 a 131 c 118 g 93 t
ORIGIN

Query Match 51.1%; Score 368; DB 37; Length 468;
Best Local Similarity 92.2%; Pred. No. 0.00e+00;
Matches 402; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Db 1 gaattcaactctcaaccatcagcgctcagcctgaagatttgcaatttatacttgcga 60
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Qy 283 GATTTACACTGAAATCAGCGCAGTGGAGGCTCAAGATGTTGGGGTTTATTTCTCGGG 342
Db 61 cagtaagaagatttgctctcaactcttcggcgaggagccaaagtgagatcaaacgaact 120
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Qy 343 CAGGTACAGAGNCTCTCCACTTTCGGCGGAGGACCAAGGTGGAATCAACGTACC 402
Db 121 gtggctgcaccatctgtctctctctccgccatctgagcagtggaatctggaact 180
|||||
Qy 403 GTGGCTGCACCATCTGCTTCTATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAC 462
Db 181 gctctgtgtgtgctgtgaaataactctatccagagagggccaaagtcagtggaag 240
|||||

Qy 463 GCCTCTGTGTGTGCTCTCAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAG 522
Db 241 gtgataaacgccctccaatcgggttaactcccagagaggtgtcacagagcagcagcaag 300
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Qy 523 GTGATAAACGCCCTCCAATCGGTTAACTCCAGGAGAGTGTACAGAGCAGCAGCAAG 582
Db 301 gacagcaactacagcctcagcagcaccctgacgtgagcaagcagactacagagaacac 360
|||||
Qy 583 GACAGCACTACAGCCTCAGCGACCCCTGACGCTGAGCAAGCAGACTACAGAAACAC 642
Db 361 aaagtctacgctgcgaagtcacccatcagggcctgagctgcgccgtcacaaagagcttc 420
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Qy 643 AAAGTCTACGCCCTGCGAAGTCCCATCAGGGCCTGAGCTGCGCCGTACAAAGAGCTTC 702
Db 421 aacagggaagagtggt 436
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Qy 703 AACAGGGGAGAGTGTT 718

RESULT 15
LOCUS A07738 754 bp DNA PAT 02-AUG-1993
DEFINITION Synthetic nucleotide sequence of the Y22 light chain.
ACCESSION A07738
NID g413214
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 754)
AUTHORS
JOURNAL Patent: WO 8912098-A 39 14-DEC-1989;

COMMENT NCBI gi: 413214
FEATURES
source
1..754
/organism="Artificial sequences"
CDS
10..720
/note="NCBI gi: 413215"
/codon_start=1
/product="Y22 light chain"
/db_xref="pid:g413215"
/translation="MTMLSLAPLLSLLLCVSDSRSTTTVTQSPISLSVATGKVTIR
CITTTDIDDDMKWYQKPGEPKLLISEGNTLRPGVPSRSSSGYGSDFVTIETLS
EDVADYYCQSDNMFPTFGSGTKLEIRRTVAAPSVFIPFSDQIKSGTASVWCLLN
FYPREAKVQWRYDNLALQSNQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEV
THQGLSSPVTKSFNRGEC"
BASE COUNT 203 a 207 c 174 g 170 t
ORIGIN

Query Match 50.6%; Score 364; DB 35; Length 754;
Best Local Similarity 83.3%; Pred. No. 0.00e+00;
Matches 455; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Db 173 tgaagtgtaccacagagcaggggaacctccaaagctctatttcagaaggaata 232
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Qy 173 TGAGTTGTTATCAGAGAAAGCCAGGCCAACCTCCAGAGCTCTGATTATTAAGCTTTCTA 232
Db 233 ctcttgctcgtgagtcctccatcccgattctccagcagtggtatggctcagattttgttt 292
|||||
Qy 233 ACCGGCACTCTGGGGTCCACAGAGATTACCGCGGAGTGGGGCAGGACAGATTTCACAC 292
Db 293 ttacaattgaaaacacgctctcagaagatgttcagattactactgtttgcaagtgata 352
|||||
Qy 293 TGAANAATCAGCGCAGTGGAGGCTCAAGATGTTGGGGTTTATTTCTCGCGGCAAGGTACAA 352

Release 2.1D John F. Collins, Biocomputing Research Unit.
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Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	525	72.9	726	19	T18060	Monoclonal antibody D	0.00e+00
2	484	67.2	729	16	T03380	Anti-IL-8 chimeric G5	0.00e+00
3	481	66.8	737	4	Q25691	Sequence of the chime	0.00e+00
4	415	57.6	9208	11	Q65629	Vector contg. TCAE 8	4.38e-263
5	411	57.1	924	10	T18172	Sequence coding human	2.71e-260
6	405	56.3	1066	8	Q49943	Human anti-HBs light	4.16e-256
7	402	55.8	4691	16	Q92546	pComb3 expression vec	5.15e-254
8	402	55.8	6166	16	Q92547	Expression vector, pp	5.15e-254

RESULT	1	
ID	T18060 standard; DNA; 726 BP.	
AC	T18060;	
DT	20-AUG-1995 (first entry)	
DE	Monoclonal antibody DNA light chain against 65 kD hCMV antigen.	
KW	Polymerase chain reaction; primer; amplify; PCR; light chain; WAB;	
KW	65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis; ss.	
OS	Synthetic.	
Key	Location/Qualifiers	
FF	1..717	
FT	CDS	
FT	/*tag= a	
FT	sig_peptide	1..60
FT	/*tag= b	
FT	mat_peptide	61..714
FT	/*tag= c	
FT	3'UTR	715..726
FT	/*tag= d	
PN	J08038178-A.	
PD	13-FEB-1996.	
PF	20-FEB-1995; 030742.	
PR	18-FEB-1994; JP-021628.	
PA	(NISN) NISSHINO IND INC.	
PA	(TANA/) TANAKA H.	

DR WP1; 96-154852/16.

DR P-PSDB; R93554.

PT Human monoclonal antibody binds to cytomegalovirus 65 kD antigen - produced by primer amplification, used in the diagnosis of hCMV

PT infection

PS Claim 7; Page 19; 22pp; Japanese.

CC The sequences given in T18059-60 encode the heavy and light chains respectively of a monoclonal antibody against a 65 kD antigen of human cytomegalovirus (hCMV). These sequences were amplified using the CC sequences given in T18040-58. The monoclonal antibody may be used CC in the diagnosis of hCMV.

SQ Sequence 726 BP; 177 A; 192 C; 199 G; 158 T;

Query Match

72.94;

Best Local Similarity 87.6%; Pred. No. 0.00e+00;

Matches 629; Conservative 0; Mismatches 86; Indels 3; Gaps 2;

Db 1 atgaagggtccccgcgtctctctgggggtgctgaatgctgtgatacctggtatgtgca 60

Qy 1 ATGAGCCTCCCTGCTCACTCTCCGGGCTGCTATTGCTCTGCTCCGGCTCCAGTGGG 60

Db 61 gatattgtatgaccagactccactctctgtccgtccacctggacagccgctctcc 120

Qy 61 GAAGTGTGTGATGACCTCTCCACTGTCCCTTCCCATCACACCTGGAGCGCGCTCC 120

Db 121 atctctcgaagtctagtccagagctctctgcatgatgagaaagacctattgtatgg 180

Qy 121 ATCTCTGTAGGCTAGTCAAGAGCCTTAACACAGTAATGAGACACCTTCTCAGTTGG 180

Db 181 tatttcagaagccagccagctccacagctctgactgactgaggtttccaaacggttc 240

Qy 181 TATCAGCAAGACCGAGCAACCTCCAGGCTCTGATTTATAAGGTTTCTAACCGGGAC 240

Db 241 tctggaagtgcagataggttcadgtggcagcgggtcaggagacagattccactgaaatc 300

Qy 241 TCTGGGGTCCACAGACAGATTCCAGCGCAGTGGGCGAGGACAGATTTCACACTCAAAATC 300

Db 301 agccgggtgaggtgaggtgtgggtttattactgcatggaagtatacagt-tcg- 358

Qy 301 ACCGAGTGGAGGCTGAGATGTTGGGTTTATTTCTCGGGGCAAGGTACAGAGACTCT 360

Db 359 -cgacttttggccagggaccagactggagatcaaacgaactgtggtgcacactgttc 417

Qy 361 CCCACTTTCGGCGGAGGACCAAGGTGGAATCAAAAGCTGCGGTGACCATCTGTC 420

Db 418 ttcatctccgcacatctgatgagcagttgaaactctggaactgctgtgtgtgcttg 477

Qy 421 TTCAFTCTTCGGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCCTCTGTTGTGCTGTG 480

Db 478 ctgaaatacttctatccccagagggccaaagtgcagtggaaagtgataacgccctccaa 537

Qy 481 CTGAATAACTTCTATCCCTAGAGAGGCCAAAGTACAGTGGAAAGGTGATTAACGCCCTCCAA 540

Db 538 tcgggttaactccagagaggtgtcacagagcaggacagcaagagacagcactacagctc 597

Qy 541 TCGGGTAACTCCCAAGAGTGTACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 600

Db 598 agcagcaccctgacgtgagcaagcagactacgagaaacacaaagtctacgcctcgaa 657

Qy 601 ACGACGACCTTGACGCTGACGAAAGGACGACTACGAGAAACACAAAGTCTACGCCCTCGAA 660

Db 658 gtccaccatcagggtgactgctgcgcctcacaaagagcttccacaggggagagtggt 715

Qy 661 GTCCCATCAGGGGCTTAGCTCGCCGCTCACAAGAGCTTTCAACAGGGGAGAGTGTT 718

RESULT 2

ID T03380 standard; DNA; 729 BP.

AC T03380;

DT 12-MAR-1996 (first entry)

DE Anti-IL-8 chimeric 6G4.2.5 light chain DNA.

KW Monoclonal antibody 6G4.2.5; MAb; interleukin-8; IL-8;

KW chimeric antibody; Fab; antibody engineering; inflammation;

KW inflammatory bowel disease; ulcerative colitis; bacterial pneumonia;

KW ds.

OS Chimeric Mus sp.;

OS Chimeric Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..729

FT /*tag= a

FT /product= fusion protein

FT sig_peptide 1..69

FT /*tag= b

FT /function= STII signal peptide

FT mat_peptide 70..726

FT /*tag= c

FT /product= mouse-human chimeric Fab

PN W09523865-A1.

PD 08-SEP-1995.

PF 01-MAR-1995; U02589.

PR 03-MAR-1994; US-205864.

PA (GETH) GENENTECH INC.

PA (INDV) UNIV INDIANA FOUND.

PI Doerschuk CM, Fong S, Herbert CA, Kim KJ, Leong SR;

DR WP1; 95-320580/41.

DR P-PSDB; R86323.

PT New anti-interleukin-8 monoclonal antibodies - useful for treating

PT inflammatory disorders, partic. ulcerative colitis, and bacterial

PT pneumonia

PS Example G; Fig 27A-B; 114pp; English.

CC A cDNA insert (T03380) in vector pchimFab codes for a mouse-human

CC chimeric Fab light chain (R86323) consisting of the light chain

CC variable region of anti-interleukin-8 mouse MAb 6G4.2.5 and the

CC light chain constant region of human IgG1. A chimeric Fab vector,

CC plasmid p66425chim2 (ATCC 97055), was constructed that encoded the

CC murine-human variable/constant regions of both the light and heavy

CC chains of 6G4.2.5.

SQ Sequence 729 BP; 192 A; 192 C; 174 G; 171 T;

Query Match

67.24;

Best Local Similarity 87.1%; Pred. No. 0.00e+00;

Matches 568; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Db 76 gtgatgacagacacaccactctccctgctgctcagtccttgagatcaggtcctcatctct 135

Qy 67 GTGATGACTCAGTCTCCACTCTCCCTTCCCATCAGACCTGGAGAGCGGCTCCATCTCC 126

Db 136 tgcagatctagtcagagcctgttacacggtattggaacacacctattacattggtactcg 195

Qy 127 TGTAGTCTACTCAAGCCTTAACACAGACTAATGGACACCTTCTCTGAGTTGTTATCAG 186

Db 196 cagaagccagccagctctccaaagctctgatctacaaagtttccaacgactttctggg 255

Qy 187 CAGAGCCAGGCGCAACCTCCAAGGCTCTCTGATTTATAGGTTTCTAACCGGAGCTCTGGG 246

Db 256 gtccagacaggttcagtgccagtggatcagggagacagatttcacactcaggtcagcaga 315

Qy 247 GTCCAGACAGATTTCAGCGGCGAGTGGGCGGAGGACAGATTTCACTGTAATAATCAGCGCA 306

Qy 610 CTGAGCTGAGCAAGCAGCTACGAGAAACACAAAGTCTACGCTGCGAGTCAACCAT 569
Db 681 caggcgctgagctcgccgtcacaaagagcttcaaccggagagtggt 729
Qy 670 CAGGGCTGAGCTCGCCGCTCAAAAGAGCTTCAACAGGGGAGAGTGTT 718

RESULT 4

ID Q65629 standard; DNA; 9208 BP.
AC Q65629;
DT 01-FEB-1995 (first entry)
DE Vector contg. TCAE 8 DNA.
KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;
KW cell lysis; ss.
OS Synthetic.
PN W09411026-A.
PD 26-MAY-1994.
PF 12-NOV-1993; U10953.
PR 13-NOV-1992; US-978891.
PR 03-NOV-1993; US-149099.
PA (IDEC-) IDEC PHARM CORP.
PI Anderson DR, Hanna N, Leonard JE, Newman RA, Rastetter WH;
PI Refine;
DR WPI; 94-183162/22.
PT Treating B cell lymphoma with chimeric antibody - against CD20,
PT causing rapid depletion of peripheral B cells, also new
PT antibodies and hybridomas
PS Disclosure; Fig 3; 101pp; English.
CC The sequence shows a vector contg. TCAE8, a gene encoding a chimeric
CC anti-CD20 antibody for treatment of B cell lymphomas. TCAE8
CC contains 4 transcriptional cassettes, human Ig light and heavy chain
CC constant regions, dihydrofolate reductase, neomycin phosphotransferase
CC and murine variable regions. The vector can be used to produce
CC antibodies which cause depletion of peripheral blood B cells,
CC including those associated with lymphoma. They mediate complement-
CC dependent lysis and lyse target cells by antibody-dependent cellular
CC cytotoxicity.
CC See also Q65629-35.
SQ Sequence 9208 BP; 2237 A; 2399 C; 2388 G; 2182 T;
Query Match 57.6%; Score 415; DB 11; Length 9208;
Best Local Similarity 88.2%; Pred. No. 4.38e-263;
Matches 479; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
Db 1143 tggttccagcagaagcagagctctcccaaaacccctggatttatgccacatccaactg 1202
Qy 178 TGGTATCAGCAGAACGCCAGCCCACTCCAAAGGCTCTGATTATAAGGTTTCTAACCGG 237
Db 1203 gttctcggagtcctgttcgtctcagtgagctgggtcgggactcttactctctcaacc 1262
Qy 238 GACTCTGGGCTCCACAGACAGATTACGGCGCAGTGGGGCAGGACAGATTTCACACTGAAA 297
Db 1263 atcagagatggaggtgaagctgccacttattactcagcagtgagctagtaac 1322
Qy 298 ATCAGCCGACTGAGCGCTGAGATGTTGGGGTTTATTCTCGGGGCAAGCTACAGGACT 357
Db 1323 ccaccacgttcggaggggagcgaagctggaatcaaacgtacggtgctgcaccatct 1382
Qy 358 CTCCCACTTTCGGCGGAGGCAAGGTGGGAATCAAACTGACGGTGGCTGCACACTCT 417
Db 1383 gttctcatctcccgcaatctgatgagcagttgaaatctggaactgctctgtgtgtgc 1442
Qy 418 GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCGCCTCTGTTGTGC 477

Db 1443 ctgctgaataacttctatccccagagagccaaagtacagtgaaggtggataaagccctc 1502
Qy 478 CTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAGGTGGATAAGCCCTC 537
Db 1503 caatcgggttaactccccagagagtgctcacagagcaggacagcaaggagcagctacage 1562
Qy 538 CANTCGGTTACTCCCGAGAGTGCTCACAGAGCAGCAGCAGCAGAGGAGGACCTACAGC 597
Db 1563 ctacagcagccacctgacgtgagcaaaagcagactacgagaaacacaaagtctacgcctgc 1622
Qy 598 CTAGCAGAGCCCTGACGCTGAGCAAGCAGACTACGAGAAACAAAGTCTACGCCCTGC 657
Db 1623 gaagtccaccatcaggccctgagctcgccctcacaagagcttcaacaggggagagtg 1682
Qy 658 GAAGTCAACCATCAGGGCTGAGTCCGCCCTCAAAAGAGGTTCAACAGGGGAGAGTGT 717
Db 1683 tga 1685
Qy 718 TGA 720

RESULT 5

ID Q71872 standard; cDNA; 924 BP.
AC Q71872;
DT 27-OCT-1994 (first entry)
DE Sequence coding human anti-IgE MAb light chain.
KW Human IgE; CH4 region; triggers mediator release;
KW Mast cells; Monoclonal antibody; allergy; Immunoglobulin; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT misc feature 4..6
FT /*tag= a
FT /note= "C or G, illegible sequence."
FT misc feature 908..910
FT /*tag= b
FT /note= "N is an unidentified base"
FT misc feature 71..394
FT /*tag= c
FT /note= "L-chain variable region"
FT CDS 11..715
FT /*tag= d
FT /product= antibody light chain
FT /note= "Human monoclonal anti-IgE antibody "
PN EP-592230-A.
PD 13-APR-1994.
PF 07-OCT-1993; 308006.
PR 07-OCT-1992; JP-293800.
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
PI Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N;
PI Yoshida T;
DR WPI; 94-120330/15.
DR P-PSDB; R52951.
PT Human monoclonal anti-IgE peptide antibody - inhibits histamine
PT release from mast cells by allergen stimulation, useful for
PT preventing allergies
PS Claim 4; Page 17; 21pp; English.
CC Q71872 encodes the light chain of a human type anti-IgE peptide
CC monoclonal antibody which inhibits the signal transmission for
CC the release of chemical mediator from mast cells and basophils
CC stimulated with allergen. The antibody can be used for the
CC prophylaxis and the therapy of allergy.
SQ Sequence 924 BP; 230 A; 277 C; 216 G; 195 T;

CC sites, an NcoI restriction site between the two cassettes, and a second cassette consisting of an expression control RBS, a PelB leader, a human consensus amino terminus spacer region comprising the sequence EVQLLE, a cloning region bordered by 5' XhoI and 3' SpeI restriction sites followed by a SfiI site, expression control stop sequences and a NotI restriction site. The pPho-TT expression vector contains a light chain stuffer that is 1200 bp in length and a heavy chain stuffer that is 300 bp in length. The nucleotide sequences of the heavy and light chain stuffers encode the heavy and light chain variable domains of a tetanus toxin-specific Fab.

SQ Sequence 6166 BP; 1416 A; 1706 C; 1629 G; 1415 T;

Query Match 55.8%; Score 402; DB 16; Length 6166;
Best Local Similarity 88.5%; Pred. No. 5,15e-254;
Matches 479; Conservative 0; Mismatches 59; Indels 3; Gaps 2;

Db 4706 tggatccagcagaacacgtggccaggctcccaggctcctcatctatgtacatccagcagg 4765
||||| ||||||| || ||||| ||||| ||||||| || ||||| || ||||| || |||||
Qy 178 TGGTATCAGCAGAGAACGCCAGCCAACTCCAAAGGCTCTGATTTATAAGTTCCTAAACCGG 237
Db 4766 gccactggcatcccaagacaggttcagtggcagtggtgtgggacagacttcactctcaacc 4825
||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| |||||
Qy 238 GACTCTGGGGTCCACAGAGATTTCAGCGCAGTGGCGCAGGACAGATTTCACACTGMAA 297
Db 4826 atcagcagactggagctgaagattttgcagtgtactactgtcagca--gtatggtggct 4883
||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| |||||
Qy 298 ATCAGCGCAGTGGAGGCTGAAGATGTTGGGTTTATTTCTGGGGCAAGGTACAGGACT 357
Db 4884 ca--ccgtggttcggccaaagggacaaaggttggaaactcaaacgaactgtggctgcacatct 4942
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Qy 358 CCTCCCACTTTCGGCGGAGGACCAAGGTGGAATCAACAGTACGGTGGCTGCACCACTCT 417
Db 4943 gtctctcatcttcccgcctctctgatgagcaggttgaactctgaactgcctctgtgtgtgc 5002
Qy 418 GTCTTCATCTTCCCGCCATCTCATGACGAGTGTGAATCTCGAACTGCCTCTCTGTGTGC 477
Db 5003 ctgctgaataactctcccagagagggccaaagtacagtggaggtggataacgcctc 5062
||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| |||||
Qy 478 CTGCTCAATAACTTCTATCCACAGAGGCCAAAGTACAGTGGAGGTGGAATAAGCCCTC 537
Db 5063 caatcggttaactcccagagaggtgtcacagagcaggacagcagacacacacacacacac 5122
||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| |||||
Qy 538 CAATCGGCTTAATCTCCAGAGAGTGTACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 597
Db 5123 ctgagcagcacctgacgtgagcaagcagactacagagaacacaaagtctacgcctgc 5182
||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| |||||
Qy 598 CTGAGCAGCAGCTGACGCTGAGCAAGCAGACTACGAGAACACAAAGTCTACGCCCTGC 657
Db 5183 gaagtccaccatcagggctgagtcgcccgtcacaaagagcttcacagggggagagtg 5242
||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| |||||
Qy 658 GAAGTCAACCATCAGGGCTGAGCTCGCCCTGCAAAAGAGCTTCAACAGGGGAGGTGT 717
Db 5243 t 5243
Qy 718 T 718

RESULT 9

ID Q67896 standard; cDNA to mRNA; 645 BP.

AC Q67896;

DT 07-AUG-1995 (first entry)

DE cDNA contg. an ORF for a globulin kappa chain for an antibody to SLE.

KW globulin kappa chain; light chain; antibody; treatment; nephritis;

KW systemic lupus erythematosus; SLE; ds.

OS Homo sapiens.
PN J06296490-A.
PD 25-OCT-1994.
PR 14-APR-1993; 109783.
PR 14-APR-1993; JP-109783.
PA (LTTK-) LTT KENYUSHO KK.
PA (TAIH) TAIHO PHARM CO LTD.
DR WPI, 95-010856/02.
PT DNA coding SLE nephritis-causing positive charge antibody - and
PT it's use in treating nephritis
PS Claim 2; Page 5; 6pp; Japanese.
CC Q67894-7 are cDNA sequences contg. an open reading frame encoding a
CC globulin kappa chain for an antibody causing systemic lupus erythematosus
CC (SLE). The nucleotide sequences can be used to aid in the treatment of
CC nephritis caused by SLE.
SQ Sequence 645 BP; 171 A; 177 C; 163 G; 134 T;

Query Match 55.7%; Score 401; DB 13; Length 645;
Best Local Similarity 87.1%; Pred. No. 2.56e-253;
Matches 471; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Db 103 tggatccagcagaagccagggaagccctaacgcgtgatctatgtcatgtgatttg 162
||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| |||||
Qy 178 TGGTATCAGCAGAGCCAGCCAACTCCAGGCTCTGATTTATAAGTTCCTAAACCGG 237
Db 163 caaagtgggtcccatcatcaagggttcagcgaggtggtatctggacagattcactctcaca 222
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Qy 238 GACTCTGGGGTCCACAGCAGATTTCAGCGCAGTGGCGCAGGACAGATTTCACACTGMAA 297
Db 223 atcagcagctgagcctgaagattttgcaacttattactgtctccagcataatagttc 282
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Qy 298 ATCAGCGCAGTGGAGGCTCAAGATGTTGGGTTTATTTCTCGGGCAAGGTACAGGACT 357
Db 283 ccgtacacattttggccagggaacaaagtgaggtcaaacgaactgtggctgcacactatc 342
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Qy 358 CCTCCCACTTTCGGCGGAGGACCAAGGTGGAATCAACAGTACGGTGGCTGCACCATCT 417
Db 343 gtctctcatcttcccgcctctgatgagcaggttgaactctggaactgcctctgtgtgtgc 402
||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| |||||
Qy 418 GTCTTCATCTTCCCGCCATCTGATGAGCAGTGTGAATCTGGAATCTGCTCTCTGTGTGC 477
Db 403 ctgctgaataactcttctcccagagagggccaaagtacagtggaggtggataacgcctc 462
||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| |||||
Qy 478 CTGCTCAATAACTTCTATCCACAGAGGCCAAAGTACAGTGGAGGTGGAATAAGCCCTC 537
Db 463 caatcggttaactcccagagaggtgtcacagagcaggacagcaagagacacactacagc 522
||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| |||||
Qy 538 CAATCGGCTTAATCTCCAGAGAGTGTTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 597
Db 523 ctacagcagcacctgagcgtgagcaagcagactacagagaacacaaagtctacgcctgc 582
||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| |||||
Qy 598 CTGAGCAGCAGCTGAGGCTGAGCAAGCAGACTTACGAGAACACAAAGTCTACGCCCTGC 657
Db 583 gaagtccaccatcagggctgagctcgcccgtcacaaagagcttcacagggggagagtg 642
||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| ||||||| ||||| |||||
Qy 658 GAAGTCAACCATCAGGGCTGAGCTCGCCCTGCAAAAGAGCTTCAACAGGGGAGGTGT 717
Db 643 t 643
Qy 718 T 718

RESULT 10

ID Q11878 standard; cDNA; 1242 BP.

[illegible]

Qy	355	ATCTCTC----	CCACTTTTGGCGCGGAGGAGGCAAGTGGAAATCAAACTACCGTGGCTGCA	411
Db	740	ccatctgtcttc	atctccgcccatctgatgagcagttgaaatctggaactgcctctggt	799
Qy	412	CCATCTGTCTTCATCT	TCCTCCGCCATCTGATGAGCAGTTCAAACTCGCCTCTGTT	471
Db	800	gttgctctgctgaata	acttctatccagagagagccaaagtcacagtggaaagtgagataac	859
Qy	472	GTGTGCTGCTGTAATA	CTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGGTGCAATAAC	531
Db	860	gccctccaatcgggt	taactccagagagagtgtcacagagcaggacaggaagcagcaacc	919
Qy	532	GCCTCCRAATCGGGTAA	CTCTCCAGGAGAGTGTCTACAGACAGGACAGCAAGCAGCAACC	591
Db	920	tacagctcagcagcac	ccacctgacgtgagcagaagcagactacgagaacacaaaagttac	979
Qy	592	TACAGCCTCAGCAGAC	ACCTCTACGGCTGAGCAACGACGACTACGAGAAACACAAAGTCTAC	651
Db	980	gcttcgcgaagt	caccatcatcaggcctgagctgcgccgtcacaaagagcttcaacagggga	1039
Qy	652	GCCTCGGAAGTCA	CCCATCAGGCGCTGAGCTGCCCGCTCAGAAAGAGCTTCAACAGGGGA	711
Db	1040	gagtgtt	1046	
Qy	712	GAGTGT	718	

RESULT 11

ID	Q70487	standard; cDNA; 646 bp.
AC	Q70487;	
DE	04-APR-1995	(first entry)
DT	04-APR-1995	Anti-tetanus toxoid light chain cDNA from vector, pC3AP313.
KW	Polymerase chain reaction; primer; mutagenesis; PCR; amplify;	
KW	diversity; antibody; complementarity determining region; CDR;	
KW	framework; constant; light; heavy; phase; immunoglobulin; library; ss.	
OS	Synthetic.	
PN	W09418219-A.	
PD	18-AUG-1994.	
PF	02-FEB-1994;	U01234.
PR	02-FEB-1993;	US-012566.
PR	28-DEC-1993;	US-174674.
PA	(SCRI)	SCRIPPS RES INST.
PI	Barbas CF, Burton DR, Leirner RA;	
DR	WPI; 94-279673/34.	
PT	Oligo-nucleotides - used as PCR primers for producing increased	
PT	diversity antibody libraries, for screening antigens	
PS	Claim 21; Page 84-85; 120pp; English.	
CC	This sequence represents the light chain coding sequence derived from	
CC	the surface display phagemid expression vector, pC3AP313. pC3AP313	
CC	contains the bacteriophage gene III and heavy and light chain variable	
CC	domain sequences for encoding human Fab antibodies against tetanus toxin.	
CC	This sequence was pref. used in the method of the invention for the	
CC	production of antibody libraries containing increased diversity. The	
CC	sequences given in Q70480-86 are primers which were used for inducing	
CC	mutagenesis in a complementary determining region (CDR) of an	
CC	immunoglobulin light chain gene. These primers contain a 3' terminus	
CC	capable of hybridising to a first framework region, a 5' terminus	
CC	capable of hybridising to a second framework region and a nucleotide	
CC	sequence between the 5' and 3' termini having the formula [NNK]n,	
CC	where n is 3-24. These primers may be used to produce antibody	
CC	libraries with increased antibody diversity by inducing mutagenesis	
CC	within the CDR regions of immunoglobulins heavy or light chains that	
CC	are displayed on the surface of filamentous phage particles comprising	
CC	the library. These primers pref. mutate the light chain CDR3.	

SQ Sequence 646 BP; 162 A; 187 C; 170 G; 127 T;
Query Match 55.6%; Score 400; DB 12; Length 646;
Best Local Similarity 88.4%; Pred. No. 1,28e-252;
Matches 478; Conservative 0; Mismatches 60; Indels 3; Gaps 2;

Db 100 tggatccagcagaacccgtggccaggtccacaggtccatcatctatggtacatccagcagg 159
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Qy 178 TGGTATACAGCAAGACCGCGCAACTCCAGGCTCTGATTTATTAAGGTTTCTTAACCGG 237
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Db 160 gccactgcacccagacagatccagtggcagtggtctgggacagacttcactctcacc 219
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 238 GACTCTGGGGTCCACAGAGATTACGGCAGTGGGCGAGGACAGATTTCACACTGAAA 297
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 220 atcagcagactggagcctgaagattttgacgtgtactactgtcagca--gtatggtgct 277
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Qy 298 ATCAGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGGGCGCAAGGTACAGGACT 357
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Db 278 ca--ccgtggttcggccaaagggaccaggtggaactcaaacgaactgtggctgcaccatct 336
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Qy 358 CTCCCACTTTCCGGCGGAGGACCAAGGTGGAAATCAAACTAGCGTGGCTGCACCATCT 417
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Db 337 gtcttcactttcccgccatctgatgagcagttgaaatctggaactgcctctgtgtgtgc 396
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Qy 418 GTCTTCATCTTCGGCCCACTGTGATGAGAGTTGAAATCTGGAACTGCTCTGTGTGTGC 477
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 397 ctgctgaataactctatccagagagggccaaactacagtgaaggtgataacgcccctc 456
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 478 CTGCTGAATAACTTCTATCCAGAGGGCCAAAGTACAGTGGAAAGTGGATTAACGGCCCTC 537
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 457 caatcgggttaactccagagaggtgtcacagagcagcagcagcagcagcagcagcagc 516
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 538 CAATCGGTAACTCCAGCAGAGTGTACAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 597
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 517 ctacgagcaccctgacgtgtgcaagcagactacgagaacacaaagtctacgctgc 576
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 598 CTGAGCAGCACCCTGACGCTGCAGAAAGCAGACTACGAGAAACAAAGTCTAGCCCTGC 657
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 577 gaagtcacccatcatgagcgtgagtcgcccgtcacaaagagcttcacaaaggagagagtg 636
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 658 GAAGTCACCCATCAGGGGCTGAGCTGCGCCGCTCAGAAAGAGCTTCAACAGGGGAGAGTG 717
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 637 t 637
Qy 718 T 718

RESULT 12

ID Q67894 standard; cDNA to mRNA; 645 BP.
AC Q67894;
DT 07-AUG-1995 (first entry)
DE cDNA contg. an ORF for a globulin kappa chain for an antibody to SLE.
KW globulin kappa chain; light chain; antibody; treatment; nephritis;
KW systemic lupus erythematosus; SLE; ds.
OS Homo sapiens.
PN J06296490-A.
PD 25-OCT-1994.
PF 14-APR-1993; 109783.
PR 14-APR-1993; JP-109783.
PA (LTKR-) LFT KENYUSHO KK.
PA (TAIH) TAIHO PHARM CO LTD.
DR WPI; 95-010856/02.
PT DNA coding SLE nephritis-causing positive charge antibody - and
PT it's use in treating nephritis

PS Claim 2; Page 4-5; 6pp; Japanese.
CC Q67894-7 are cDNA sequences contg. an open reading frame encoding a
CC globulin kappa chain for an antibody causing systemic lupus erythematosus
CC (SLE). The nucleotide sequences can be used to aid in the treatment of
CC nephritis caused by SLE.
SQ Sequence 645 BP; 179 A; 178 C; 158 G; 130 T;

Query Match 55.4%; Score 399; DB 13; Length 645;
Best Local Similarity 86.9%; Pred. No. 6.36e-252;
Matches 470; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Db 103 tggatccagcagaacccaggaagcccttaagcgcctgatctatcttgcacccagctcg 162
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 178 TGGTATACAGCAAGACCGCAACTCCAGGCTCTGATTTATTAAGGTTTCTTAACCGG 237
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 163 caaagtgggtcccatcaaggttcagcggcagtgatctgagacagaattcactctcaca 222
|| || ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 238 GACTCTGGGGTCCACAGAGATTACGGCAGTGGGCGAGGACAGATTTCACACTGAA 297
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 223 atcaacagcgtcgagcctgaagattttgcaacttattactgtctgcagcagaatagttac 282
||||| || || || ||||||| || || ||||||| || || ||||||| || || ||||||| || || ||
Qy 298 ATCAGCGCAGTGCAGGCTCAAGATGTTGGGGTTTATTTCTGGGGCAAGGTACAAAGCAT 357
||||| || || || ||||||| || || ||||||| || || ||||||| || || ||||||| || || ||
Db 283 ccgtggacctacgccaagggaccagagtggaatcaaacgaactgtggctgcacacatct 342
||||| || || || ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 358 CTCCCACTTTCCGGCGGAGGACCAAGGTGGAAATCAAACTAGCGTGGCTGCACCATCT 417
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 343 gtcttcactttcccgccatctgatgagcagttgaaatctggaactgcctctgtgtgtgc 402
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 418 GTCTTCATCTTCGGCCCATCTGATGAGCAGTTGAAATCTGGAACTGCTCTGTGTGTGC 477
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 403 ctgctgaataactttatccagagagggccaaactacagtgaaggttgataacgcccctc 462
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 478 CTGCTGAATAACTTCTATCCAGAGAGGCGCAAACTACAGTGGAAAGTGGATTAACGGCCCTC 537
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 463 caatcgggttaactccagagaggtgtcacagcagcagcagcagcagcagcagcagcagc 522
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 538 CAATCGGTAACTCCACAGCAGTGTACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 597
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 523 ctacgagcagcctgacgtgagcagaagcagactacgagaacacaaagtctacgctgc 582
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 598 CTCAGCAGCACCCTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTAGCCCTGC 657
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 583 gaagtcacccatcagggcctgagctcggccgtcacaaagagcttcacaaaggggagagtg 642
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 658 GAAGTCACCCATCAGGGGCTGAGCTGCGCCGCTCAGAAAGAGGCTTCAACAGGGGAGAGTG 717
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 643 t 643
Qy 718 T 718

RESULT 13

ID Q67895 standard; cDNA to mRNA; 645 BP.
AC Q67895;
DT 07-AUG-1995 (first entry)
DE cDNA contg. an ORF for a globulin kappa chain for an antibody to SLE.
KW globulin kappa chain; light chain; antibody; treatment; nephritis;
KW systemic lupus erythematosus; SLE; ds.
OS Homo sapiens.
PN J06296490-A.
PD 25-OCT-1994.
PF 14-APR-1993; 109783.
PR 14-APR-1993; JP-109783.

PA (LTTK-) LTT KENYUSHO KK.
PA (TAIH) TAIHO PHARM CO LTD.
DR WPI; 95-010856/02.
PT DNA coding SLE nephritis-causing positive charge antibody - and
PT it's use in treating nephritis
PS Claim 2; Page 5; 6pp; Japanese.
CC Q67894-7 are cDNA sequences contg. an open reading frame encoding a
CC globulin kappa chain for an antibody causing systemic lupus erythematosis
CC (SLE). The nucleotide sequences can be used to aid in the treatment of
CC nephritis caused by SLE.
SQ Sequence 645 BP; 180 A; 179 C; 154 G; 132 T;

Query Match 55.1%; Score 397; DB 13; Length 645;
Best Local Similarity 87.5%; Pred. No. 1.58e-250;
Matches 475; Conservative 0; Mismatches 66; Indels 2; Gaps 2;

Db 102 ttggtatcagcagaaacagggaagccctaaagctcctgatcttcgatgcatgcaattt 161
|||||
Qy 177 TTGGTATCAGCAGACAGCCAGCGCCACCTCCAAAGGCTCCTGATTATAAGGTTCTTAACCG 236
Db 162 gcaaacagggtcccatcaaggttcagtggaagtggatatgggacagatttcaatttcac 221
|||||
Qy 237 GCACTCTGGGTCCTCAGACAGATTACAGCGGAGTGGGGCAGGACAGATTTCACTGAA 296
Db 222 catcagcgcctcagcgtgaagatattgcaacattactgtcaaccaggtttacagtta 281
|||||
Qy 297 AATCAGCGCAGTGGAGGTGAAGATCTTGGGGTTTATTTCG-CGGGCAAGGTACAAGGA 355
Db 282 cccctcc-acgttcggccaaaggaccagagtggaatcaaacgaactgtggctgcacct 340
|||||
Qy 356 CTCTCCCACTTTCGGCGAGCGACAGGTGGAATCAACGTACGGTGGCTGCACCAT 415
Db 341 ctgcttcacatctccgcctcatctgatgagcagttgaaatctggaactgcctctgtgt 400
|||||
Qy 416 CTGTCTCATCTCCCGGCATCTGATGAGCAGTTGAAATCTGGAACTCGCTGTGTGT 475
Db 401 gctcgtgaataactctatcccagagagccaaagtacagtgaaggtgataacqccc 460
|||||
Qy 476 GCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGATAACGCC 535
Db 461 tccaatcgggttaactcccagagagtgatgtcacagagcaggacagcaagacacactaca 520
|||||
Qy 536 TCCATCGGGTAACTCCAGGAGAGTGTACAGAGCAGCAGCAGCAGCAGCAGCTACA 595
Db 521 gctcagcagcaccctgacgtgagcaagcagactacgagaacacacaagtctacgcct 580
|||||
Qy 596 GCCTCAGCAGCAGCTGACGCTGAGCAAGCAGACTACAGAGAACACAAAGTCTACGCCT 655
Db 581 qcgaagtcacccatcagggctcagctgcgccctcacaagagcttcaacagggagagt 640
|||||
Qy 656 GCGAAGTCACCCATCAGGGGCTGAGCTGCCCTGTCAAAAGAGCTTCAACAGGGGAGGT 715
Db 641 gtt 643
|||
Qy 716 GTT 718

RESULT 14

ID Q67897 standard; cDNA to mRNA; 645 BP.

AC Q67897;

DT 07-AUG-1995 (first entry)

DE cDNA contg. an ORF for a globulin kappa chain for an antibody to SLE.

KW globulin kappa chain; light chain; antibody; treatment; nephritis;

KW systemic lupus erythematosis; SLE; ds.

OS Homo sapiens.
PN J06296490-A.
PD 25-OCT-1994.
PF 14-APR-1993; 109783.
PR 14-APR-1993; JP-109783.
PA (LTTK-) LTT KENYUSHO KK.
PA (TAIH) TAIHO PHARM CO LTD.
DR WPI; 95-010856/02.
PT DNA coding SLE nephritis-causing positive charge antibody - and
PT it's use in treating nephritis
PS Claim 2; Page 5; 6pp; Japanese.
CC Q67894-7 are cDNA sequences contg. an open reading frame encoding a
CC globulin kappa chain for an antibody causing systemic lupus erythematosis
CC (SLE). The nucleotide sequences can be used to aid in the treatment of
CC nephritis caused by SLE.
SQ Sequence 645 BP; 175 A; 179 C; 152 G; 139 T;

Query Match 54.4%; Score 392; DB 13; Length 645;
Best Local Similarity 86.2%; Pred. No. 4.83e-247;
Matches 467; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Db 102 ttggtatcagcagaaacagggaagccctaaagctcctgatattactatgcacccagttt 161
|||||
Qy 177 TTGGTATCAGCAGACAGCCAGCGCCACCTCCAAAGGCTCCTGATTATAAGGTTCTTAACCG 236
Db 162 gcaagtgggggcccatcaaggtttcagtgagtgatctggacagatttcacgctcac 221
|||||
Qy 237 GGACTCTGGGTTCCACAGACAGATTCAAGCGGAGTGGGGCAGGACAGATTTCACTGAA 296
Db 222 catcagcagtgccaacttgaaagactttgcaacttacttctcgcagcagacttacagtac 281
|||||
Qy 297 AATCAGCGCAGTGGAGGCTGAAGATCTTGGGGTTTATTCTCGGGCAAGGTACAAGGAC 356
Db 282 cctctcacccttcggccaaaggacagcagctggagattaaacgaactgtggctgcaaccac 341
|||||
Qy 357 TCCTCCCACTTTCGGGGAGGGACCAAGTGGAAATCAAAAGCTAGCTGGCTGCCACCATC 416
Db 342 tgtcttcattctccgccactctgatgagcagttgaaatctggaactgcctctgtgtgtg 401
|||||
Qy 417 TGCTTTCATCTTCGCCCATCTGATGAGCAGTTGAATCTGGAATCTGGAATCTGTTGTG 476
Db 402 cctgctgaataacttctatcccagagagccaaagtacagtggagtggaataacgcct 461
|||||
Qy 477 CTGCTGAATTAACCTTATCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATAACGCCCT 536
Db 462 ccaatcgggttaactcccaggagagtgtcacagacagagcagcaaggacagcactacag 521
|||||
Qy 537 CCAATCGGGTAACTCCAGGAGAGTGTCAAGCAGCAGCAGCAGCAGCAGCAGCTACAG 596
Db 522 cctcagcagcaccctgacgtgagcaaaagcagactacgagaaaacacaaagtctacgcctg 581
|||||
Qy 597 CCTCAGCAGCACCCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAAGTCTACGCCCTG 656
Db 582 cgaagtcaccatcagggctgagctgcgccctcacaagagcttcaacaggggagagtgt 641
|||||
Qy 657 CGAAGTCACCCATCAGGGCTTGAGCTGCCCTCACAAGAGAGCTTCAACAGGGGAGAGTG 716
Db 642 tt 643
||
Qy 717 TT 718

RESULT 15

ID T03363 standard; cDNA; 714 BP.

AC T03363;
DT 03-APR-1996 (first entry)
DE Anti-IL-8 MAB 5.12.14 VL/human IgG1 CL cDNA.
KW Monoclonal antibody 5.12.14; Mab; interleukin-8; IL-8;
KW chimeric antibody; Fab; antibody engineering; inflammation;
KW inflammatory bowel disease; ulcerative colitis; bacterial pneumonia;
KW ds.
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
FH Key Location/Qualifiers
FT sig_peptide 1..69
FT /*tag= a
FT /product= STII signal peptide
FT mat_peptide 70..396
FT /*tag= b
FT /product= Murine 5.12.14 light chain variable region
FT mat_peptide 397..713
FT /*tag= c
FT /product= Human IgG1 light chain constant region
PN W09523865-A1.
PD 08-SEP-1995.
PF 01-MAR-1995; U02589.
PR 03-MAR-1994; US-205864.
PA (GETH) GENENTECH INC.
PA (INDV) UNIV INDIANA FOUND.
PI Doerschuk CM, Fong S, Herbert CA, Kim KJ, Leong SR;
DR WPI; 95-320580/41.
DR P-PSDB; R86319.
PT New anti-interleukin-8 monoclonal antibodies - useful for treating
PT inflammatory disorders, partic. ulcerative colitis, and bacterial
PT pneumonia
PS Example E; Fig 19; 114pp; English.
CC A cDNA insert (T03363) in vector pA51214VL' codes for the light
CC chain variable region of anti-human interleukin-8 mouse monoclonal
CC antibody 5.12.14 and human IgG1 light chain constant region. The
CC cDNA was obtd. by amplification of cDNA derived from 5.12.14-producing
CC hybridoma cells using primers (T03352-55) based on light chain
CC sequences. It is used with cDNA (T03364) coding for the heavy chain
CC variable region in the prodn. of anti-IL-8 mouse-human chimeric Fab.
SQ Sequence 714 BP; 193 A; 188 C; 167 G; 166 T;

Query Match 54.3%; Score 391; DB 16; Length 714;
Best Local Similarity 86.1%; Pred. No. 2.41e-246;
Matches 466; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Db 172 tggatcaacaagaacagggaactctctaagacactgatttactcgtcatcctaccgg 231
||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Qy 178 TGGTATCAGCAGAAGCCAGGCAACCTCCAGGCTCTGATTATTAAGGTTTCTTAACCGG 237

Db 232 tacagtggagtcctcgtccttcacagggcagtgatctgggacagatttcactcacc 291
|| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 238 GACTCTGGGGTCCACAGAGATTTCAGGCGCAGTGGGGCAGGACAGATTTCACACTGAAA 297

Db 292 atcagccatgacgtctgaagacttggcagactatttctgtcagcaataacatctat 351
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 298 ATCAGCGCAGTGGAGGCTGAAGATGTGGGCTTTATTTCTCGGGCAAGGTACAGGACT 357

Db 352 cctctcagcttcggtcctgggacaaagctggagcttcgaagagctgtggctgacacctct 411
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 358 CTTCCCACTTTCCGGCGGAGGAGCAAGGTGGAATCAAACTAGCTGGCTGCACCAATCT 417

Db 412 gcttcacgtctccgccatctcgtgagcaggttgaatctggaactgctctcgttgtgac 471
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 418 GTCTTCATCTTCGCCGCCATCTGTAGCAGTGTGAATCTGGAACCTGCCTCTGTTGTGTC 477

Db 472 ctgctgaataacttctatccccagagagggccaaaagtacagtggaggtggataaacgcctc 531
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 478 CTGCTGAATAACTTTCTATCCACAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTC 537

Db 532 caatcgggttaactccccaggagagtggtcacagagcaggacagcaaggacagcactacagc 591
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 538 CAATCGGGTAACTCCCGAGGAGTGTTCACAGAGCAGGACAGCAAGGACAGCAGCTACAGC 597

Db 592 ctcagcagcacctctgacgtgagcaagcagactacgagaaacacaaagtctacgcctgc 651
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 598 CTACGAGCAGCCCTGACGCTGAGCAAGGACGACTACGAGAAACACAAAGTCTACGCCCTGC 657

Db 652 gaagtcacccatcagggcctgagctcgccctcacaagagcttcaacagggagagagt 711
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 658 GAAGTCACCCATCAGGGCTGAGGTCGCCCGCTCAAAAGAGGTTTCAACAGGGGAGAGTGT 717

Db 712 t 712
Qy 718 T 718

Search completed: Tue Dec 17 21:56:29 1996
Job time : 69 secs.

Dec 17 21:47

US-08-487-550-5.fst

3

LOCUS H25972 391 bp mRNA EST 10-JUL-1995
DEFINITION y156d07.r1 Homo sapiens cDNA clone 162253 5' similar to gb:S49006
IC KAPPA CHAIN C REGION (HUMAN);
ACCESSION H25972
NID g895095
KEYWORDS EST.
SOURCE human clones:162253 library=Soares breast 3NbHst vector=pT7T3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13Rp1 Rsite1=Not I Rsite2=Eco RI Adult human.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TCTTACCAATCTGAAGTGGGCGCGCCCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT7T3 vector (Pharmacia). Library went through one round
of normalization to a Cot = 20. Library constructed by Bento Soares
and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 391)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskie, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project

Unpublished (1995)

JOURNAL

Unpublished (1995)

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 307

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

NCBI gi: 895095

Location/Qualifiers

1..391

/organism="Homo sapiens"

/clone="162253"

/note="human"

BASE COUNT 111 a 104 c 100 g 75 t 1 others

ORIGIN

Query Match 46.0%; Score 331; DB 11; Length 391;
Best Local Similarity 94.6%; Pred. No. 0.00e+00;
Matches 351; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Db 7 taaagtccccgtacagatttggccaggagaccacactggacatcgaacaaagactgtggc 66

Qy 348 TACAAGGACTCTCCCACTTTTGGCGGCGGAGCAAGGTCGAATCAACAGCTACGCTGGC 407

Db 67 tgcaccatctgtcttcattctcccgccatctgtgagcaggttgaactgtgaactgctc 126

Qy 408 TGCACACTCTCTCTTCACTCTCCCGCCACTCTCATGACAGCTTGAATCTGGAAGCTGCCTC 467

Db 127 tgtgtgtgcctgtgaaataacttctatcccgagagagccaaagtacagtggaggtgga 186

Dec 17 21:47

US-08-487-550-5.fst

4

Qy 468 TGTGTGTGCTGCTGTGAATACTTCTATCCAGAGCGCCAAAGTACAGTGGAGGTGGA 527
Db 187 taacgcccctccaatcggttaactcccaggagagtggtcacagagcaggacagcaagacag 246
Qy 528 TAAAGCCCTCCAAATCGGGTAACCTCCAGGAGAGTGTACAGAGAGGAGCAGCAAGCAG 587
Db 247 cacctacagctctcagcagcagccctgacgctgagcaaaagcagactacgagaaaacacaaact 306
Qy 588 CACCTACAGCCTCAGCAGCACCCTGACCTGAGCAAAAGCAGACTACGAGAAACACAAAGT 647
Db 307 ctacgctcggaagtaccatcaccatcaggcctgagctcgccgtgtacaaagagctttaacag 366
Qy 648 CTACGCGCTCGGAAGTTCAGCCATCAGGCGCTGAGCTCGCGCTCACAAGAGAGCTTCAACAG 707
Db 367 gggagagtggt 377
Qy 708 GCGAGAGTGT 718

RESULT 2

LOCUS R79141 448 bp mRNA EST 09-JUN-1995
DEFINITION y186f10.r1 Homo sapiens cDNA clone 146155 5' similar to gb:M63438
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);

ACCESSION R79141

NID g855422

KEYWORDS EST.

SOURCE human clones:146155 library=Soares placenta Nb2HP vector=pT7T3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13Rp1 Rsite1=Not I Rsite2=Eco RI Female placenta
obtained at birth (full term). 1st strand cDNA was primed with a
Not I - oligo(dT) primer [5'
ACTCGAAGAAATTCGCGCGGAGGAATTTTTTTTTTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified pT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 448)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskie, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

TITLE

JOURNAL

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 347

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

NCBI gi: 855422

KEYWORDS
SOURCE

KEYWORDS
EST.
SOURCE
human clone=187094 library=Soares breast 3NbHbSt vector=pT733D (Pharmacia) with a modified polylinker host=DHI08 (ampicillin resistant) primer=M13P1 Rsite1=Not I Rsite2=Eco RI Adult human. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACCAATCTGAAGTCGGAGCGCCGCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and ligated into the Not I and Eco RI sites of a modified pT733 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fátima Bonaldo.

ORGANISM

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE AUTHORS

AUTHORS
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 297
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
source

```
source
1..398
/organism="Homo sapiens"
/clone="187094"
/note="human"
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BASE COUNT	106 a	110 c	102 g	76 t	4 others
ORIGIN					

Query Match 43.2%; Score 311; DB 69; Length 398;
Best Local Similarity 96.8%; Pred. No. 0.00e+00;
Matches 335; Conservative 0; Mismatches 8; Indels 3; Gaps 3;

Db 3 gggacgaagctggagatcaaacgaaactgtaggctgcaccatctgtcttcatntttccgcc 62
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qv 376 ggacccaaggttgcaattcaaacgttagcgtgcacctgtcttcttcattcttcccgcca 435

Db 63 tctgatgagcagtggtgaaatcttggaactgcctctgttgtgtgcctgctgaataacttcttat 122
|||||
Ov 436 TCTGATCAGCAGTGTGAAATCTGGAACTGCCTCTGTGTGCTGCTGCTGAAATCACTTCTAT 495
|||||

Qy 436 TCTGATCAGCGAGTTGAAATCTGGAACTGCCTCTGTGTGTGCTGCTGAATAACTTCTAT 495

Db 123 ccacagagaggccaaactacagtggaggtggataaacgcctccaatcgggtaactcccag 182

Qy 496 CCCAGAGGCCAAACTACAGTGAAGGTGGATAACGCCCTCCAAATCGGGTAACTCCCAG 555

Db 183 gagagtgtcacagagcaggaagacagcacctacagcctcagcagcacctgacg 242

QY	556	GAGAGTGTACAGAGCAGGACAGCAAGAGACAGACCTACGCCTCAGCAGACCCCTCAGG	615
Dd	243	ctgacgaagcagact acyagaacaacaaact ct acgcgtcgaggt caccattcagg	302
QY	616	CTGACAAGCAGACTACCGAAACACAAAGCTTACGCCTCGGAAGTCACCAT-CAGGG	674
Dd	303	cctgagcttgcgccgtcacaaagagtcttcacacagggagagatntt	348
QY	675	CCTTGAGCT-CCCCCGTCAAAAGAGTT-CAACAGGGGAGAGTGT	718

RESULT	5				
LOCUS	H25329	378 bp	mRNA	EST	10-JUL-1995
DEFINITION	yI46c07.r1 Homo sapiens cDNA clone 161292 5' similar to gb:s49006 IG KAPPA CHAIN C REGION (HUMAN) :				

ACCESSION H25329
NID g894452
KEYWORDS EST.

SOURCE

human clone=161292 library=Soares breast 3NbHbSt vector=p773D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13R1 Rsite1=Not I Rsite2=Eco RI Adult human. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTCGAGGCGCCGCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chosnata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
AUTHORS

AUTHORS
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.

TITLE	JOURNAL	COMMENT
1. The Role of the Teacher in the Classroom	Journal of Educational Research	1980, Vol. 83, No. 1, pp. 1-10
2. The Impact of Technology on Education	Journal of Educational Technology	1981, Vol. 5, No. 2, pp. 1-10
3. The Role of the Parent in the Classroom	Journal of Educational Research	1982, Vol. 85, No. 1, pp. 1-10
4. The Impact of the Environment on Learning	Journal of Educational Research	1983, Vol. 86, No. 1, pp. 1-10
5. The Role of the Student in the Classroom	Journal of Educational Research	1984, Vol. 87, No. 1, pp. 1-10
6. The Impact of the Teacher on Learning	Journal of Educational Research	1985, Vol. 88, No. 1, pp. 1-10
7. The Role of the Parent in the Classroom	Journal of Educational Research	1986, Vol. 89, No. 1, pp. 1-10
8. The Impact of the Environment on Learning	Journal of Educational Research	1987, Vol. 90, No. 1, pp. 1-10
9. The Role of the Student in the Classroom	Journal of Educational Research	1988, Vol. 91, No. 1, pp. 1-10
10. The Impact of the Teacher on Learning	Journal of Educational Research	1989, Vol. 92, No. 1, pp. 1-10

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 337
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL; contact
IMAGE Consortium (info@image.linnl.gov) for further information.

NCBI gi: 894452	Location/Qualifiers				
FEATURES	source	1..378	/organism="Homo sapiens"		
			/clone="161292"		
			/note="human"		
BASE COUNT		101 a	108 c	95 g	71 t
ORIGIN					3 others

Query Match 42.8%; Score 308; DB 11; Length 378;

Dec 17 21:47

US-08-487-550-5.rst

9

Best Local Similarity 97.9%; Pred. No. 0.00e+00;
Matches 323; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

Db 2 atcaagaactgtgggtgaccatctgtcttcatcttccgcctatctgatgagcattt 61
||||||| 11 |||||
Qy 391 ATCAACGTAGCGTGG-CTGACCATCTGCTTCATCTTCCGCCCATCTGATGACGATT 449
Db 62 gaaactgtgaactgctctgtgtgctgctgaataaacttctatccagagagccaa 121
|||||||
Qy 450 GAAATCGAACTGCCCTGCTGTGCTGCTGCTGAATAACTTCTATCCAGAGAGCCAA 509
Db 122 agtacagtgaagtgagtaaacgcctccaatcgggttaactccaaggagagtgctcacaga 181
|||||||
Qy 510 AGTACAGTGAAGTGTGATGATGAGCGCCCTCCAATCGGTAACCTCCAGGAGAGTGTACACAGA 569
Db 182 gcaggacagcagcagcaactcagcctcagcagcaccctgacgtgagcaagcaga 241
|||||||
Qy 570 GCAGGACAGCAAGCAGCAGCACTACAGCTCAGCAGCACCTGACGCTGAGCAAGCAGA 629
Db 242 ctacgagaacacaaagtctacgctgctgaagtcacccatcaggcctgagctcgccct 301
|||||||
Qy 630 CTACGAGAAACACAAAGTCTAGGCTCGGAGCTCAGCCATCAGGCGCTGAGCTGCCCGT 689
Db 302 nacaagagtttcaacagagggagagtggtt 331
|||||||
Qy 690 CACAAAGAGCTTCAACAGGGG-AGAGTGT 718

RESULT 6
LOCUS H44560 451 bp mRNA EST 31-JUL-1995
DEFINITION yo75g10.r1 Homo sapiens cDNA clone 183810 5' similar to gb:549006
IG KAPPA CHAIN C REGION (HUMAN);
ACCESSION H44560
NID G920612
KEYWORDS EST.
SOURCE human clones=183810 library=Soares breast 3NbH8st vector=pT7T3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13Rp1 Rsite=Not I Rsite2=Eco RI Adult human.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGCGCCCTTTTTTTTTTTTTTTT 3']
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT7T3 vector (Pharmacia). Library went through one round
of normalization to a Cot = 20. Library constructed by Bento Soares
and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonotia; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 451)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaekie, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilton RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

Dec 17 21:47

US-08-487-550-5.rst

10

Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 340
Source: IMAGE Consortium, LBNL
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.lbnl.gov) for further information.

NCBI gi: 920612
FEATURES
Location/Qualifiers
source 1..451
/organism="Homo sapiens"
/clone="183810"
/note="human"
BASE COUNT 106 a 142 c 102 g 98 t 3 others
ORIGIN

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Best Local Similarity 99.7%; Pred. No. 0.00e+00;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 caccatctgtcttcatcttccgcctatctgatgagcagttgaaatctggaactgacctg 60
|||||||
Qy 410 CACCATCTGCTTTCATCTTCCGCCCATCTCATGACAGTTTGAATCTGGAATCTGCTCTG 469
Db 61 ttgtgtgctgctgaataacttctatcccgagagggccaaagtacagtgaagtgagata 120
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Qy 470 TTGTGTGCTGCTGAATACTTCTATCCAGAGAGGCCAAAGTACAGTGGAGGTGGATA 529
Db 121 acgcctccaatcgggttaactcccgagaggtgtcacagcagcagcagcagcagcagca 180
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Qy 530 AGCCCTCCCAATCGGTTACTCCAGGAGAGTGTCCAGAGCAGCAGCAGCAGCAGCACA 589
Db 181 cctacagctcagcagcacctgagctgagcagcagcagcagcagcagcagcagcagcagc 240
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Qy 590 CCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 649
Db 241 acgctgcaagtcacccatcagggcctgagctgagctgagctgagctgagctgagctgag 300
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Qy 650 AGCGCTGCGAAGTCACCATCAGGCGCTGAGCTCGCCCGCTCACAAGCAGCTTCAACAGGG 709
Db 301 gagagtggtt 309
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Qy 710 GAGAGTGT 718

RESULT 7
LOCUS H45568 432 bp mRNA EST 31-JUL-1995
DEFINITION yo72g01.r1 Homo sapiens cDNA clone 183504 5' similar to gb:007989
IG KAPPA CHAIN V-I REGION (HUMAN);
ACCESSION H45568
NID G921620
KEYWORDS EST.
SOURCE human clones=183504 library=Soares breast 3NbH8st vector=pT7T3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13Rp1 Rsite=Not I Rsite2=Eco RI Adult human.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGCGCCCTTTTTTTTTTTTTTTT 3']
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT7T3 vector (Pharmacia). Library went through one round
of normalization to a Cot = 20. Library constructed by Bento Soares
and M.Fatima Bonaldo.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Db 121 catgtcttcattccccccatctgatgagcagttgaaatctggaactgcctctgtt 180

QY	413	CATCTGCTTTCATCTTCCCGCCATCTGATGAGCAGTGAATATCGAACTGCCTCTGTTG	472
Db	181	tgtgcctgctgaataaacttctatccacagaggccaaagtacagtgaagtggaataacg	240
QY	473	TGTGCTGCTGTAATAACTTCTATCCACAGAGGCCCAAGTACAGTGGAAAGGTGCATAACG	532
Db	241	ccctccaatcgggtaaetccccaggagagagtgcacagagcaggacagcaaggacagcacc	300
QY	533	CCCTCCAATCGGTAACTCCACAGGAGAGGACAGCAAGACAGCAGCACC	591
Db	301	tacagctctcagcagcaccttggacgtgagcaagcaggagactcaggganacacaaactt	360
QY	592	TACAGCCTCAGCAGCACCTTG-ACGCTGAGCAAGCAG-ACTACG-AGAAACACAAAGTC	648
Db	361	ttacgctctgmaagattcacccenttcaggggcttgagctnctcggttcacaaagagcttt	420
QY	649	T-ACGCTTGGGAAGT-CACCCAT-CAGGGCCT-GAGCT-CGCCCGT-CACAAACAGCTT-	701
Db	421	caacaggggagagctttt	437
QY	702	CAACAGGGGAGAGCTGTT	718

RESULT	12
LOCUS	T89330 489 bp mRNA EST 20-MAR-1995
DEFINITION	yel3ell.s1 Homo sapiens cDNA clone 117644 3' similar to gb:M63438 IG KAPPA CHAIN PRECURSOR V-JII REGION (HUMAN);.
ACCESSION	T89330
NID	g717843
KEYWORDS	EST.
SOURCE	human clone=117644 library=Stratagene lung (#937210) vector=pBluescript SK- host=SOLR cells (kanamycin resistant) primer=-21m13 tsaitet=EcoRI Rsaite=XhoI Normal lung tissue from a 72 year old male. Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence: 5'-GAATTGGGCACGAG-3'; 3' adaptor sequence: 5'-CTCGAGTTTTTTTTTTT-3'.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 489)

REFERENCE
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Rifkin, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Raitan, L., Rohlfing, T., Tan, F., Trevasik, E.,
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
WashU-Merck EST Project
JOURNAL Unpublished (1995)

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 420
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

```

FEATURES
NCBI gi: 717843
Location/Qualifiers
1..489
/organism="Homo sapiens"

```

BASE COUNT	104 a	114 c	151 g	116 t	4 others
ORIGIN	/clone="117644" /note="human"				
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Best Local Similarity	99.3%; Pred. No. 0.00e+00;				
Matches 303; Conservative	0; Mismatches 1; Indels 1; Gaps 1;				
Db	168	aacactctccctgtgaagctctttgtgacggcgagctcaggccctgatgggtgacct 227			
Cp	718	AACACTCTCCCTCTGTGAAGCTCTTTGTGACGGCGAGCTCAGGCCCTGATGGGTGACTT 659			
Db	228	cgacggcgtgagactttgtttctcgtagctcgtcttctcagcgtcagggtcgtcgtga 287			
Cp	658	CGACGGCGTAGACTTTGTGTTCTGTGAGTCTGCTTCTCAGCGTCAGGGTGCTCTGA 599			
Db	288	ggctgagtgctgtccttgctgtcctgtcctgtgacactctcctgggagttcaocgat 347			
Cp	598	GGCTGTAGTGCTGTCTTGGCTTGGCTGTGTGACACTCTCTGGG-AGTTACCGGAT 540			
Db	348	tggaggcggttatccacattccactgtactttggctctctgggatagaagatttcagc 407			
Cp	539	TGAGAGGGCGTTATCCACCTTCACCTGTACTTTGGCTCTCTGGGATAGAGTTATTTCAGC 480			
Db	408	aggcacacaagaggcagttccagattccaactgctcatcagatggccggaagatgaag 467			
Cp	479	AGGCACACAAGAGGCAGTTCCAGATTTCACCTGCTCATCAGATGGCGGGAAGTGAAG 420			
Db	468	acaga 472			
Cp	419	ACAGA 415			

RESULT	13				
LOCUS	H44320	429 bp	mRNA	EST	31-JUL-1995
DEFINITION	yp04d12.r1 Homo sapiens cDNA clone 186455 5' similar to gb:M63438 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN) ;.				

Accession H4320
 NID 9920372
 Keywords EST.
 Source human clone=186455 library=Soares breast 3NbHBst vector=pf7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13R1 Rsite1=Not I Rsite2=Eco RI Adult human. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGCGCGCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pf7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcotryyli; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 429)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasaks, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

(TM)

20

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WPrch nn n.a. - n.a. database search, using Smith-Waterman algorithm

```
Run on: Tue Dec 17 22:07:24 1996; MasPar time 850.41 Seconds
1284,318 Million cell updates/sec
Tabular output not generated.
```

```

Title:
Description:
Perfect Score:
N.A. Sequence:
Comp:

```

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0
Searched: 270440 seqs. 380027776 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: **embl-new3**
1: BCT 2: FUN 3: INV1 4: INV2 5: INV3 6: MAM 7: ORG 8: PLN
9: PRI1 10: PRI2 11: PRO 12: ROD 13: SYN 14: UNC 15: VRT
16: VIR1 17: VIR2

Database:

genbank92

18:BC1 19:BC2 20:BC3 21:BC4 22:BC5 23:BC6 24:BC7
25:BC8 26:BC9 27:INV1 28:INV2 29:INV3 30:INV4 31:INV5
32:INV6 33:MAM1 34:MAM2 35:PAT1 36:PAT2 37:PAT3 38:PHG
39:PLM1 40:PLM2 41:PLN3 42:PLN4 43:PLN5 44:PLN6 45:PLN7
46:PLN8 47:PR1 48:PR2 49:PR3 50:PR4 51:PR5 52:PR6
53:PR7 54:PR8 55:PR9 56:PR10 57:PR11 58:PR12
59:PR13 60:ROD1 61:ROD2 62:ROD3 63:ROD4 64:ROD5 65:ROD6
66:ROD7 67:STR 68:SVN 69:UNA 70:VRL1 71:VRL2 72:VRL3
73:VRL4 74:VRL5 75:VRL6 76:VRL7 77:VRT1 78:VRT2 79:VRT3

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Database:
genbank-new1
80:BCT 81:INV1 82:INV2 83:MAM 84:PHG 85:PLN 86:PRI
87:ROD 88:STR 89:SYN 90:UNA 91:VRL 92:VRT
u-emb145_92
93:part1

Database:

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Statistics: Mean 11.574; Variance 4.914; scale 2.355

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.	
1	1114	77.5	1549	36	A21385	Plasmid DNA with huma	0.00e+00
2	1045	72.7	1599	56	HUM1GHEPAH	Human (hybridoma H210	0.00e+00
3	1008	70.1	1135	37	I093303	Sequence 5 from paten	0.00e+00
4	1008	70.1	1135	37	I07069	Sequence 15 from pate	0.00e+00
5	1007	70.1	1465	59	S79307	Ig gamma =Immunoglobu	0.00e+00
6	998	69.5	1341	35	A07562	DNA sequence of chime	0.00e+00
7	762	53.0	1359	38	MAC1GHWCDR	Macaca fascicularis i	0.00e+00
8	695	48.4	768	51	HS1GQ4FCA	H.sapiens mRNA for Im	0.00e+00
9	693	48.2	1163	51	HS1GQVDJ1	H.sapiens rearranged	0.00e+00
10	608	42.3	1089	56	HUM1GHAF	Human Ig gamma3 heavy	0.00e+00
11	588	40.9	1547	34	MVI1GVDVJ	Mink immunoglobulin q	0.00e+00
12	585	40.7	1551	34	PT1G1GHVCA	S.domesticus immunogl	0.00e+00
13	494	34.4	1594	34	OA1GGISA	O.aries mRNA for immu	0.00e+00
14	489	34.0	1235	34	RAB1IGHCJ	Rabbit Ig active gamma	0.00e+00
15	479	33.3	1179	34	MVI1GGJC	Mink immunoglobulin g	0.00e+00
16	468	32.6	1563	34	PT1G1HVC	S.domesticus immunogl	0.00e+00
17	466	32.4	1581	33	BT1G1GHXC	B.taurus mRNA for imm	0.00e+00
18	456	31.7	1079	34	SSU03779	Sus scrofa Ig gamma 2	0.00e+00
19	454	31.6	1079	34	SSU03780	Sus scrofa Ig gamma 2	0.00e+00
20	442	31.2	1079	34	SSU03781	Sus scrofa Ig gamma 3	0.00e+00
21	442	30.8	1093	34	PT1G1HVCB	S.domesticus IgG chai	0.00e+00
22	443	30.8	1488	75	PVY1B	Potato virus Y immuno	0.00e+00
23	443	30.8	1544	63	MUS1G1BH1	Mouse mRNA for immuno	0.00e+00
24	440	30.6	1079	34	SSU03778	Mouse scrofa Ig gamma 1	0.00e+00
25	418	29.1	1581	60	MM1GHC2AA	M.musculus mRNA for m	0.00e+00
26	414	28.8	1106	66	R1G1G2C	R.rattus mRNA for Ig	0.00e+00
27	414	28.8	1106	63	MUS1G3ALL	Mus musculus germline	0.00e+00
28	414	28.8	1341	37	I07390	Sequence 4 from paten	0.00e+00
29	397	27.7	1095	60	MM1G66	Mouse mRNA for gamma-	0.00e+00
30	397	27.6	1347	37	I08674	Sequence 2 from paten	0.00e+00
31	393	27.3	1561	87	CM0117166	Cricetulus migratoriu	0.00e+00
32	393	27.3	1561	60	CM0117166	Cricetulus migratoriu	0.00e+00
33	393	27.3	1561	12	CM17166	Cricetulus migratoriu	0.00e+00
34	390	27.1	1140	34	OA1G62	O.aries mRNA for Ig g	0.00e+00
35	384	26.7	928	34	SSU03782	Sus scrofa Ig gamma 4	0.00e+00
36	358	24.9	1332	62	MUSH21C	Mus musculus rearrang	0.00e+00
37	357	24.8	675	55	HUM1GCVHX	Human immunoglobulin	0.00e+00
38	356	24.8	870	33	CD1G6C	C.dromedarius mRNA fo	0.00e+00
39	352	24.8	1515	59	GS6761	Anti-colorectal carc	0.00e+00
40	355	24.7	1530	63	MUS1GFCBA	Mouse immunoglobulin	0.00e+00
41	354	24.6	1395	35	A07558	DNA sequence of monoc	0.00e+00
42	352	24.5	1505	60	MM1G66	M.musculus mRNA for a	0.00e+00
43	349	24.3	1518	63	MUS1GACZA	Mouse immunoglobulin	0.00e+00
44	341	23.7	711	36	HUM1GHZZA	Mouse Ig rearranged g	2.00e-302
45	341	23.7	1492	63	MUS1GHGZA	Homo sapiens Ig rearr	1.66e-294
46	341	23.7	1492	63	MUS1GHGZA	Mouse germline immuno	1.66e-294

ATTEMPTING

RESULT	1	PAT	19-DEC-1994
LOCUS	A21385	1549 bp	RNA
DEFINITION	Plasmid DNA with human cDNA insert.		
ACCESSION	A21385		
NID	g983507		
KEYWORDS	.		
SOURCE	unidentified.		
ORGANISM	unidentified		
	unclassified.		

Dec 17 22:07

US-08-487-550-7.rge

5

LOCUS HUMIGEPAH 1599 bp mRNA PRI 08-OCT-1993
DEFINITION Human (hybridoma H210) anti-hepatitis A IgG variable region,
constant region, complementarity-determining regions mRNA, complete
cde.
ACCESSION M87789
NID g185361
KEYWORDS complementarity-determining region; constant region;
immunoglobulin gamma-chain; immunoglobulin heavy chain;
variable region.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhini; Catarrhini; Homiidae.
REFERENCE 1 (bases 1 to 1599)
AUTHORS Lewis, A.P., Lemon, S.M., Barber, K.A., Murphy, P., Parry, N.R.,
Peakman, T.C., Sims, M.J., Worden, J. and Crowe, J.S.
TITLE Rescue, expression, and analysis of a neutralizing human
anti-hepatitis A virus monoclonal antibody
JOURNAL J. Immunol. 151 (5), 2829-2838 (1993)
MEDLINE 93367243
COMMENT NCBI gi: 185361
FEATURES
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1..1599 /organism="Homo sapiens"
1..34 /note="putative"
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92..472 /note="variable region; putative"
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/note="complementarity-determining region 1; putative"
239..289
/gene="CDR2"
/note="complementarity-determining region 2; putative"
386..439
/gene="CDR3"
/note="complementarity-determining region 3; putative"
473..1462
/note="constant region; putative"
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1463..1599
/note="putative"
1566..1571
/note="putative"
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BASE COUNT

Dec 17 22:07

US-08-487-550-7.rge

6

ORIGIN
Query Match 72.7%; Score 1045; DB 56; Length 1599;
Best Local Similarity 87.4%; Pred. No. 0.00e+00;
Matches 1256; Conservative 0; Mismatches 175; Indels 6; Gaps 3;
Db 35 atggactggacctggaggttcctctttgtggtggcagcagctacaggtgtccagtccag 94
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Qy 1 ATGGGTGGAGCCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 95 atcaggtggtgcagctctggggtcgaagtaagaagcctgggtcctcggtgacggtcc 154
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 61 GTCAACTCGTGGAGTCTGGGGAGGCTTGGTCCAGCCTGGCGGCTCCGTGAGAGTCTCC 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 155 tgaagcatctggagcaccctcagcaactatgctatcagctgggtggcagcagggccct 214
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Qy 121 TGTGAGTCTCTGGATTCACTTCACTGACCACTACATCTATTGTTGGTTCGGCAGGCTCCA 180
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Db 215 ggacaagggttggtggtggg----agg-gat-catccctctttttgttacaccaacc 268
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 181 GGAAGGGCGCGAATGGGTAGGTTTCATTAGAAAACAACCGACGCTGGGACACAGAA 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 269 tactcacagaacttccaggcgaggtcacgattaccggcgacaaatccaccagcacagcc 328
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Qy 241 TAGCGCGCTCTGTGAAGAAGACATTCACCATCTCCAGAGATGATCCAAAGACATCGCC 300
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Db 329 cacatggagctgacagctgagatctgagacagcgcggtgtattactgtgcagagat 388
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Qy 301 TATCTCAAAATGACAGCCTCAAAAATCGAGGACACGGCGCTATTACTGTACTACATCC 360
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Db 389 cgctacagggcaggaatttggacggcgccgggttgctggttcgacccctggggccag 448
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 361 TACATTTACATTGTCGGGTGGTGTCTGCTATGGAGGTTACTTCGAATTTCTGGGGCCAG 420
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 449 ggcacccctggtcacgtctcctcagctccaccaaggcccatcggtcttccccctggca 508
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 421 GGGCCCTGGTCACTCTCTCAGTAGCACACAGGGCCATCGGTCTTCCCTCCCTGGCA 480
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 3 109303 1135 bp PAT 14-NOV-1994

LOCUS 109303 Sequence 5 from patent WO 8902922.

DEFINITION 109303

ACCESSION 109303

NID g587989

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1135)

AUTHORS Capon,D.J. and Gregory,T.J.

TITLE ADHESON VARIANTS

JOURNAL Patent: WO 8902922-A 5 06-APR-1989;

COMMENT NCBI gi: 587989

FEATURES Location/Qualifiers

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LOCUS 107069 1135 bp PAT 14-NOV-1994

DEFINITION Sequence 15 from patent EP 0314317.

ACCESSION 107069

NID g590384

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1135)

AUTHORS Capon,D.J. and Gregory,T.J.

TITLE Adhesion variants, nucleic acid encoding them and compositions

comprising them

JOURNAL Patent: EP 0314317-A1 15 03-MAY-1989;

COMMENT NCBI gi: 590384

FEATURES Location/Qualifiers

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RESULT 5

LOCUS

DEFINITION

ACCESSION

NID

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REMARK

5 S79307 1465 bp mRNA PRI 10-JUL-1992
Ig gamma =immunoglobulin heavy chain [rats, humanized lympholytic
MoAb CAMPATH-IH, mRNA, 1465 nt].

S79307
g243865
human humanized lympholytic MoAb CAMPATH-IH.
Homo sapiens
Unclassified.

1 (bases 1 to 1465)
Crown,J.S., Hall,V.S., Smith,M.A., Cooper,H.J. and Tite,J.P.
Humanized monoclonal antibody CAMPATH-IH: myeloma cell expression
of genomic constructs, nucleotide sequence of cDNA constructs and
comparison of effector mechanisms of myeloma and Chinese hamster
ovary cell-derived material

Clin. Exp. Immunol. 87 (1), 105-110 (1992)
92127884
GenBank staff at the National Library of Medicine created this
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This sequence comes from Figure 2.a.

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ACCESSION    A07562
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KEYWORDS     .
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ORGANISM     unidentified
REFERENCE    1 (bases 1 to 1341)
AUTHORS      Kaluza, B. and Lenz, H.
TITLE        Diagnostic method using chimeric antibodies
JOURNAL      Patent: EP 0378175-A 13 18-JUL-1990;
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RESULT 8
LOCUS H10G4FCA 768 bp RNA PRI 21-JAN-1994
DEFINITION H.sapiens mRNA for Immunoglobulin G1, Fc fragment.
ACCESSION X70421
NID g33068
KEYWORDS immunoglobulin; protein A binding.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; mitochondria; eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcophylla; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Carnivora; Hominidae; Homo.
REFERENCE 1 (bases 1 to 768)
AUTHORS Filpula,D.
TITLE H. sapiens mRNA for immunoglobulin G1, Fc fragment
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 768)
AUTHORS Filpula,D.R.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-1993) to the EMBL/GenBank/DBJ databases. D.R.
Filpula, Enzon Labs, 16020 Industrial Drive, Gaithersburg, Maryland
20877, USA
COMMENT NCBI gi: 33068
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DEFINITION H.sapiens rearranged IgG VH-D-JH-Hinge-CH2-CH3 region.
ACCESSION X81695
NID g940515
KEYWORDS constant region; immunoglobulin heavy chain; variable region.
SOURCE human.
ORGANISM Homo sapiens
           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
           Vertebrata; Osteichthyes; Sarcopterygii; Mammalia; Eutheria;
           Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1163)
AUTHORS Khamlichi, A.A., Aumontier, P., Preud'homme, J.L. and Cogne, M.
TITLE Structure of abnormal heavy chains in human heavy-chain-deposition
       disease
JOURNAL Eur. J. Biochem. 229 (1), 54-60 (1995)
MEDLINE 9526287
REFERENCE 2 (bases 1 to 1163)
AUTHORS Khamlichi, A.A.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-1994) to the EMBL/GenBank/DBSJ databases. A.A.
       Khamlichi, CNRS URA 1172, LAB. IMMUN. AND GENETICS, IBMIG FACULTY OF
       SCIENCES, F-86022 POITIERS CEDEX, FRANCE
COMMENT NCBI gi: 940515
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Best Local Similarity 99.4%; Pred. No. 0.00e+00;
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RESULT 12
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DEFINITION S.domesticus immunoglobulin rearranged gamma chain mRNA, VJC
region, complete cds.
ACCESSION M81769
NID g164502
KEYWORDS C-region; D-region; J-region; V-region;
immunoglobulin gamma-chain; immunoglobulin heavy chain;
processed gene.
SOURCE Sus scrofa (individual isolate 5063-3, strain Minnesota miniature
swine, sub_species domesticus) adult spleen cDNA to mRNA.
ORGANISM Sus scrofa
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Artiodactyla; Suiformes; Suidae.
REFERENCE 1 (bases 1 to 1551)
AUTHORS Bosch,B.L., Beaman,K.D. and Kim,Y.B.
JOURNAL Unpublished (1991)
COMMENT NCBI gi: 164502
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Db 139 ctctgagactctctgtgtggtctggaattcaccttcagtaattatgaatcagctggg 198
Qy 107 CCCTGAGAGTCTCTGTCGAGTCTCTGATTACCTTCAGTCAGCAGTACATGATTGCT 166

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Qy 167 TCCGCCAGGCTCCAGGAGGGGCGGATGGGTAGGTTTCATTAGAAACCAACCGACG 226

Db 259 gtggtgacacactactcagcagactctgtgaagggccgattcaccatctccagcacaact 318
Qy 227 GTGGGACACAGATACGCCCGCTGTGTCAAGACAGATTCACCATCTCCAGAGTAT 286
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Qy	347	ACTGTACTACATCTTACATTTCTCGGGGTGGTCTGCTGATGAGGTTACTTCGC	406
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Qy	407	AATTCTGGGGGAGGGCGCCTGGTCA CGGTC TCTCAGCTAGCA CCAAGGGCCCATCGG	466
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Qy	527	TGCTCAAGGACTACTTCCCGCAACCGGTGACGCTGCTGGAACTCAGGCGCCTGACCA	586
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Qy	647	TGCTGACGCTGCCCTCCAGGACGCTTGGGACCCAGACCTTACATCTGCAAGTGTAATCA	706
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Qy	707	AGCCGACGACACCAAGGTGGA CAGAAGCAGACGCCCAAACTTGTGACAAACTTCAC	766
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Qy	887	ACGTGAGCCACGAACACCTGAGTCAAGTTCAACTGGTACGTGCGCGCGCTGAGGTGC	946
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Qy	947	ATAATGCCAAGACAAAGCGGGGAGGACGATACACAGCAGCTACCTGTGTGTCAGCG	1006
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Qy	1007	TCTCAGCGCTCTGCACGAGCACTGCCTGAATGGCAAGGATCAAGTGAAGTCTCCA	1066
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Qy	1127	AACCAAGGTGTACACCTGCGCCCCATCCCGGGATGAGCTGACCAAGAACACAGTGACGC	1186
Db	1201	taacctgccttgctattggcttctaccacacctgacatcgatgtcgagtgcaagaagacg	1260
Qy	1187	TGACCTGCTGTTCAAGGGTTCTATPCCCGACGACATCGCGCTGCAGTGGGAGCAATG	1246

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Qy	1301	CCTTCTCTCTACAGCAAGCTCACTCGGTGACAAAGACAGGCTGCACAGCGGGAAGCTCT	1360
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Qy	1361	TCTCATGCTCCGATGATCATGAGGCTTGCACACCACTACGACGAAGAGCGCTCTCC	1420
Db	1441	agactccgggtaaatga	1457
Qy	1421	TGTCCTCGGCTAAATGA	1437

RESULT	13
LOCUS	OATGGISA 1594 bp RNA MAM 16-FEB-1993
DEFINITION	O.aries mRNA for immunoglobulin gamma chain secreted form.
ACCESSION	X69797
NID	q1268
KEYWORDS	Ig heavy chain; immunoglobulin gamma-1.
SOURCE	sheep.
ORGANISM	Ovis aries
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovoidae; Bovidae; Caprinae; Ovis.
REFERENCE	1 (bases 1 to 1594)
AUTHORS	Nau, F.
TITLE	Direct Submission
JOURNAL	Submitted (15-DEC-1992) to the EMBL/GenBank/DBJ databases. F. Nau, CNRS/Universite de Poitiers, IBMIC, Lab d'Immunologie Moleculaire, Faculte des Sciences de Poitiers, 40 avenue du Recteur Pineau, 86022 Poitiers Cedex, FRANCE
REFERENCE	2 (bases 1 to 1594)
AUTHORS	Patri, S. and Nau, F.
JOURNAL	Unpublished
COMMENT	NCBI gi: 1268
FEATURES	Location/Qualifiers
source	1..1594
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	/tissue type="spleen"
	/clone="382"
sig_peptide	<1..49
	/gene="Ig gamma-1"
CDS	<1..1424
	/note="secreted form; NCBI gi: 388235"
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	/product="immunoglobulin gamma-1 chain"
	/db_xref="PID:g38235"
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Best Local Similarity 75.9%; Pred. No. 0.00e+00;
Matches 789; Conservative 0; Mismatches 241; Indels 9; Gaps 6;
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Qy 405 CGAATCTGGGGCCAGGGCCCTGCTCAGCTCTCTCAGCTAGCAGCAGGCGCCATC 464
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Db 448 agtccacctctgacttctgtgaggagacaggtccagctccatgtagccctgggtg 507
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Qy 465 GGTCTTCCCTGGCACCCTCCTCAAGAGCAGCTCTGGGGGCACAGCGGCCCTGGG 524
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Qy 525 CTGTGCAAGGACTACTTCCCGAACCAGGCTGACGGTGTCTGGAACCTCAGCGCCCTGAC 584
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Db 568 cagcggtgcaacactccggccactcctgagctcctccgggtctactctctcagcag 627
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Qy 585 CAGCGGGTGCACACTTCCCGGCTCTCTACAGCTCTCTCAGGACTCTACTCCCTCAGCAG 644
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Db 628 cgtgtgacctgcgagccagacctcagagcccagacctctcatctgcaagctagccca 687
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Qy 645 CGTGTGACCGTCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCA 704
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Db 688 ccgcccagcagcacaaggtgacaagcgtgttgagcccgatgccgagcccatg-ca 746
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Qy 705 CAAGCCAGCAACAACAAAGGTGGACAGAAAGACAGAGCCCAATCTTGTCAAAACTCA 764
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Qy 765 CACATGCCACCTGCCAGCAGCTCAACTCTCTGGGGGACCGTCAGTCTCTCTTCCC 824
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Db 865 ggaactggccagatgaccccgaggtgagttctctgtgtgtgtgtgtgtgtgtgtgt 924
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Qy 885 GGACGTGAGCCAGAGACCTGAGTCAAGTTCAACTGAGTGGAGCGGCGTGAGGT 944
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Db 925 ggcacgagcagacaaagccgagagagagagagagagagagagagagagagagag 984
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Qy 945 GCATAATGCCAACAAGAGCGCGGAGGAGCAGTACAAACAGCAGTACCTGTGTGTG 1004
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Db 985 cgccctgccatccagcacaagctgagctgagagaaagaggttcaagtcaaggtcca 1044
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Qy 1005 CGTCTCAGCGTCTCTGCACAGGAGTGTGCTGATGGAAGGAGTCAAGTCAAGGTCTC 1064
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Db 1165 cgtcaactcgtgtgacccggctctaccagactacatccgctggagtgagaaaaa 1224
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Qy 1185 CTGACCTGCTGTGTAAGAGCTTCTATCCAGCAGCATCGCCGTGAGCTGGGAGAGCAA 1244
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Db 1225 tgggcagcctgagtcggaggaagaagtaacgacacacacatcccagctggagcgcagcg 1284
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Qy 1245 TGGCAGCGCGGAGACAACACTAAG-AC--CAGC-CCTC--CCGTGCTGGACTCCGACGG 1298
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Qy 1359 CTTCCTAGCTCCGTGATGAGGCTCTGCAACACCTACACGAGCAGACGCTCTTC 1418
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Db 1405 taagcctcgggttaataga 1423
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Qy 1419 CTTCTCTCCGGTAAATGA 1437
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RESULT 14
LOCUS RABIGHAD 1235 bp mRNA MAM 23-MAR-1995
DEFINITION Rabbit Ig active gamma H-chain (allotype Vha2 del2,14) mRNA.
ACCESSION K00752 M12187 M24226
NID g165127
KEYWORDS C-region; D-region; J-region; V-region;
heavy chain allotype Vha2; heavy chain allotype del2,14;
immunoglobulin gamma-chain; immunoglobulin heavy chain;
processed gene.
SOURCE Rabbit (haplotype F-I; Vha2 del2,14 allotype) spleen, cDNA to mRNA,
clone p-gamma-BI-12,14.
ORGANISM Oryctolagus cuniculus
Eukaryota; Amalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Lagomorpha; Leporidae.
REFERENCE 1 (bases 1 to 1235)
AUTHORS Bernstein,K.E., Alexander,C.B. and Mage,R.G.
TITLE Nucleotide sequence of a rabbit Ig heavy chain from the
recombinant F-I haplotype
JOURNAL Immunogenetics 18 (4), 387-397 (1983)
MEDLINE 84030930
COMMENT Original entry prepared by Dr. Rose Mage. The V-region is compared
[1] with the Vha2 allotype p-mu-3 and the human genomic VH26
sequence. The two rabbit V-regions are 89.5% homologous, and this
sequence is 77% homologous with the human segment. This sequence,
as well as the p-mu-3 sequence, shows remarkable homology with the
human CDR2 and D minigenes. The C-region is compared [1] with two
rabbit C-regions, one of del1,15 allotype and the other of e15 and
unknown d allotype.

NCBI gi: 165127 Location/Qualifiers
source 1..1235
/organism="Oryctolagus cuniculus"
CDS <1..1209
/note="Ig gamma chain; NCBI gi: 165128"
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/translation="MSVRQAPKLEWIGYISYSGSAYTASWAKSRSTITRNMENT
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VAHPATNKVDKTVAPSTCSKTCPPPELLGGSVFIFPPKPKDTLMISRTPEVTCV
VDSODDPEVQFTWYINNEQVTRAPPIREQFNSTIRVSTLPI THQDMILRKEFK
KVHKKALPAP IEKTIISKARQPLEPKVTMGPPREELSSRSVSLTOMINGFYPSDISV
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198...199
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BASE COUNT      278 a 423 c 341 g 193 t
ORIGIN           9 bp upstream of Avail site.

Query Match      34.0%; Score 489; DB 34; Length 1235;
Best Local Similarity 78.9%; Pred. No. 0.00e+00;
Matches 81; Conservative 0; Mismatches 196; Indels 21; Gaps 9;

Db 203 tctggggccagcaccctggtcacggtctctccagggacacccaagctcaagctcaagctcattcagctct 262
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Qy 410 TCTGGGGCCAGGGCGCCCTGGTGCACGCTCTCTCCTCAGTAGCACCAGAGCCCATCGGTCT 469

Db 263 tcccactggccccctgctgctgggggacacccaagctccacggtgacccctgggtgacctg 322
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Qy 470 TCCCCCTGGCACCCCTCTCTCCAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGGCTGG 529

Db 323 tcaaggctacctccccggagcagctgacctgacctggaactcgggacacctcaccaatg 382
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Qy 530 TCAAGGACTACTTCCCCCAACCCGTCACGGTCTGCTGGAATCTAGCGGCCCTGACCAAGC 589

Db 383 gggtagcgaacctccccctccgctcggcagctcctcaggtcctcactcgtgagcagcgtg 442
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Qy 590 GGTGCAACACTTCCGGGCTGCTTACAGTCTCTCAGGACTTACTCCCTCAGCAGCGTGG 649

Db 443 tgagcgtgacctcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 493
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Qy 650 TGACCGTCCCTCCAGAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCAACAGC 709

Db 494 ccaccaacacaaagtggacaaacccgttgaccc---tc---gacatg---cag-caa 542
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Qy 710 CCAGCAACACCAGAGTGGACAGAAAGCAGAGCCCAATCTTGTGCAAAACTCACACAT 769

Db 543 gccac-gtgcacccccctgaactctgggggagcgtctgtttcattcttccccca 601
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Qy 770 GCCCAGCTGCCAGCAGCTGACTCTGGGGGACCGTCACTCTCTCTTCCGCCCA 829

Db 602 aacccaagcacccctcatgatctcagcaccccccaggtcacatcgctggtggtgagc 661
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Qy 830 AACCCAGGACCCCTCATGATCTCCGGGACCCCTCAGGTACATCGGTGGTGGAGG 889

Db 662 tgagccaggatgaccgcagggtgcagttcacatggtacataaacaacagcagcaggtgcga 721
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Qy 890 TGAGCCAGCAAGACCCCTGAGGTCAAGTTCAACTGCTGAGCGGCGCTGGAGGTGCATA 949

Db 722 ccgccccgcgcgcctacgggagcagcaggttcaacagcagcagctccgctgggtcagcc 781
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Qy 950 ATGCCAAGCAAAAGCCGGGAGGAGCAGTACACAGCAGCAGCTGCTGTGTGAGGCTCC 1009

Db 782 tcccactcagcaccagcagctggctgaggggcaaggaggttcaagtgcaaaagtccacaaca 841
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Qy 1010 TCACGCTCTGCACGAGACTGCTGATGTCAGAGGAGTACAGTGCAGAGTCTCAACA 1069

Db 842 aggcactccgcgcgccctcagaaacacatctccaaagccagagggcagccctggagc 901
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Qy 1070 AGCCCTCCCGAGCCCTCATGAAAGACATCTCCAAAGCCAAAGGCGAGCCCGCAGAAC 1129

Db 902 cgaaggtctacacctgggctcccccggaggagcgtgagcagcaggtcggtcagcctga 961
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Qy 1130 CACAGGTGTACACCCCTG-CCCCATCCCGGATGAGCTGACCAACCAACAGGTCTCAGCTGA 1189

Db 962 cctgcatgatcaacggctctacacctccgacatctcgggtggagtgaggagagacggga 1021
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Qy 1190 CTTGCTGCTCAAAGGCTTCTATCCACGACATCGCGCTGGAGTGGAGAGCAATGGGC 1249

Db 1022 agcgaggagcaactaagaccacgcgcgctgctggacagcagcggtcctcactcc 1081
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Qy 1250 AGCGGAGACACTACAGACACCGCTCCGCTGCTGACTCCGAGCGGCTCTTCTTCC 1309

Db 1082 tctacaacaagctctcagtgcccacagtgagtgccagcggggcgagcgtcttcacgtct 1141
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1310 TCTACAGCAAGCTCACCGTGACAGAGCAGGCTGGCAGCGAGGGGAACGCTTCTCATGCT 1369

Db 1142 ccgtgatgcagggagccttgacaacacactacacgagaagtcacatcccgctctccgg 1201
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Qy 1370 CCGTGATGATGAGGCTCTGCACAACACTACAGCAGAGAGGCTCTCCCTGCTCCGG 1429

Db 1202 gtaaatga 1209
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Qy 1430 GTAATGA 1437

RESULT 15
LOCUS      MVIIGGJC 1179 bp mRNA MAM 14-DEC-1992
DEFINITION Mink immunoglobulin gamma heavy chain (IGHG) joining region and
            hinge region mRNA, 3' end.
ACCESSION 107788
NID        .g164255
KEYWORDS   J-region; gamma chain; heavy chain; hinge region; immunoglobulin;
            serum protein.
SOURCE     Mustela vison spleen cDNA to mRNA.
ORGANISM   Mustela vison
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Carnivora; Caniformia; Musteloidae; Mustelidae.
REFERENCE 1 (bases 1 to 1179)
AUTHORS    Belousov, J.S., Alabyev, B.Y., Najakshin, A.M., Christensen, J., Stor
            Gaard, T., Aasted, B. and Taranin, A.V.
TITLE       Molecular cloning of cDNA encoding mink immunoglobulin gamma chain
JOURNAL     Unpublished (1992)
COMMENT     NCBI gi: 164255
FEATURES    Location/Qualifiers
            source          1..1179
                        /organism="Mustela vison"
                        /sequenced_mol="cDNA to mRNA"
                        /tissue_type="spleen"
            CDS             <1..1032
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                        /codon_start=1
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BASE COUNT 243 a 423 c 313 g 200 t
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Query Match 33.3%; Score 479; DB 34; Length 1179;
Best Local Similarity 76.0%; Pred. No. 0.00e+00;
Matches 787; Conservative 0; Mismatches 236; Indels 12; Gaps 4;

Db	4	t t c t g g g c a a g g g a g a c t c a g t c a a c g t g t c t c a g t t c a a c a c g g c c c a t c g g t t	63
Qy	409	T T C T G G G C C A G G G C G C C T G G T C A C G T C T C T C A G T A G C A C A A G G G C C A T C G G T C	468
Db	64	t t c c a a c t g g c c c c a g t g c g g g g g c a c c c c g a c c a c a g t g g c c t g g c c t g c c t g	123
Qy	469	T T C C C C T G G C A C C C T C T C T C A A G A C A C C T C T G G G G G C A C A G G C C C T G G G T C G G T	528
Db	124	g t g c e g g c t a c t t c c c t g a c c t g t c a c t g t c c t g g a a c c g g c t c c t t g a c c a g c	183
Qy	529	G T C A A G A C T A C T T C C C G A A C C G G T G A C G G T G T G T G A C T C A G G C G C C T G A C C A G	588
Db	184	g g t g t g c a a c t t c c c g t c c g t c c g t c c t c g g g c t c t a c t c t c a g c a g c a t g	243
Qy	589	G G G T G C A C A C C T T C C C G G C T G T C C T A C A G T C C T A G A G T C T A C T C C C T A G A G G G T G	648
Db	244	g t a a c c t g c c t c c a g c a g t g g c c a g c a a c c t c a t c a c a c c t g g c c a c c a	303
Qy	649	G T A C C G T G C C C T C A G A G A G T T G G G C A C C C A G A C C T A C T C T C A A C G T G A A T C A A G	708
Db	304	g c a g t a a c a c c a g g t g a c a a g a g a g t c c c c c a g a a a a a t t c c t c g c c a t g c a a	363
Qy	709	C C C A C A A C A C C A A G G T G G A A G A A G C A G A G C C A A T C T T G T G A A A A A C A C A C A	768
Db	364	t g t c c c c a a g t g a a a t g t a t a t g t c g g a g a c e t t c a g t c t t a t g t c c c c g	423
Qy	769	T G C C C A C G T G C C C A C C A C T G A A C T C T G G G G G A C C T C A G T C T T C C T C C C C C A	828
Db	424	a a c c c a g g a c a c c t c t c a t t c c c g a a c c c c g a g t c a c a t g c a t g g t g t g a c	483
Qy	829	A A C C C A A G A C A C C T C A T G A T C T C C G G A C C C T G A G T C A T G C G T G T G G T G G A C	888
Db	484	c t g ----- g a a g a c c t c a g g t c c a g a t c a g t g g t g g t g g a a c c a g g a g a t g c a c	537
Qy	889	G T A G C A C A G A G A C C C T G A G G T C A A G T T C A A C T G T A G T G G A C G C G C T G A G G T G C A T	948
Db	538	a c g g c a a g a c a a t t c a c a g a g a c a g t t c a a c a g c a c c t c c g t g t g t c a g t g t c	597
Qy	949	A A T G C C A A G A C A A A G C C G G G A G A G A C A C A G C A C G T A C C G T G T G T C A G C G C T	1008
Db	598	c t c c c c t c a g a c c a c c a g g a c t g g t c a a g g g a a g t c t c a a g t g a a g g t c a a c a c	657
Qy	1009	C T C A C G G T C T G C A C C A G A C T G G C T G A A T G C C A A G A G A C A A G T C C A A G C T C T C C A A	1068
Db	658	a a a g t c t c c c a t c c c c a t t g a g a g a c c a t c t c c a a g t c a a g g g a a g c c c a t c a g	717
Qy	1069	A A A G C C T C C C A G C C C C A C T G A A A A A C C A T T C C A A A G C C A A A G G C A C C C C A G A A	1128
Db	718	c c c a g t g t a t g t c c t g c c c c c a t c c g g a c g a g c t g a g c a a a c a c a g g t c a g t g t g	777
Qy	1129	C C A C A G G T G T A C A C C T G C C C C A T C C C G G A T C A G C T G C C A A G A A C C A G A C C G T C A G C C T G	1188
Db	778	a c c t g c a t g g t c a a a g a c t c t a c c a c c t g a c a t g a t g g a g t g g a g a c a c a g c g c	837
Qy	1189	A C C T G C C T G T C A A A G G C T T C T A T C C C A G A C A C A T C C G C T G A G T G G A G A G A A T G G G	1248
Db	838	c a a c a g t t t c a a g a g g c a g t g t g c a a a a c c c c c a c g t g a t c a g a c g a c c a c	897
Qy	1249	A G A A C A A C A A G A C C A C G C C T C C G C T G C T G C A C T C G A C G G C T C C	1302
Db	898	t a c t t c t c t a c a a g a y c t c t c g g t g a c a a g g c g c t g g a g g g g g a g a a c t t c	957
Qy	1303	T T T C T C T T A C A G A A S C T C A C C C T G A C A G A G A G G T G C C A G C A G G G A A C T C T T C	1362

Db	958	acgtgftgcggfctgcatgaagccctacacacacacacacagcagagagacatctccag	1017
Qy	1363	TCATCTCCGCTGATGATGATGGCTCTGCACCAACCATACACGCAGAAGGCTCTCCCTG	1422
Db	1018	tctccgggtaaatga	1032
Qy	1423	TCTCCGGTAAATCA	1437

Search completed: Tue Dec 17 22:21:53 1996
Job time : 869 secs.

US-08-487-550-7.mg

Release 2.1D John F. Collins, Blocomputing Research Unit.
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MPsrch mn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 22:22:12 1996; MasPar time 118.25 Seconds
Tabular output not generated. 947.093 Million cell updates/sec

Title: >US-08-487-550-7

Description: (1-1437) from US08487550.seq

Perfect Score: 1437

N.A. Sequence: 1 ATGGGTCGAGCCTCATCTT.....CCCTGTCTCCGGGTAAATCA 1437

Comp: TACCCACCTCGGAGTAGAA.....GGGACAGAGCCCATTTACT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 102519 seqs, 38967980 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-genseq24

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 9.414; Variance 6.114; scale 1.540

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1144	79.6	1386	8	Q49834	0.00e+00
2	1112	77.4	1549	3	Q20066	0.00e+00
3	1043	72.6	1617	6	Q35099	0.00e+00
4	1032	71.8	1576	8	Q49944	0.00e+00
5	1014	70.6	1431	19	T18059	0.00e+00
6	1012	70.4	9208	11	Q65629	0.00e+00
7	1007	70.1	1467	4	Q23570	0.00e+00
8	1006	70.0	1135	1	N90736	0.00e+00

9	1005	69.9	1136	1	N90779	Sequence of the linker	0.00e+00
10	1005	69.9	1458	4	Q23571	Reshaped CD4 antibody	0.00e+00
11	1003	69.8	1458	4	Q23581	Reshaped CD4 antibody	0.00e+00
12	1001	69.7	6557	18	T15932	Anti-IgE VH expressio	0.00e+00
13	1000	69.6	1641	9	Q54655	chiT84.12 H3 heavy ch	0.00e+00
14	988	68.8	1412	4	Q25692	Sequence of the chime	0.00e+00
15	987	68.7	8540	11	Q65628	Vector contg. TCAE 8	0.00e+00
16	981	68.3	1174	9	Q51547	Human kappa immunogl	0.00e+00
17	824	57.3	1006	17	T12663	Synthetic IgG4 cDNA.	0.00e+00
18	692	48.2	768	17	Q96101	IgG1 hinge, CH2, CH3	0.00e+00
19	689	47.9	693	15	Q87592	Human IgG1 antibody F	0.00e+00
20	689	47.9	1164	17	T12658	IL4.Y124D/IgG1 gene f	0.00e+00
21	689	47.9	6367	17	T12661	Vector COSFclink.	0.00e+00
22	689	47.9	6926	17	T12662	IL-4.Y124D/IgG1 fusio	0.00e+00
23	687	47.8	1231	15	Q87593	Human Fas/Fc fused OR	0.00e+00
24	685	47.7	699	9	Q35339	cDNA sequence for a h	0.00e+00
25	685	47.7	705	18	Q74083	Immunoglobulin G1 Fc	0.00e+00
26	686	47.7	745	9	Q55943	Polylinker/Fc fragmen	0.00e+00
27	686	47.7	745	15	Q92273	Fc cDNA.	0.00e+00
28	686	47.7	745	13	Q75425	Antibody Fc mutein co	0.00e+00
29	686	47.7	745	9	Q58428	Human IgG1 Fc-polylin	0.00e+00
30	684	47.6	740	6	Q41508	Human IgG1 Fc.	0.00e+00
31	683	47.5	705	7	Q42589	Human Fc polypeptide	0.00e+00
32	682	47.5	1050	5	Q28684	LFA-3-Ig fusion gene	0.00e+00
33	682	47.5	1347	12	Q67347	VCAM 2D-IgG.	0.00e+00
34	682	47.5	2043	9	Q55340	tICAM(453)IgG immuno	0.00e+00
35	681	47.4	1317	17	T00829	Plasmid pDC406/OX40/F	0.00e+00
36	680	47.3	1050	6	Q40423	DNA sequence of LFA3T	0.00e+00
37	675	47.0	1557	10	Q45225	Sequence encoding a r	0.00e+00
38	675	47.0	1587	10	Q63958	P-selectin ligand-IgG	0.00e+00
39	675	47.0	1587	16	T02490	P-selectin ligand/Fc	0.00e+00
40	662	46.1	884	2	N70398	Portion of plasmid pp	0.00e+00
41	658	45.8	765	2	N70257	Part of the nucleotid	0.00e+00
42	658	45.8	765	1	N82142	Immunoglobulin G Fc d	0.00e+00
43	645	44.9	6889	18	T15931	DHFR/intron (WTrasSD)	0.00e+00
44	631	43.9	1425	6	Q41516	Human CD40-L/Fc fusio	0.00e+00
45	631	43.9	1765	10	Q71873	Sequence coding human	0.00e+00

ALIGNMENTS

RESULT 1
ID Q49834 standard; cDNA; 1386 BP.
AC Q49834;
DT 27-APR-1994 (first entry)
DE Anti-HIV-1 recombinant antibody 447-52D heavy chain coding sequence.
KW Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;
KW HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
KW acquired immune deficiency syndrome; chimeric antibody;
KW surface glycoprotein gp120, V3 loop; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS
FT /tag= a
FT /note= "encodes recombinantly modified 447-52D
FT heavy chain"
FN M09319785-A.
PD 14-OCT-1993.
PF 23-MAR-1993; U02629
PR 01-APR-1992; US-861701.
PA (MERI) MERCK & CO INC.
PA (JOHN) JOHNSON L.S.
PA (PFAR) PFAR D.S.
PI Conley AJ, Emami EA, Johnson LS, Mark GE, Pfarr DS;

Db 1112 caccagactgctgaatggcaagagtcacagtgcaaggtctccaaagagccctccca 1171
 Qy 1021 CACCAGGACTGGCTGAATGGCAAGAGTACAAGTCAAGTCTCCAACAAAGCCCTCCCA 1080
 Db 1172 gcccccatcgagaaaccatctccaaagccaaagggcagcccccagaaacacaggtgtac 1231
 Qy 1081 GCCCCCATCGAAMAAACCATCTCCAAAGCCAAAGGCGACGCCCGGAGAACCCACAGGTGTAC 1140
 Db 1232 acctgcccctccatcccggtgatgactgaccagaaccaggtcagctgacctgcctggtc 1291
 Qy 1141 ACCCTGCCCCATCCCGGATGACCTGACCAAGAACCCAGGTGAGCTGACCTGCTGTC 1200
 Db 1292 aaaggtttctatcccacgacatcccggtggagtgagagcaatgggcagccggagaac 1351
 Qy 1201 AAGGCTTCTATCCAGGACGATCCCGTGGAGTGGGAGCAATGGGAGCGGAGAAC 1260
 Db 1352 aactacaagaccgctcccggtgactccagcgctctctctctctctctctctctctctct 1411
 Qy 1261 AACTACAAGACCAGCTCCCGTGGACTCCGACGGCTCTTCTCTACAGCAAG 1320
 Db 1412 ctcaactggcaagagcaggtggcagcggggaacgtctctctctctctctctctctctct 1471
 Qy 1321 CTCACGCTGGCAAGAGCAGGTGGCAGCAGGGAACGCTCTCTCATGCTCCGTCATGAT 1380
 Db 1472 gaggtctgcacaaacctacacagagaagcctctccctgtctccggtaaatga 1528
 Qy 1381 GAGGCTCGCAACCACTACACGACAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1437

RESULT 3
 ID Q35099 standard; DNA; 1617 BP.
 AC Q35099;
 DE 19-MAY-1993 (first entry)
 DE Antibody D heavy chain.
 KW Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;
 KW lymphocyte; hepatitis A virus; HAV; sero; positive; patient;
 KW murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H; ss.
 OS Synthetic.
 FH Key
 FT Key Location/Qualifiers
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 FT sig peptide 35..91
 FT /*tag= b
 FT /*tag= c
 FT /label= FR1
 FT misc RNA 182..196
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 FT /label= CDR1
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 FT misc RNA 386..439
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 PN EP-523949-A.
 PD 20-JAN-1993.
 PF 14-JUL-1992; 306420.
 PR 15-JUL-1991; GB-015284.
 PR 01-AUG-1991; GB-016594.
 PR 23-MAR-1992; GB-006284.
 PA (WELL) WELLCOME FOUND LTD.
 PI Crowe JS, Lewis AP;
 DR WPI; 93-019951/03.
 DR P-PSDB; R31024.
 Prodn. of recombinant primate antibodies - useful for treating
 infections caused by hepatitis A, B and C, herpes,
 cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,
 arthritis etc.
 PS Disclosure; Fig 2; 35pp; English.
 CC The sequences given in Q35099-100 encode the heavy and light chains
 of Antibody D respectively. Antibody D is a monoclonal antibody which
 was derived from peripheral blood lymphocytes from a hepatitis A virus
 (HAV) sero positive patient. Antibody D is closely related in nature
 to murine antibody B5B3. Total RNA was isolated from antibody D
 expressing cells and polyadenylated RNA was extracted. These polyA
 RNA's were used to prepare a cDNA library which was screened for human
 kappa light (L) chains and two positive clones were detected.
 CC Further heavy (H) chain clones were also isolated.
 SQ Sequence 1617 BP; 375 A; 526 C; 441 G; 275 T;

FT misc RNA 473..763
 FT /*tag= j
 FT /label= CH1
 FT misc RNA 764..811
 FT /*tag= k
 FT /label= HINGE
 FT misc RNA 812..1141
 FT /*tag= l
 FT /label= CH2
 FT misc RNA 1142..1462
 FT /*tag= m
 FT /label= CH3
 FT TATA signal
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 PN EP-523949-A.
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 PF 14-JUL-1992; 306420.
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 PR 23-MAR-1992; GB-006284.
 PA (WELL) WELLCOME FOUND LTD.
 PI Crowe JS, Lewis AP;
 DR WPI; 93-019951/03.
 DR P-PSDB; R31024.
 Prodn. of recombinant primate antibodies - useful for treating
 infections caused by hepatitis A, B and C, herpes,
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 arthritis etc.
 PS Disclosure; Fig 2; 35pp; English.
 CC The sequences given in Q35099-100 encode the heavy and light chains
 of Antibody D respectively. Antibody D is a monoclonal antibody which
 was derived from peripheral blood lymphocytes from a hepatitis A virus
 (HAV) sero positive patient. Antibody D is closely related in nature
 to murine antibody B5B3. Total RNA was isolated from antibody D
 expressing cells and polyadenylated RNA was extracted. These polyA
 RNA's were used to prepare a cDNA library which was screened for human
 kappa light (L) chains and two positive clones were detected.
 CC Further heavy (H) chain clones were also isolated.
 SQ Sequence 1617 BP; 375 A; 526 C; 441 G; 275 T;

Query Match 72.6%; Score 1043; DB 6; Length 1617;
 Best Local Similarity 87.3%; Pred. No. 0.00e+00;
 Matches 1255; Conservative 0; Mismatches 176; Indels 6; Gaps 3;

Db 35 atggactggacctggagggtctctcttgggtggcagcagctacaggtgtccaggtcccag 94
 Qy 1 ATGGGTTGGAGCGCTCACTTGTGCTCTCTCTTGTGCGCTGTTCAGCGGTGCCAGTGTGAG 60
 Db 95 atgcaggtgtgcagctctggggctgaagtaagagcctgggtcctcggtgacggtctcc 154
 Qy 61 GTGCAACTGTGTGGAGCTCTGGGGAGGCTTGTGTCAGCGCTGGCGGGTCCCTCAGAGTCTCC 120
 Db 155 tgaaggcctatctggaggcacccttcagcactatgctatcagctgggtgacagagccct 214
 Qy 121 TGTGCAGTCTCTGGATTTCACCTTCAGCTGACCACTACATGTATTGGTTCCGCCAGGCTCCA 180
 Db 215 ggacaagggttgagtgatggg----agg-gat-catccctctttttgtgtacacacac 268
 Qy 181 GGGAGGGGGCGGAATGGGTAGTTTTTATTAGAACAAACCCGAACGGTGGGACACAGAA 240
 Db 269 tactcacagaacttccagggcagagtcacgattaccgcgggacacaaatccaccagcacgcc 328
 Qy 241 TACGCCCGCTGTGTGAAGACAGAGATTCCCATCTCCAGAGATGATTTCCAAAGCATGCC 300

Db 329 cacatggagctgactagctgagatctgagacacggcggtgtattactgtcgacagat 388
Qy 301 TATCTGCAATTCAGACCGCTGAAATTCGAGGACACGGCGCTTATTACTACTACATCC 360
Db 389 cgtacagcagcagcaaatatttgacccgggcccgggtgtgctggttcgacccctggggccag 448
Qy 361 TACATTTACATTTGTCGGGGTGGTGTCTGTATGAGGTTACTTCGAATTCGTGGGGCCAG 420
Db 449 ggcacccctgggtcacgctctctcagcctccacaaaggggcccacatcggtctccccctggca 508
Qy 471 GGGCGCCCTGCTACCGCTCTCTCAGTACACACCAAGGGCCCATCGGTCTTCCCCCTGGCA 480
Db 509 cccctctccaagagcacctctggggccacagcggccctgggtgctgctggtcaaggactac 568
Qy 481 CCCCTCTCAAGAGCACCTCTGGGGGACACGGGCCCTGGGTGCTGAGGACTAC 540
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Db 629 ttcccggctgtcctacgctcctcaggactctactccctcagcagcgtggtgacgctgcc 688
Qy 601 TTCCGGGCTGTCTACAGTCTCAGGACTCTACTCCTCAGCAGCGTGGTGACCGTCCGC 660
Db 689 tccagcagcttgggcccagacactacatctgcaacgtgaatcacaagcccagcaaac 748
Qy 661 TCACGACCTGGGGACCCAGCACTACATCTGCAACGTGAATCATCAGCCGACCAACC 720
Db 749 aaggtggacaagaaagtgtagcccaaatctgtgacaaaactcacacatgccaccgtgc 808
Qy 721 AAGGTGGACAAGAAACAGAGCCCAATCTTGTGCAAAACTTCACATGCCCCACCGTGC 780
Db 809 ccagcacctgaaactcctggggggcagctcagctcttctctcccccaaaacccaagac 868
Qy 781 CCAGCACCTGAACTCTCTGGGGGACCGTCACTCTCTCTTCCCGCCCAAAACCAAGGAC 840
Db 869 accctcatgatctcccggaaccttgaggtcacatgacgtggtggtggcgtgagccacgaa 928
Qy 841 ACCCTCATGATCTCCGAGACCCCTGAGGTTCATGCGTGGTGGTGAGGTGAGGCACGAA 900
Db 929 gacctgaggtcaagttcaactgtagctggacggcgtgaggtgcatatgcaataatgcaagaca 988
Qy 901 GACCTGAGGTCAAGTTCACTGTTAGTGCAGCGCGTGGAGGTGCAATATGCCAAGACA 960
Db 989 aagccggggagagcagtcacaacagcacgtaccgtggtggtcagcgtcctcacgctcctg 1048
Qy 961 AAGCCGGGAGGAGGACAGTACACAGCAGCTACCGTGTGTGTCAGCGTCTCACGGTCCGT 1020
Db 1049 caccaggaactggctgaaatggcaagagtaacagtgcaaggtctccaacaagccctccca 1108
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Qy 1141 ACCCTGCCCCCATCCCGGATGAGCTGACCAAGAACCGGTCAGCTGACCTGCTGCTGCTC 1200
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Qy 1201 AAAGGCTTCTATCCCGACATCCCGCTGGAGTGGGAGCAATGGCGACGCCGAGAAC 1260

Db 1289 aactacaagacacagcctccgctgactgagactccgacggctctctctctctacaagaag 1348
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Qy 1321 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCCGTATGCAT 1380
Db 1409 gaggctctgcacaaccactacacgacgaagagcctctccctgctctccgggtaaatga 1465
Qy 1381 GAGGCTCTGCACAACCACTACACGCGACGAGACGCTCTCCCTGTCTCCGGGTAAATGA 1437
RESULT 4
ID Q49944 standard; cDNA; 1576 BP.
AC Q49944;
DT 29-APR-1994 (first entry)
DE Human anti-HBs heavy chain.
KW Antibody; Ab; light; heavy; chain; hepatitis B;
KW HB; surface antigen; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 15..1394
FT /*tag= a
FT sig_peptide 15..41
FT /*tag= b
FT mat_peptide 42..1391
FT /*tag= c
FT /note= *Claim 2, page 27*
FN W09320205-A.
PD 14-OCT-1993.
PF 30-MAR-1993; J00396.
PR 30-MAR-1992; JP-074678.
PA (SUNR) SUNTORY LTD.
PI Arima K, Kurihara T, Matsukura S, Nishihara T, Tsuruoka N;
DR WPI; 93-336913/42.
DR P-PSDB; R42066.
PT Human anti-hepatitis B surface antigen antibody gene - can be
PT used to produce L and H chains of the antibody in large quantity
PT Disclosure; Fig 6-8; 46pp; Japanese.
CC Polynucleotides encoding the L and H chains of human anti-HBs
CC Ab are given in Q49943-Q49944. The Ab can be easily produced in
CC large quantities for therapeutic use.
SQ Sequence 1576 BP; 394 A; 483 C; 426 G; 273 T;
Query Match 71.8%; Score 1032; DB 8; Length 1576;
Best Local Similarity 91.9%; Pred. No. 0.00e+00;
Matches 1279; Conservative 0; Mismatches 85; Indels 27; Gaps 16;
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Qy 47 GTGTCCAGTGTGAGGTGCAACTGGTGGAGTCTGGGGGAGGCTTGTCCAGCCTGGCGGGT 106
Db 91 cccgtgagactctcctgtgcagcctctgagttcaccttcagtagcaattctatgcactggg 150
Qy 107 CCCTGAGAGTCTCCTGTGCAGTCTCTCGATTCCCTTCAGTCACCACTACATGTTTGGT 166
Db 151 tccgccagcctccagcaggggttgagtggtggcagttatattatgatg-gaaa- 208
Qy 167 TCCGCCAGGCTCCAGGGAAGGGGGCCGAATGGGTAGTGGTTTCATTAGAAACAAACCGAACG 226
Db 209 -tc--ataa-attctacgcagactccgtgaaggccgattccaccatttccagagacaatt 264
Qy 227 GTGGCAACAAGAAATACGCCCGCTCTGTGAAGACAGATTCACCATCTCCAGAGATGATT 286

Qy 468 CTTCCCCCTGGCACCTCTCTCAAGAGCACCTCTGGGGGACACAGCGCCCTGGGCTGCCT 527

Db 519 ggtcaaggaactacttccccgaaccggtgacggtgtcgtggaactcagcgccctgaccag 578
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Qy 528 GGTCAAGGACTACTTCCCGAGACGGGTGACGGTCTGCTGGAACTCAGCGCCCTGACCAG 587
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Db 579 cggcgtgcacaccttccccggtgtcctacagtcctcaggactctactccctcagcagcgt 638
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Qy 588 CGCGGTGCACACCTTCCGGCTGTCTAGAGTCTCAGGACTCTACTCCCTCAGCAGCGT 647
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Db 639 ggtgacctgccctccagcagcttgggacccagacctatctgaaagtgaaatacaaa 698
|||||

Qy 648 GGTGACCGTGCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGCTGAATCACAA 707
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Db 699 gcccagcaacacccaagtggaagaagaagtgagcccaaatcttgtgacaaactcacac 758
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Qy 708 GCCAGCAACACCAAGGTGGAGAGAAAGCAGAGGCCAAATCTTGTGACAAAATCACAC 767
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Db 759 atgccaccgtgccagcacctgaactcctgggggaccgtcagttcttcttcccccc 818
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Qy 768 ATGCCACCGTCCCGACGACCTGACTCTCTGGGGGACCGCTCAGTCTCTCTTCCCCC 827
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Db 819 aaaccccaagcacacctcatgatctcccgaccctgaggtcacatgctggtgga 878
|||||

Qy 828 AAAAAACCAAGACACCTCATGATCTCCGGGACCCCTGAGGTCAATGGGTGGTGA 887
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Db 879 cgtgaccagaagaacctgaggtcaagttcaactggtacgtgacggtgaggtgca 938
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Qy 888 CGTGAGCCACGAAGACCCCTGAGGTCAAGTTCACTGGTACGTGGACGGGTGCA 947
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Db 939 taatgccagaacaaagccgggagagcagtaacacagcagctacogtgtggtcagcgt 998
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Qy 948 TAATGCCAAGCAAAAGCCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGTCAGCGT 1007
|||||

Db 999 cctcaccgtcctgcaccaggtggtcgaatggcaaggagtacaagtcaaggtctccaa 1058
|||||

Qy 1008 CTTACCGTCTCCACGAGCTGGCTGATGGCAGAGGAGTACAGTGCAAGGTCTCCAA 1067
|||||

Db 1059 caaagccctcccagcccctcagagaaaccatctccaaagccaaagggcagcccgaga 1118
|||||

Qy 1068 CAAAGCCCTCCAGGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGA 1127
|||||

Db 1119 accacaggtgtacacacctgccccatcccgggatgagtgaccaagaaccaggtcagcct 1178
|||||

Qy 1128 ACCACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACAGGTACGCT 1187
|||||

Db 1179 gacctgacctcaaggtctctatcccagcgacatcgccgtggagtgggagagaatagg 1238
|||||

Qy 1188 GACCTGCCTGTTCAAGGCTTCTATCCAGCGACATCGCGGTGGAGTGGGAGAGCAATGG 1247
|||||

Db 1239 gcagcggagaacaaactacaagaccgctcccgtgctggactccgagcggtccttctt 1298
|||||

Qy 1248 GCAGCGGAGAGAACACTCAAGACACAGCGCTCCCGTGTGTGACTCGACGGGTCTCTTT 1307
|||||

Db 1299 cctctacagaagctcacgtggacaagcagcaggtggcagcaggggaacgtcttctcatg 1358
|||||

Qy 1308 CTTCTACAGCAAGCTCAACGGTGAAGAGCAGGTGGCAGAGGGAGGTCTTCTCATG 1367
|||||

Db 1359 ctcggtgatgatgaggtctctgacaaccactacacgagaagagctctccgtctcc 1418
|||||

Qy 1368 CTCGGTGTGATGATGAGGTCTGTGCACAACCACTACACCGCAGAGAGCGCTCTCCCTGTCTCC 1427
|||||

Db 1419 gggtaaatga 1428
|||||

Qy 1428 GGTAAATGA 1437

RESULT 6

ID Q65629 standard; DNA; 9208 BP.
AC Q65629;
DT 01-FEB-1995 (first entry)
DE Vector contg. TCAE 8 DNA.
KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;
KW cell lysis; ss.
OS Synthetic.
PN W09411026-A.
PD 26-MAY-1994.
PF 12-NOV-1993; U10953.
PR 13-NOV-1992; US-978891.
PR 03-NOV-1993; US-149099.
PA (IDEC-) IDEC PHARM CORP.
PI Anderson DR, Hanna N, Leonard JE, Newman RA, Rastetter WH;
PI Refine;
DR WPI; 94-183162/22.
PT Treating B cell lymphoma with chimeric antibody - against CD20,
PT causing rapid depletion of peripheral B cells, also new
PT antibodies and hybridomas
PS Disclosure; Fig 3; 101pp; English.
CC The sequence shows a vector contg. TCAE8, a gene encoding a chimeric
CC anti-CD20 antibody for treatment of B cell lymphomas. TCAE8
CC contains 4 transcriptional cassettes, human Ig light and heavy chain
CC constant regions, dihydrofolate reductase, neomycin phosphotransferase
CC and murine variable regions. The vector can be used to produce
CC antibodies which cause depletion of peripheral blood B cells,
CC including those associated with lymphoma. They mediate complement-
CC dependent lysis and lyse target cells by antibody-dependent cellular
CC cytotoxicity.
CC See also Q65629-35.
SQ Sequence 9208 BP; 2237 A; 2399 C; 2388 G; 2182 T;
Query Match 70.4%; Score 1012; DB 11; Length 9208;
Best Local Similarity 98.7%; Pred. No. 0.00e+00;
Matches 1025; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 2775 taettcaatgtctggggcgagggagacacggtcacagctctctgcagctagcacaaggcc 2834
|||||

Qy 400 TACTTCAATTTCTGGGGCCAGGGCCCTGCTGACCGTCTCTCAGCTAGCAGCAGGGC 459
|||||

Db 2835 ccacgtgcttccccctggcaccctcctccaagagcacctctggggcacagcgccctg 2894
|||||

Qy 460 CCAATCGGTCTTCCCTTGGCACCTCTCTCAAGAGACCTCTGGGGGACAGCGGCCCTG 519
|||||

Db 2895 ggcctgctgtgcaagactacttcccgaaccggtgacggtgctggaactcagcgcc 2954
|||||

Qy 520 GGTGCTGCTGTAAGGACTACTTCCCGAAACGGGTGACGCTGTCTGGAACCTCAGGCC 579
|||||

Db 2955 ctgaccagcgctgcacaccttccccgctgtcctacagtcctcaggactctactccctc 3014
|||||

Qy 580 CTGACCAAGCGGTGACACCTTCCCGGTGTCTCAGTCTCTCAGGACTCTACTCCCTC 639
|||||

Db 3015 agcagcgtggtgacctgacctccagcagcttgggacccacagacctacatctgcaacgtg 3074
|||||

Qy 640 AGCAGCGTGGTCCCTGCCCTCCAGCAGCTTGGGACCCAGCAGCTACTCTGCAAGCTG 699
|||||

Db 3075 aatcacaagccagcaacacaaaggtggacaagaagcagagcccaaatcttgtgacaaa 3134
|||||

Qy 700 AATCACAGCCCAACCAACACAGGTGGAGAAAGAACAGACGCCCAAAATCTTGTGACAAA 759
|||||

Db 3135 actcacatgccacgctgcccagcactgaactcctctggggagccgtcagctctcttc 3194
|||||
Qy 760 ACTCACATGCCACCTGCCGACACCTGAACCTCTGGGGGACCGTCACTCTCCTC 819
Db 3195 ttcccccaaaacccaagagacacccctcatgatctccggagccctgaggtcacatggtg 3254
|||||
Qy 820 TTCCCCCAAAACCCCAAGGACACCTCATGCTCTCCGGACCCCTGAGGTCAATGGCTG 879
Db 3255 gtggtggagctgagccagcaagacccctgaggtcaagtccaactggtgagcggtg 3314
|||||
Qy 880 GTGGTGAGCTGAGCCACCAAGACCTGAGGTCAAGTTCACCTGGTAGCTGGACGGGCTG 939
Db 3315 gagggtcataatgccaaagcaaaacccgggagagcagtcacacagcagctacogtgg 3374
|||||
Qy 940 GAGGTGCATATGCCAAGCAAAACCCGGGAGGAGGAGTACACACAGCTACCGCTGTC 999
Db 3375 gtccagctcctcaccgtcctgcaccagagctggctgaatggcgaacagtcgaagtgaag 3434
|||||
Qy 1000 GTCCAGCGCTCTCACCGCTCTGCACCAAGGACTGGCTGAATGCCAAGGAGTACAAGTGAAG 1059
Db 3435 gtctccaaagaagccctccagcccccatcgagaaaaccatctccaaagccaaagggcag 3494
|||||
Qy 1060 GTCTCCAAAGAGCCCTCCAGCGCCCATCCGAGAAACCATCTCCAAAGCCAAAGGGCAG 1119
Db 3495 ccccgagaaaccacaggtgtacacccctgcccccatcccgggatgaggtgaccgaagaccag 3554
|||||
Qy 1120 CCGCGAGAACACAGGTGTACACCTGCGCCCATCCGGGATGAGCTGACCAAGAACAG 1179
Db 3555 gtccagctgaactgctggctcaaaaggctctatccagcgacatcgccgtggagtggag 3614
|||||
Qy 1180 GTACGCTGACCTGCTGTGTAAGGCTTCTATCCAGGACATCGCGCTGAGTGGAG 1239
Db 3615 agcaatggcgagcggagaaacaactacaagaccagcctcccgctgctggactccgagcgc 3674
|||||
Qy 1240 AGCAATGGGACGCGGAGAACATACAAAGACACGCTCCGCTGCTGGAGCTCGACGGC 1299
Db 3675 tccttctcctcacaagaagctaccgtggagaagcagaggtggcagcaggggaagctc 3734
|||||
Qy 1300 TCCCTCTCTCTACAGCAAGCTCACGCTGGACAAAGAGAGGCTGGCAGGGGGAAGCTC 1359
Db 3735 ttctcatgctccgtgatgatgaggtctgcacaaccactacacgcagagagcctctcc 3794
|||||
Qy 1360 TTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACACGCAAGAGGCTCTCC 1419
Db 3795 ctgtctccgggtaaatga 3812
|||||
Qy 1420 CTGTCTCCGGGTAATGA 1437
|||||

RESULT 7

ID Q23570 standard; DNA; 1467 BP.
AC Q23570;
DT 20-OCT-1992 (first entry)
DE Reshaped CAMPATH-1 antibody heavy chain cDNA.
KW Antigen; CD8; complementarity determining region; graft rejection;
KW autoimmune diseases; rheumatoid arthritis; allergy; ss.
OS Rattus rattus.
FH Key Location/Qualifiers
FT CDS 36..1448
FT /*tag= a
FT misc feature 183..197
FT /*tag= b
FT /*note= "Complementarity determining region 1"
FT misc feature 240..296

FT /*tag= c
FT /*note= "Complementarity determining region 2"
FT misc feature 392..422
FT /*tag= f
FT /*note= "Complementarity determining region 3"
PN W09205274-A.
PD 02-APR-1992.
PF 16-SEP-1991; G01578
PR 17-SEP-1990; GB-020282.
PA (GORM/) GORMAN S D.
PI Clark M R, Cobbold S P, Gorman S D, Waldmann H.
DR WP1; 92-132139/15.
DR P-PDB; R22757.
PT Humanisation of antibodies binding to human CD4 antigen - by
PT mutation of framework-encoding regions of DNA encoding variable
PT domain of rat or mouse antibody chain
PS Disclosure; Fig 5; 74pp; English.
CC The sequence is that of the reshaped CAMPATH-1 heavy chain cDNA.
CC Reshaped CD4 antibody can be used to induce tolerance against an
CC antigen. It can also be used to alleviate autoimmune diseases such
CC as rheumatoid arthritis, and to prevent graft rejection. Tolerance
CC to a graft, e.g. an organ graft or a bone marrow transplantation can
CC also be achieved. See also Q23566-Q23581.
CC also be achieved. See also Q23566-Q23581.
SQ Sequence 1467 BP; 352 A; 467 C; 384 G; 264 T;
Query Match 70.1%; Score 1007; DB 4; Length 1467;
Best Local Similarity 98.6%; Pred. No. 0.00e+00;
Matches 1021; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Db 414 ttgattactgggtcaagcagcctcgtcacagtcctctcagcctccaccagggccca 473
|||||
Qy 403 TTCCGAATTCGGGCCAGGGCCCTGGTCACCGCTCTCTCAGCTAGCACCAAGGGCCCA 462
Db 474 tegtgttccccctggaccctcctccaaagagcacctctgggggcacagggccctgggc 533
|||||
Qy 463 TCGGTCTTCCCCCTGGCACCTCTCTCCAGAGCACCTCTGGGGGACAGGGCCCTGGGC 522
Db 534 tgcctgtcaaggaactaattccccgaaccggtgacggtgtcgtggaactcagggccctg 593
|||||
Qy 523 TGCCTGCTCAGGACTACTTCCCGCAACCGGTGACGGTGTCTGGAACCTCAGGCCCTG 582
Db 594 accagcggcgtgcacacttcccggtgtcctacagtcctcaggactctactccctcagc 653
|||||
Qy 583 ACCAGCGCGCTGCACACCTTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCTCAGC 642
Db 654 agcgtggtgacgtgacctccagcagcttggggcaccagacacctacatctgcaacgtgaat 713
|||||
Qy 643 AGCGTGTGACGCTGCCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACCTGAAT 702
Db 714 cacaagcccaacacacaaaggtggacaagaagtggagcccaaatcttgtgacaaaact 773
|||||
Qy 703 CACAGGCCCAACACACAGAGGTGGACAGAAAGACAGACCCCAATCTTCTGACAAACT 762
Db 774 cacacatgcccaaccgtgccacagcactgaaactcctgggggagccgtcagctctctcttc 833
|||||
Qy 763 CACACATGCCACCGCTGCCAGCACCTGAACTCTCTGGGGGAGACCGTCAGTCTCTCTTC 822
Db 834 ccccccaaaacccaagggagacacctcatgatctcccgaccctgaggtcacatgcgtggtg 893
Qy 823 CCCCCAAAACCAAGGACACCTCATGATCTCCCGACCCCTGAGTCACTGAGTCACTGCTG 882
Db 894 gtgagcgtgagccacgaagacccctgaggtcaagttcaactggtacgtggagcgtggag 953
|||||

|||||
Qy 1124 GAGAACACAGGCTACACCTGCCCTCCCGATGCCGATGAGTGAACACACAGGTCA 1183
Db 870 gctgactgctggtcacaaggtctatcccagagacatcccggtgagtgaggagagca 929
|||||
Qy 1184 GCTTGACCTGGCTGGTCAAGGCTTCTATCCAGCGACATCCGCGTGGAGTGGGAGACA 1243
Db 930 atgggagccgagagaaactacaagaccacgctcccggtgctggactccgaggtcct 989
|||||
Qy 1244 ATGGGACGCGGAGAACAACTACAAGACACCGCTCCCGTGGTGGACTCCGACGGCTCT 1303
Db 990 tcttctctacagcaagctcaacctggacaagacaggtggcagcagggaagctctct 1049
|||||
Qy 1304 TCTTCTCTACAGCAAGCTCAGCTGGACAGAGCAGGTGGCAGCAGGCAAGCTCTTCT 1363
Db 1050 catgtccgtgatgatgaggtctgcacaaccactacacgacagagagctctccctgt 1109
|||||
Qy 1364 CATGCTCCGTGATGAGGCTCTGCACACCACTACAGCAGAGGCTCTCCCTGT 1423
Db 1110 ctccgggtaaatga 1123
|||||
Qy 1424 CTCGGGTAAATGA 1437
|||||

RESULT 9
ID N90779 standard; DNA; 1136 BP.
AC N90779;
DT 14-MAY-1990 (first entry)
DE Sequence of the linked immunoglobulin gamma chain fragment
KW Immunoglobulin gamma chain; IgG1 heavy chain constant region.
FH Key Location/Qualifiers
FT CDS
FT 8...1123
FT /*tag= a
PN EP-314317-A.
PD 03-MAY-1989.
PF 03-OCT-1988; 309194.
PR 28-SEP-1988; US-250785, US-104329.
PA (GETH) Genentech Inc.
PI Capon DJ, Gregory TJ;
DR WPI; 89-131855.
DR P-PSDB; P91918.
PT Compns. contg. adhesion variants
PT - useful in therapy and diagnostics, eg CD4 variants
PT which are therapeutically useful for treating human
PT immuno-deficiency virus
PS Figure 4a-4b; 36pp; English.
CC The polypeptide it codes for may be fused to the first 180 N-terminal
CC residues of CD4 at the C-terminus. The fusion protein may be used for
CC antiviral of immunomodulatory therapy particularly in treatment of HIV
CC infection.
SQ Sequence 1136 BP; 256 A; 385 C; 303 G; 192 T;

Query Match 69.9%; Score 1005; DB 1; Length 1136;
Best Local Similarity 98.7%; Pred. No. 0.00e+00;
Matches 1018; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 90 tcgacctggggcctgggaacctgggtcacggtctcctcgtgctccacaaagggcccat 149
|||||
Qy 404 TCGAATTCGTGGGGCGAGGCGCTGTGTCACCGTCTCTCAGCTAGCACCAAGGCGCCAT 463
Db 150 cgggtctccctcgtgacacctctccaagacacgtctgggggcacagcgccctgggct 209
|||||
Qy 464 CGGTCTTCGCCCTGGACCCCTCTCTCGAGAGCAGCTCTGGGGGCGACAGCGGCGCTGGGCT 523
|||||

Db 210 gcttggctcaagactacttcccgaaccggtgacggtgctcgtggaactcaggccctga 269
|||||
Qy 524 GCCTGCTGAAGACTACTTCCCGCAACCGGTGACGGTCTCTGGAACCTCAGCGGCTCA 583
Db 270 ccagcgggtgcacaccttcccggtgtcctacagtcctcaggactctactccctcagca 329
|||||
Qy 584 CCAGCGGCTGCACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCA 643
Db 330 ggttggtagcgtgccctccagcagcttgggcccacagacctacatctgcaacgtgaatc 389
|||||
Qy 644 GCCTGGTAGCCTGCCCTCCAGAGCTTGGGCACCAGACCTACATCTGCAAGCTGAATC 703
Db 390 acaagccagcaacacccaaggtggacaagaagtggcccacaaatcttggacaaaactc 449
|||||
Qy 704 AGAAGCCGACGACACCCAGGTGGACAGAAAGCAGAGGCCAAATCTTGTGACAAACTC 763
Db 450 acacatgccaccgtgccagcacctgaactcctgggggacgctcagctctctctctcc 509
|||||
Qy 764 ACACATGCCACCGCTGCCAGCACCTGAACCTCTCTGGGGGACCGCTCAGTCTCTCTCTCC 823
Db 510 ccccaaaaccaaaggacacctcatgatctccgggacctcaggtcaeatgctggtgg 569
|||||
Qy 824 CCCCCAAAACCAAGGACACCTCATCTCTCCGGAGCCCTTCAGGTGCATGCGTGGTGG 883
Db 570 tggagtgagccacyaagacctgaggtcaagtccaactggtacgtggacgggtggagg 629
|||||
Qy 884 TGGAGCTGAGCCACGAAGACCCCTGAGGTCAAGTCAACTGGTACGTGGAGCGGCTGGAGG 943
Db 630 tgcataatccaagacaaaagccgggagagcagctacaacagcagctaccgggtggtca 689
|||||
Qy 944 TGCATATGCCAAGACAAAGCCGCGGAGGACGAGTACACAGCAGCTACCGTGTGTGTC 1003
Db 690 gcttctcacggtcctgcacacgactggtgaatggcaagagtcacaagtcaagtgct 749
|||||
Qy 1004 CGGTCTCTACCGTCTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGTTCT 1063
Db 750 ccaacaaagccctcccagcccccatcgagaaaacccatctccaaagccaaagggagcccc 809
|||||
Qy 1064 CCAACAAAGCCCTCCAGGCCCATTCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC 1123
Db 810 gagaacacaggtgtacacctgcccccatcccgggtgagctgagctgaccaaagaccaggtca 869
|||||
Qy 1124 GAGAACCAAGCTGTACACCTTGGCCCTCCCGGATGAGCTGACCAAGACCAAGGTCA 1183
Db 870 gctgacctgctggtcaaggtcttctcccagcgacatcccggtgagtgaggagagca 929
|||||
Qy 1184 GCCTGACCTGCTCGTCAAGGCTTCTATCCCGGACATCCGCGTGGAGTGGGAGAGCA 1243
Db 930 atgggagccgagagaaactacaagaccacgctcccggtgctggactccgagcgtcct 989
|||||
Qy 1244 ATGGGACGCGGAGAACAACTACAAGACACCGCTCCCGTGGTGGACTCCGACGGCTCT 1303
Db 990 tcttctctacagcaagctcaacctggacaagagcaggtggcagcagggaagacctctct 1049
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Qy 1304 TCTTCTCTACAGCAAGCTCAGCGTGGACAGAGCAGGTGGCAGCGGCAAGCTCTTCT 1363
Db 1050 catgtccgtgatgatgaggtctgcacaaccactacacgacagagagctctcctcgt 1109
|||||
Qy 1364 CATGCTCCGTGATGAGGCTCTGCACACCACTACAGCAGAGGCTCTCCCTGT 1423
Db 1110 ctccgggtaaa 1120
|||||
Qy 1424 CTCGGGTAAA 1434
|||||

RESULT	10
ID	Q23571 standard; DNA; 1458 BP.
AC	Q23571;
DT	20-OCT-1992 (first entry)
DE	Reshaped CD4 antibody heavy chain cDNA CD4VHNEW-Thr30
KW	Antigen; CDR; complementarity determining region; graft rejection; autoimmune diseases; rheumatoid arthritis; allergy; ss.
OS	Rattus rattus.
FS	Key
FT	Location/Qualifiers
FT	CDS 36..1439
FT	FT **tag= a
FT	FT misc_feature 183..197
FT	FT **tag= b
FT	FT /note= "Complementarity determining region 1"
FT	FT misc_feature 240..290
FT	FT **tag= c
FT	FT /note= "Complementarity determining region 2"
FT	FT misc_feature 387..413
FT	FT **tag= d
FT	FT /note= "Complementarity determining region 3"
PN	WO9205274-A.
PD	02-APR-1992.
PF	PF 16-SEP-1991; G01578.
PR	PR 17-SEP-1990; GB-020282.
PA	(GORM/) GORMAN S D.
PI	Clark M R, Cobbold S P, Gorman S D, Waldmann H.
DR	WPI; 92-132139/16.
DR	P-PSDB; R22758.
PT	PT Humanisation of antibodies binding to human CD4 antigen - by
PT	mutation of framework-encoding regions of DNA encoding variable
PT	domain of rat or mouse antibody chain
PS	Disclosure; Fig 6; 74pp; English.
CC	CC The sequence is that of the reshaped CD4 antibody heavy chain cDNA
CC	CC CD4VHNEW-Thr30. Reshaped CD4 antibody can be used to induce tolerance
CC	CC against an antigen. It can also be used to alleviate autoimmune diseases
CC	CC such as rheumatoid arthritis, and to prevent graft rejection. Tolerance
CC	CC to a graft, e.g. an organ graft or a bone marrow transplantation can
CC	CC also be useful to alleviate allergies. Tolerance to allergens could
CC	CC also be achieved. See also Q23566-Q23581.
SC	SC Sequence 1458 BP; 345 A; 467 C; 385 G; 261 T;
Query Match	69.9%; Score 1005; DB 4; Length 1458;
Best Local Similarity	98.9%; Pred. No. 0.00e+00;
Matches	1016; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Db	413 ctgggtcaaggcagctctccaagagcactctgggggcacagcgccctggctgctgctt 472
Qy	411 CTGGGGCCAGGGGCCCTGGTCACCGCTCCTCCTACGTAGACACAGGGCCCATGGCTCTT 470
Db	473 ccccttggcaccctcctccaagagcactctgggggcacagcgccctggctgctgctt 532
Qy	471 CCCCCCTGGGACCCCTCTCCACAGACACTCTGGGGGACACAGCGGCCCTGGGCTGGCTGT 530
Db	533 caaggaactctcccgaaaccggtgacggtgtcgtggaactcaggcgccctgacacagcg 592
Qy	531 CAAGGACTACTTCCCGGAAACCGGTGACGGTGTCTGTGGAACCTACGGCGGCCCTACCAAGCGG 590
Db	593 cgtgcaacacttcccggtgtgcttcaagtcctcaggactctactccctcagcagcgtggt 652
Qy	591 CGTGCACACTTCCGGGTCTCTACAGTCTCTCAGGACTTACTCCCTCAGACGCTGT 650
Db	653 gaccgtgccctccagcajcttggggcaccacagcactacatctgcaacgtgaatcacaaagc 712

Qy	651	GACCGTGCCTTCAGCAGCTTGGGCACCCAGCATACATCTGCAAGCGTGAATCAAGCC	710
Db	713	cagcaaccacaaagttgacagaagaadtTgagcccaaatcttTgacaaaactcacacatg	772
Qy	711	CAGCAACACCAAGGTGCAAGAAGACGAGCCAAATCTTGTGACAAAATCACACATG	770
Db	773	cccaactgcgtccagcaacctgaactcctctggggggagccgtcagdtctctcttcccccaaa	832
Qy	771	CCCAACGCTGCCAGCAGCTGAATCTCTGGGGGACCGTCACTCTTCTTCCCGCCAAA	830
Db	833	accaagagcacacctcatgctctcccggaccctcTgaggtcacatcgctgggtgggtgagct	892
Qy	831	ACCCAAGACACACCTCATGATCTCTCGGACCCCTGAGGTGCATCGCTGGTGGCGCT	890
Db	893	gagccacgaagaccctgaggtcaagttcaactggtacgtggacgtggcgtggaggtgcataa	952
Qy	891	GAGCACACGACACCTTGAGGTCAAGTTTCAACTGGTACGTGACGGCTGGAGGTGCATAA	950
Db	953	TGCCAGCAAAACCGCGGGAGGAGCAGTCAACACGACGCTACCGTGTGGTCAAGCTCT	1012
Qy	951	TGCCAGCAAAACCGCGGGAGGAGCAGTCAACACGACGCTACCGTGTGGTCAAGCTCT	1010
Db	1013	cacgtcctgcaccaggactgctgaattgcaaggaggtacaagtgcaaggtctcccaaaa	1072
Qy	1011	CACCGTCTCTCAGCAGGACTGGCTGAATGGCAAGAGTACAAGTGCAGGCTCTCCAACA	1070
Db	1073	agccctcccagcccccactcgagaaaaccattctcaagccaaaagggcagcccgagacc	1132
Qy	1071	AGCCCTTCCAGCCCGCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAAC	1130
Db	1133	acaggtgtacacctgcccccattcccggatgagctgaccaagaaccaggtcagcctgac	1192
Qy	1131	ACAGGTGTACACCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGC	1190
Db	1193	ctgcctggtcaaaagctctatccagcagcatcgccgtggagtgagagcaatggcca	1252
Qy	1191	CTGCCTTGGTCAAAAGCTTCTATCTCAGCGCATCGCGGTGGAGTGGAGCAATGGCCA	1250
Db	1253	gccgagacaactacagacacgcctcccgtgctggactccgacgctctcttctct	1312
Qy	1251	GCCGAGAAACATCAAGACCAACGCTCCGCTGCTGGACCTCCGACGGCTCTTCTCTCT	1310
Db	1313	ctcagcaagctcacgtgacaagagcaggtggcagcaggggaacgtctctctcatgctc	1372
Qy	1311	CTACAGCAAGTCAACCGTGGACAAGCAGGTGGCAGCGGGAGCGTCTTCTCATGCTC	1370
Db	1373	cgtgatgcatgaggtctgcacaaacctacacgcagagaagcctctccctgtctccggg	1432
Qy	1371	CGTGATGATGAGGCTCTGCACACCACTACACGACGAGGAGGCTCTCCCTGTCTCGGG	1430
Db	1433	taaatga 1439	
Qy	1431	TAAATGA 1437	
RESULT	11		
ID	Q23581	standard; DNA; 1458 BP.	
AC	Q23581;		
DT	20-OCT-1992	(first entry)	
DE	Reshaped CD4 antibody heavy chain cDNA CD4VHNEW-Ser30		
KW	Antigen; CD4; complementarity determining region; graft rejection;		
KW	autoimmune diseases; rheumatoid arthritis; allergy; as.		
OS	Rattus rattus.		
FS	Key	Location/Qualifiers	

413	ctggggtcaaggcagcctctgcacagtctctcagcctccaccaaggggccatcggttt	472
Db		
411	CTGGGGCGAGGGCGCCTGGTCAACCGTCTCTCAGCTAGACCAAGAGGGCCATCGGTCTT	470
Qy		
473	ccccctggcaacctcctccaagagcaactctgggggcacagcgccctgggctgctggt	532
Db		
471	CCCCCTGGCAACCTCTCCAAAGACACCTCTGGGGGCACAGCGGCTTGGGGCTGCTGTT	530
Qy		
533	caaggactacttccccgaaccggtgacggtgtcgtgnaactcaggggccctgaccacgg	592
Db		
531	CAAGGACTACTTCCCGCAACCGGTGACGGTGTCTGGAACTCAGCGCGCTGACCAGCGG	590
Qy		
593	cgtgcacacttccggctgtctcaagctcctcaggactctactcctcgcagcagcgtggt	652
Db		
591	CGTGCACACCTTCCCGCTGCTCTACAGTCTCTCAGGACTCTACTCCTCAGCAGCGGTGTT	650
Qy		
653	gaccgtgcctccagcagcttgggcccaccagacctacatctgcaacgtgaatcacaaGCC	712
Db		
651	GACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGTAATCACAGCC	710
Qy		
713	cagcaacaccaagttggacagaagaagttagccccaatctgtgacaaaactcacacatg	772
Db		
711	CAGCAACACACAGGTGGACAAAGACAGAGGCCCAAACTCTTGTGCAAAACTCACACATG	770
Qy		
773	cccacggtgcccagcactgaactcctctgggggacgctcagctcttctccccccaaa	832
Db		
771	CCACCGTGGCCACAGCTGAACCTCTCTGGGGGGACCGTCAGTCTTCTCTTCCCCC AAAA	830
Qy		

RESOLU. 12	ID	T15932 standard; DNA; 6557 BP.
	AC	T15932;
	DT	20-JUN-1996 (first entry)
	DE	Anti-IgE VH expression vector.
	RE	Recombinant host cell; dihydrofolate reductase; selectable marker;
	KW	DHER1; ras splice donor; dicistronic vector; gene expression;
	KW	IgE; immunoglobulin; antibody; ds.
	OS	Synthetic.
	PN	W09604391-A1.
	PD	15-FEB-1996.
	PF	28-JUL-1995; 009576.
	PR	05-AUG-1994; US-286740.
	PA	(GETH) GENENTECH INC.
	PI	Crowley CW;
	DR	WPI; 96-129407/13.
	PPT	Improved process for the selection of recombinant host cells
	PPT	expressing high level of a desired product - uses eukaryotic host
	PPT	cells contg. a DNA construct comprising a selectable gene

QY 394 GGAGGTACTTCGAATTCCTGGGCGAGGGCGCTGGTCAACGGTCTCCTCAGCTAGACACC 453

Db 502 aaggccceatcggtcttccccctggaccctctccaagagacacctctctggggcagcagcg 561
|||||

QY 454 AAGGGCCCTCGGTCTTCCCGCTGGGACCGCTCTCCAGACACCTCTGGGGGACAGGG 513
|||||

Db 562 gccctgggctgacctggtcaagactacttccccgaaccgggtgacggtgctgctggaactca 621
|||||

QY 514 GCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCGAACCGGTGAGGGTGTCTGGAACCTCA 573
|||||

Db 622 ggcgcctgacacagcggtgcaaccttcccggtgctctacagtcctcaggaactctac 681
|||||

QY 574 GGGCCCTGACGAGCGGGTGCACACTTCCCGGGTGTCTCAGACTCTCAGGACTCTAC 633
|||||

Db 682 tccctcaagacgctggtgacctgacctccagcagcttgggcaaccagacctacatctgc 741
|||||

QY 634 TCCCTCAGAGCGTGTGACCGTGGCTCCAGCAGGTTGGCGACCCAGACTACATCTGC 693
|||||

Db 742 aacgtgaatcacagccacgacacccaaggtggacaagaagttagcccaaatcttgt 801
|||||

QY 694 AAGGTGAATCACAAAGCCAGACACCAAGGTGGACAAAGCAAGGCCCAATCTTGT 753
|||||

Db 802 gacaaactcacatgcccacgctgccacgacctgaactcctggggagacctcagtc 861
|||||

QY 754 GACAAACTCACACATGCCACCGCTGCCACGACCTGAACCTCTGGGGGAGCCGTGAGTC 813
|||||

Db 862 ttcccttcccccaaaacccaagagacacctcatgatctccggaccctgaggtcaaa 921
|||||

QY 814 TTCCTCTTCCCGCCAAAACCAAGAGACACCTCATGATCTCCGGACCCCTCAGGTCA 873
|||||

Db 922 tgcgtggtggtgagcgcgagccgaagacctgaggtcaagttcaactggtgacgtggac 981
|||||

QY 874 TGGCTGCTGGTGACGCTGAGCCGACGAACCTTGAGTCAAGTTCACCTGCTGCTGGAC 933
|||||

Db 982 ggcgtggaggtgcaataatgccaaagacgacgagcggtggagagcagtcacacagacgctac 1041
|||||

QY 934 GGGCTGAGGTGCATAATTCAGACAAAGCCGGGAGGAGCAGTACACAGCAGCTAC 993
|||||

Db 1042 cgtggtggtcagcgtcctcaccgctcctgaccagagctggctgaatggcaagagatcaaa 1101
|||||

QY 994 CGTGTGGTCAAGCGTCTCAACGCTCTGCACCAAGGACTGGCTGAATGGCAAGAGTACAA 1053
|||||

Db 1102 tgaaggtctcaaaagacgctcccgcccccatcgagaaaccatctccaaagccaaa 1161
|||||

QY 1054 TGCAGGCTTCCAAACAAAGCCCTCCAGCGCCCATCGAATAACCATCTCCAAAGCCAAA 1113
|||||

Db 1162 gggcagccccgagaaacacaggtgtacacctgcccccatcccggtgagctgacctgaccaag 1221
|||||

QY 1114 GGGCAGCCCGAGACACACAGGTGTACACCTCTGCCCCCATCCCGGGATGAGCTGACCAAG 1173
|||||

Db 1222 aaccaggtcagcgtgacctgctggtcaaaagcttctatcccgagcagatcgccgtggag 1281
|||||

QY 1174 AACCAAGTCAAGCTGACCTGCTGTCAAAGGCTTATTCACAGCAGATGCCGCTGGAG 1233
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Db 1282 tggagagcaatggcgagccgagaaactacaagaccgctcccgctgctgactcc 1341
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QY 1234 TGGGAGCAATGGCGACGGGAAACACTACAAGACCGCTCCCGTGGACTCC 1293
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Db 1342 gacgctctcttctctctacacgaagctcacgctggacaagacaggtggcagcagggg 1401
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QY 1294 GAGGGCTCTTCTCTCTACAGCAAGCTCACCGTGGCAAGAGCAGGTGGCAGAGGGG 1353
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Db 1402 aacgtctctcatgctcggtgcatgaggtctgtgcaaaccaactacacgagaagagc 1461
|||||

QY 1354 AAGCTCTTCTCATGCTCGTCATGCGTCAGTCAGGCTCTGCACAACCACTACAGCAGAGAGC 1413

Db 1462 ctctccctgtctccgggtaaatga 1485
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QY 1414 CTCTCGCTGCTCCGGGTAAATGA 1437

RESULT 14

ID Q25692 standard; cDNA; 1412 BP.

AC Q25692;

DT 28-DEC-1992 (first entry)

DE Sequence of the chimeric H chain cDNA contained in pTB1373

KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;

KW antithrombotic agent; myocardial infarction therapy; ss.

OS Synthetic.

FH Key Location/Qualifiers

FT sig_peptide 13..69

FT /*tag= a

FT /product= Leader

FT CDS 70..414

FT /*tag= .b

FT /product= VH

FT CDS 415..708

FT /*tag= c

FT /product= CH1

FT CDS 709..753

FT /*tag= d

FT /product= hinge

FT CDS 754..1083

FT /*tag= e

FT /product= CH2

FT CDS 1084..1407

FT /*tag= f

FT /product= CH3

PN EP-491351-A.

PD 24-JUN-1992.

PF 17-DEC-1991; 121591.

PR 18-DEC-1990; JP-413829.

PR 11-NOV-1991; JP-294464.

PA (TAKE) TAKEDA CHEM IND LTD.

PI Iwasa S, Taka H, Watanabe T, Tada H;

DR WPI; 92-209528/26.

DR P-PSDB; R24812.

PT Chimeric monoclonal antibodies - contain anti-human fibrin

PT antibody light and heavy chain variable and constant for treating

PT thrombotic conditions e.g. myocardial infarction

PS Example; Figure 11; 87pp; English.

CC Plasmid pTB1373 contains the whole length of a mouse-human

CC chimeric anti-human fibrin heavy chain cDNA open reading

CC frame. It was prepd. using Poly(A) + RNA from the anti-fibrin

CC chimeric Ab-producing transformant FIB1-H01/X63 as a template

CC to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as

CC a primer for first strand cDNA synthesis and the 5'CZH and 3'EH

CC primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding

CC encoding cDNA and an anti-fibrin antibody VH cDNA and a leader.

CC peptide cDNA were amplified using the primers 3'EH, 3'CZH and 3'CLH

CC respectively as a primer for first strand cDNA synthesis and the

CC primer combination of 5'CLH and 3'CZH, of 5' LH and 3'CLH and of

CC 5'SH and 3' LH respectively as primers for PCR. The amplified gene

CC products were isolated and used to produce plasmids. After

CC confirmation of the cDNA sequence of each plasmid, the cDNA

CC encoding LH, VH, CH1 and CH2CH3 were joined together to give

CC plasmid pTB1373 contg. the whole length chimeric H chain

Db 2332 ggactctactccctcagcagcgtggtgacctgcccctccagcagcttcggcaccagacc 2391
|||||
Qy 625 GGACTCTACTCCCTCAGCAGGTGGTGACCGTCCCTCCAGAGCTTGGCACCCAGACC 684
Db 2392 tacatctgaacgtaatacacaagccagacacacaaggtggacaagaagagagagccc 2451
|||||
Qy 685 TACATCTGCAACGCTGAATCAGAAGCCAGCAACCAAGGTGGACAGAAGACAGAGCCC 744
Db 2452 aaatcttgtacaaaactcacacatgccaacgctgccacagacctgaactcctgggggga 2511
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Qy 745 AAATCTTGTGACAAAATCACATGCCACCGTGCCAGCACCTGAATCCTCTGGGGGA 804
Db 2512 ccgtcagctcttctcttcccccaaaagcacacctcatgatctccccggaccct 2571
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Qy 805 CCGTCAGCTTCTCTCTTCCCCCAAAACCCAGGACACCCCTCATGATCTCCCGGACCCCT 864
Db 2572 gaggtcacatgcgtggtggtgagcgtgagccagcagacctgaggtcaagttcaactgg 2631
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Qy 865 GAGGTCAATGCGTGGTGGACGTGAGCCAGCACCAAGACCCCTGAGGTCAAGTTCAACTGG 924
Db 2632 tacgtgacggcgtggaagtgataatgccaaagacaaagccgggagggagcagtaaac 2691
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Qy 925 TAGGTGACGGCGTGGAGTGCATAATGCCAAGCAAAAGCCGGGAGGAGCAGTACAAC 984
Db 2692 agcacgtaccggtggtgcagctcctcacgtcctgcaccagcagctgggtgaatggcaag 2751
|||||
Qy 985 AGCAGGTACCGTCTGGTCAGCGTCTCAGCGTCTGCACAGGAGCTGGCTGAATGGCAAG 1044
Db 2752 gactacaagtcgaagctcccaaaaagccctcccagcccccatcgaaaaaccatctcc 2811
|||||
Qy 1045 GAGTACAGTGCAGGTCTCCACAAAGCCCTCCAGGCCCCATCGAANAACCATCTCC 1104
Db 2812 aaagccaaaggcagcccgagaaacacaggtgtacacctgcccccatcccggtatgag 2871
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Qy 1105 AAAGCCAAAGGGCAGCCCGAGAAACACAGGTGTACACCTTGCCCCCATCCCGGGATGAG 1164
Db 2872 ctgaccaggaacaggtcagcctgacctgctggtcctaaaggcttatccccagcgacatc 2931
|||||
Qy 1165 CTGACCAAGAACACAGGTCAAGCTGCTGCTGCTGCTCAAGGCTTCTATCCAGCGACATC 1224
Db 2932 gccgtggagtgggagagaatggcagccggagagaacaactacaaagaccacgctcccgtg 2991
|||||
Qy 1225 GCCGTGGAGTGGGAGAGCAATGGCAGCGCGAGACAACACTACAAGACACGCCCTCCCGTG 1284
Db 2992 ctggactccgagcgtctcttctctcagcaagctcacccgtggacaagagcaggtgg 3051
|||||
Qy 1285 CTGGACTCCGACGGCTCTCTCTCTTCTTCTACAGAGCTCACCCGTGGACACAGCAGGTGG 1344
Db 3052 cagcaggggaacgtctctcatgctccgtgcatgcatgaggtctcgacaaccactacag 3111
|||||
Qy 1345 CAGCAGGGGAACGCTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACTACACG 1404
Db 3112 cagaagagcctctccctgtctccgggtaaatga 3144
|||||
Qy 1405 CAGAAGAGCCTCTCCCTGTCTCGGGTAATGA 1437

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPerch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 22:43:23 1996; MasPar time 436.62 Seconds
1237.697 Million cell updates/sec

Tabular output not generated.

Title: >US-08-487-550-9

Description: (1-711) from US08487550.seq

Perfect Score: 711

N.A. Sequence: 1 ATGAGGTCGCCGCTCAGCT.....CCCCACAGATGTTTCATGA 711

Comp: TACTCCAGGGCGGAGTCGA.....GGGATCTCTACAGTACT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 270440 seqs, 380027776 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: emb1-new3

1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLN

9:PRI1 10:PRI2 11:PRO 12:ROD 13:SYN 14:UNC 15:VRT

16:VIR1 17:VIR2

Database: genbank92

18:BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7

25:BCT8 26:BCT9 27:INV1 28:INV2 29:INV3 30:INV4 31:INV5

32:INV6 33:MAM1 34:MAM2 35:PAT1 36:PAT2 37:PAT3 38:PHG

39:PLN1 40:PLN2 41:PLN3 42:PLN4 43:PLN5 44:PLN6 45:PLN7

46:PLN8 47:PRI1 48:PRI2 49:PRI3 50:PRI4 51:PRI5 52:PRI6

53:PRI7 54:PRI8 55:PRI9 56:PRI10 57:PRI11 58:PRI12

59:PRI13 60:ROD1 61:ROD2 62:ROD3 63:ROD4 64:ROD5 65:ROD6

66:ROD7 67:STR 68:SYN 69:UNA 70:VRL1 71:VRL2 72:VRL3

73:VRL4 74:VRL5 75:VRL6 76:VRL7 77:VRT1 78:VRT2 79:VRT3

Database: genbank-new1

80:BCT 81:INV1 82:INV2 83:MAM 84:PHG 85:PLN 86:PRI

87:ROD 88:STR 89:SYN 90:UNA 91:VRL 92:VRT

Database: u-emb145_92

93:part1

Statistics: Mean 10.89; Variance 4.490; scale 2.426

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	548	77.1	870 51	HSIGLV	Human mRNA for Ig lam	0.00e+00
2	540	75.9	750 51	HSIGLV027	Human rearranged immu	0.00e+00
3	534	75.1	747 51	HSIGLV006	Human rearranged immu	0.00e+00
4	528	74.3	827 51	HSIGLV021	Human rearranged immu	0.00e+00
5	522	73.4	802 51	HSIGLV032	Human rearranged immu	0.00e+00
6	520	73.1	810 51	HSIGLV025	Human rearranged immu	0.00e+00
7	492	69.2	915 51	HSIGLV009	Human rearranged immu	0.00e+00
8	484	68.1	819 51	HSIGLV029	Human rearranged immu	0.00e+00
9	480	67.5	642 59	S42404	Ig lambda chain=anti-	0.00e+00
10	470	66.1	663 52	HS007991	Human lymphoma immuno	0.00e+00
11	470	66.1	663 9	HS007991	Human lymphoma immuno	0.00e+00
12	459	64.6	877 56	HUMIGHEPAL	Human (hybridoma H210	0.00e+00
13	455	64.0	623 59	S77011	(pseudogene) Ig V lam	0.00e+00
14	448	63.0	783 51	HSIGLV001	Human rearranged immu	0.00e+00
15	447	62.9	756 51	HSIGLV034	Human rearranged immu	0.00e+00
16	444	62.4	666 9	HS007992	Human myeloma immunog	0.00e+00
17	444	62.4	666 52	HS007992	Human myeloma immunog	0.00e+00
18	435	61.2	806 51	HSIGLV005	Human rearranged immu	0.00e+00
19	430	60.5	872 56	HUMIGLAM2	Human Ig rearranged l	0.00e+00
20	426	59.9	664 51	HSIGLV004	Human rearranged immu	0.00e+00
21	423	59.5	652 56	HUMIGLV0CX	Human immunoglobulin	0.00e+00
22	423	59.5	737 51	HSIGLV023	Human rearranged immu	0.00e+00
23	423	59.5	803 51	HSIGLV022	Human rearranged immu	0.00e+00
24	421	59.2	755 51	HSIGLV033	Human rearranged immu	0.00e+00
25	417	58.6	747 51	HSIGLV031	Human rearranged immu	0.00e+00
26	400	56.3	780 51	HSIGLV011	Human rearranged immu	0.00e+00
27	398	56.0	725 51	HSIGLV002	Human rearranged immu	0.00e+00
28	392	55.1	839 51	HSIGLV026	Human rearranged immu	0.00e+00
29	391	55.0	838 51	HSIGLV01	Human mRNA for Ig lam	0.00e+00
30	384	54.0	791 51	HSIGLV028	Human rearranged immu	0.00e+00
31	375	52.7	820 51	HSIGLV024	Human rearranged immu	0.00e+00
32	358	50.4	600 56	HUMIGTAT7F	Homo sapiens (clone t	0.00e+00
33	358	50.4	600 10	HSIGTAT7F	Homo sapiens (clone t	0.00e+00
34	358	50.4	600 86	HUMIGTAT7F	Homo sapiens (clone t	0.00e+00
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36	354	49.8	495 86	HUMIGTAT3A	Homo sapiens (clone t	0.00e+00
37	354	49.8	495 10	HSIGTAT3A	Homo sapiens (clone t	0.00e+00
38	354	49.8	780 51	HSIGLV030	Human rearranged immu	0.00e+00
39	345	48.5	881 56	HUMIGLYM1	Human immunoglobulin	0.00e+00
40	342	48.1	498 86	HUMIGTATAC	Homo sapiens (clone t	0.00e+00
41	342	48.1	498 10	HSIGTATAC	Homo sapiens (clone t	0.00e+00
42	342	48.1	498 56	HUMIGTATAC	Homo sapiens (clone t	0.00e+00
43	340	47.8	776 33	HRSTGLF	Equus caballus (clone	0.00e+00
44	334	47.0	900 33	BTICLCXX	B.taurus mRNA for imm	9.55e-299
45	329	46.3	585 56	HUMIGTATAB	Homo sapiens (clone t	1.21e-293

ALIGNMENTS

RESULT	LOCUS	DEFINITION	Accession	NID	KEYWORDS	SOURCE	ORGANISM
1	HSIGLV	Human mRNA for Ig lambda-chain.	X14583	933394	Ig light chain; immunoglobulin; lambda-immunoglobulin.	human.	Homo sapiens
							Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;

REFERENCE 1 (bases 1 to 870)
AUTHORS Kishimoto, T.
TITLE Direct Submission
JOURNAL Submitted (03-MAR-1989) Kishimoto T., Yoshitomi Pharmaceutical Industries Ltd, Research Labs, 7-25 Koyata 3-chome, Iruma Shi, Saitama, 358 Japan
2 (bases 1 to 414)
AUTHORS Kishimoto, T., Okajima, H., Okumoto, T. and Taniuchi, M.
TITLE Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of a human monoclonal antibody with broad reactivity to malignant tumor cells
JOURNAL Nucleic Acids Res. 17 (11), 4385 (1989)
MEDLINE 89296497
COMMENT hybridoma; clone=4G12 L6
Data kindly reviewed (03-JUL-1989) by Kishimoto T.

NCBI gi: 33394
Location/Qualifiers
1..870
/organism="Homo sapiens"
/tissue_type="lymph node"
/cell_type="lymphocyte"
/cell_line="4G12"
25..84
/note="signal peptide (AA -20 to -1)"
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/note="pid:g33395; NCBI gi: 33395"
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/product="lambda-chain precursor (AA -20 to 215)"
/db_xref="PID:g33395"
/translation="MTCSPLLLTLLIHCTGSAQSVLTQPPSVSAAPCQKVTISGSG
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BASE COUNT 206 a 285 c 213 g 166 t
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Best Local Similarity 92.34; Pred.(No. 0.00e+00;
Matches 598; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
Db 83 agtctgtgtgacgagccgcccctcagtgctgctgcccagacagagtgcaaccatct 142
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Qy 62 AGTCTGCTGACACAGCGCCCTCAGTGTCTGGGCCCCAGGCGGACAGAGTCACCATCT 121
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Db 143 cctgtctgtggaagcagctccaaattgggaataattatgtatctggtaaccagcgtcc 202
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 122 CGTGCACTGGGACGACCTCCCAATGGAGGTTATGATCTACATCTGGTACCAAGCTCC 181
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 203 caggacagcccccaactcctcatttatgacaataataagcgaccctcagggtattctg 262
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Qy 182 CAGGACGGCCCCCAAACTCTCATCTATGACATTTAAACAGCGACCCCTCAGGAATTTCTG 241
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Db 263 accgatctctggctccaaagtctggcagctcagccaccctggcgatccaccgactccaga 322
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Qy 242 ACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCTCCCTGGCATCTGGGCTCCAGA 301
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 323 ctggggagcaggccgattactcgggaacatcggtggtatgagcagcctgagtgctgggtat 382
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Qy 302 CTGAGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGAGCCTGAATGCTCAGGTAT 361
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Qy 362 TCGGAGGAGGAGCCCGCTGACCGTCTTAGGTGAGCCCAAGGCTGCCCTCGGTCACTC 421
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Db 443 tgtccgcctcctctgagagcttcaaggccaagggccacactgggtgtctcataa 502
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Qy 422 TGTTCGCCCTCTCTGAGGAGCTTCAAGCCCAACAGCCACACTGGTGTCTCATAA 481
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Db 503 gtgactctaccgggagccgctgacagtgccctggaagcagatagcagcccgcaag 562
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Qy 482 GTGACTTCTACCGGGAGCCCTGACAGTGGCCTTGAAGGAGATAGCAGCCCTCAAGG 541
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Db 623 atcgagcctgagcctgagcagtggaagtcaccagagctacagctgccaggtcacgc 682
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Qy 602 ACCTGAGCCTGAGCGCTGAGCAGTGGAGTCCCAAGAGCTACAGCTGCCAGGTCAAGC 661
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Db 683 atgaaggagcagcctggaagacagtgccctcacagaatgtcat 730
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 662 ATGAGGAGCAGCCGCTGGAGAGACAGTGGCCCTTACAGAAATGTTCAAT 709
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RESULT 2
LOCUS HSTGL027 750 bp RNA PRI 20-JUL-1995
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION X57817
NID g33733
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.
REFERENCE 1 (bases 1 to 750)
AUTHORS Klobbeck, H.G.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G. Klobbeck, Inst fuer Physiologische Chemie, Physiologische Biochemie und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany
REFERENCE 2 (bases 338 to 384)
AUTHORS Combrato, G. and Klobbeck, H.G.
TITLE V lambda and J lambda-C lambda gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism
JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE 91257162
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

NCBI gi: 33733
Location/Qualifiers
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Db 137 cctgtctgtggacagcttccaaatcggggcaggttcattcattgctgtgctaccagaag 196
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Qy 122 CGTGCACTGGGACACCTCCACATGG---AGTTATGATCTACATTGCTACACGACGC 178
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Db 197 ttccaggacagcccccacaaactcctcatctatgctgacaaatcggccctcagggtcc 256
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Db 257 ctgaccgaatctctggtccaagtggcgacttcagctccctggccatcactgggtcc 316
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RESULT 5
LOCUS HSIGVL032 802 bp RNA PRI 04-NOV-1994
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION X57822
NID 933743
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcosterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Carnivora; Hominiinae; Homo.
REFERENCE 1 (bases 1 to 802)
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AUTHORS Klobeck, H.G.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.
Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie
und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000
Muenchen 2, Germany
REFERENCE 2 (bases 342 to 388)
AUTHORS Combriato, G. and Klobeck, H.G.
TITLE V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism
JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE 91257162
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

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Best Local Similarity 90.3%; Pred. No. 0.00e+00;
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Qy 62 AGTCTGTCTGTACACAGCGCCCTCAGTGTCTGGGGCCCGCAGGCGAGAGGTCAACATCT 121
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QY 542 CGGAGTGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGCCAGCAGCT 601

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QY 602 ACCTGAGCCTGAGCGCTGACGACTGGAAGTCCACAGAGGCTACAGCTGCCAGGTCAAG 661

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QY 662 ATGAAGGAGCAGCTGGAGACAGTGGCGCCCTACAGATTTTCAT 709

RESULT 7

LOCUS H5IGVL009 915 bp RNA PRI 04-NOV-1994

DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.

ACCESSION X57809

NID g33714

KEYWORDS Ig lambda light chain; immunoglobulin.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 915)

AUTHORS Klobeck, H.G.

TITLE Direct Submission

JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G. Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany

REFERENCE 2 (bases 452 to 498)

AUTHORS Cambriato, G. and Klobeck, H.G.

TITLE V lambda and J lambda-C lambda gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism

JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)

MEDLINE 91257162

COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

FEATURES

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Matches 585; Conservative 0; Mismatches 57; Indels 6; Gaps 4;

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QY 422 TGTTCGGCGCCCTCTCTGAGAGCTTCAGCCCAACAGCCACACTGCTGTCTCTATA 481

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 RESULT 9
 LOCUS S42404 642 bp mRNA PRI 15-NOV-1992
 DEFINITION Ig lambda chain=anti-Rh (D) antibody [human, mRNA Partial, 642 nt].
 ACCESSION S42404
 NID g253701
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 642)
 AUTHORS Chouchane, L., Van Spronsen, A., Breyer, J., Guglielmi, P. and Strosberg, A. D.
 TITLE Molecular characterization of a human anti-Rh (D) antibody with a DH segment encoded by a germ-line sequence
 JOURNAL Eur. J. Biochem. 207 (3), 1115-1121 (1992)
 MEDLINE 92362614
 REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 11063] from the original journal article. This sequence comes from Fig. 4.
 COMMENT NCBI gi: 253701
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 Author-given protein sequence is in conflict with the conceptual translation. NCBI gi: 253702"
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Qy 122 CGTGCACTGGGAGCACCTCCACATTGGAGGTTATCA--TCTACAT--TCGTACCAGCAGC 178
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RESULT 15
LOCUS HSIGVL034 756 bp RNA PRI 04-NOV-1994
DEFINITION Human rearranged immunoglobulin lambda light chain mRNA.
ACCESSION X57824
NID g33747
KEYWORDS Ig lambda light chain; immunoglobulin.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 756)
AUTHORS Klobeck,H.G.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1991) to the EMBL/GenBank/DBJ databases. H.G.
Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie
und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000
Muenchen 2, Germany
REFERENCE 2 (bases 344 to 390)
AUTHORS Combratio,G. and Klobeck,H.G.
TITLE V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism
JOURNAL Eur. J. Immunol. 21 (6), 1513-1522 (1991)
MEDLINE 91257162
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.

NCBI gi: 33747 Location/Qualifiers
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Matches 564; Conservative 0; Mismatches 81; Indels 6; Gaps 5;

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Dbb 119 cctgattggaccagcagtcagtcgtgtcttattttctcctgggtaccagcaat 178
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Dbb 416 ctctgttcccgctctcttgaggagcttcaagccaagaaggccacactggtgtctca 475
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Dbb 476 taagtgacttctaccgggagccgtgacagtggcctggaaggcagatagcagcccgctca 535
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Dbb 536 gggcgaggagtggagaccacacacctccaaacaagaagcaacaagtaacgcgccagca 595
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Dbb 596 gctatctgagcctgacg-ctgagcagtggaagtcacacagaagctacagctgccaggtca 655
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Dbb 656 cgcataaggaggagaccjtggaagaagcagtggtccctacagaatgttcat 706
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PD	15-FEB-1990.	
PF	05-AUG-1988; 196647.	
PR	05-AUG-1988; JP-196647.	
PP	(YOSH) Yoshitomi Pharm. Ind. KK.	
PA	WPI; 90-094983/13.	
DR	P-PSDB;R05555.	
PT	DNA base sequence coding for 4G12 monoclonal antibody - which reacts	
PT	specifically with human lung cancer and oesophageal carcinoma.	
PS	Disclosure; Page 549; 9pp; Japanese.	
CC	Sequence is cloned and synthetic DNA/RNA of human Ab L chain C regions	
CC	is used as probe to obtain sequences coding for 4G12 Mab.	
CC	See also 003607-003610.	
SQ	Sequence 884 BP; 219 A; 286 C; 212 G; 166 T; 1 Others;	
Query Match 76.8%; Score 546; DB 1; Length 884;		
Best Local Similarity 92.1%; Pred. No. 0.00e+00;		
Matches 597; Conservative 0; Mismatches 51; Indels 0; Gaps 0;		
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Db	263 accgatctctgtgctcgaagtctgcagctcagccaccctggccatccagcgactccaga 322	
Qy		
	242 ACCGATCTCTGGGCTCCAAGTCTGGTACCGCGGCCCTCCCTGGCCATCTACTGGGCTCACA 301	
Db	373 ctgggagcagggccgatttaactgcggaacatgggatatagcagctgagtcggggtat 382	
Qy		
	302 CTGAGGATCAGGCTGATTACTGCCAGTCTCTATGACAGCAGCCCTGAATGCTCAGGTAT 361	
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Qy		
	362 TCGGAGGAGGCACGGGCTGACCGCTTAGCTAGCTCAGCCCAAGGCTGGCCCTCGGTCACTC 421	
Db	443 tgtcccgccctcctctgaggagcttcaaagccaaagggccacactggtgtctcataa 502	
Qy		
	422 TGTTCCCGCCCTCCTCTGAGGAGCTTCAGCCAACAGGCCACACTGGTGTGTCTCATTA 481	
Db	503 gtgaecttctaccgggagccgtgacagtggcctggaaaggcagatagcagcccgctcaagg 562	
Qy		
	482 GTGACTTCTACCCGGAGCCGTGTGACAGTGCCCTTGGAGGCAGATAGCAGCCCCTCAAG 541	
Db	563 cgggagtggagaccacc acacccctccaaaagaagcaacaagtlacggcccgagcagct 622	
Qy		
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	602 ACCTGAGCCTGACGCCCTGAGCAGTGGAAGTGCCACAGAACTACAGCTGCCAGGTCAAG 661	
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Qy		

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QY 662 ATGAGGAGCAGCGGTGGAGAGACAGTGGCCCTTACAGAAATGTCAT 709

RESULT 2
ID Q49835 standard; cDNA; 654 BP.
AC Q49835;
DT 27-APR-1994 (first entry)
DE Anti-HIV-1 recombinant antibody 447-52D light chain coding sequence.
KW Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;
KW HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
KW acquired immune deficiency syndrome; chimeric antibody;
KW surface glycoprotein gp120; V3 loop; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..654
FT /*tag= a
FT /note= "encodes recombinantly modified 447-52D
FT light chain"
FT FT
PN W09319785-A.
PD 14-OCT-1993.
PF 23-MAR-1993; U02629.
PR 01-APR-1992; US-861701.
PA (MERI ) MERCK & CO INC.
PA (JOHN/) JOHNSON L S.
PA (PFAR/) PFARR D S.
PI Conley AJ, Emin EA, Johnson LS, Mark GE, Pfarr DS;
DR WPI; 93-336600/42.
DR P-PSDB; R42163.
PT New recombinant human antibody - with HIV neutralising activity
PT against at least two isolates, useful for preventing or treating
PT infection in diagnosis, etc.
PS Example 9; Fig 2B; 154pp; English.
CC EBV-transformed cell lines and mouse-human heterohybridomas
CC producing human MAb's specific for the gp120 V3 loop of HIV-1 MN
CC isolate were obtained. MAb 447-52D was found to recognise the
CC tetrapeptide motif GPCR, i.e. the Principal Neutralising
CC Determinant common to the V3 loop of different HIV isolates.
CC A recombinant Ab was produced in which the L chain V region was
CC derived from 447-52D and to which a signal sequence and a L chain
CC intronic sequence are appended, fused to a fragment contg. a short
CC lambda 2 constant encoding domain.
CC Sequence 654 BP; 156 A; 199 C; 178 G; 121 T;
SQ

Query Match 73.1%; Score 520; DB 8; Length 654;
Best Local Similarity 91.1%; Pred.No. 0.00e+00;
Matches 593; Conservative 0; Mismatches 55; Indels 3; Gaps 1;

Db 2 agctgtgtgaagcagcgccctcagtgctgtcgggcccccaggacagaaggtaccatct 61
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Db 62 cctgtcttggagcagctcccaactatgtggaataattatgttggaccagagttcc 121
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QY 122 CGTGCACTGGGAGCACCTCAACATTGGAGGTTATGATCTACATTGGTACCAGACGCTCC 181
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Db 122 caggaacagccccaaactcctcatttggcaataataagcgacctcaggagttcctg 181
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QY 182 CAGAACAGCGCCCCAACTCTCTATCTATGACATTACAGGACGCCCTCAGGAATTCG 241
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Db 182 accgatctctgtggctcgaactctgcacgtcagccaacctgggcatcaaccggaactccaga 241
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QY 242 ACCGATTTCTTGGCTCAAGTCTGGTACCGCGGGCTCCCTTGGCCATCATCTGGCGCTCCAGA 301
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Db 507 taagtgaacttaccgggagccgtgacagtgccgtggaaggcagatagcagcccgctca 566
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Qy 479 TAAAGTCACTTCTACCGGGAGCCGTGACAGTGGCTGGAGGCGCAGATAGCAGCCCGCTCA 538
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Db 567 agcggggagtgagagaccaccacccctccaacaagaagcaacaacaagtcagcggcgagca 626
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Qy 539 AGCGGGAGTGGAGCACCACACCCCTCCAAACAAGCAACAACAAGTACGGCGCGCAGCA 598
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Db 627 gctatetgagctgacgctgagcagtggaagtgccacacagaagctacagctgccaggtca 686
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Qy 599 GCTACCTGAGCTGAGCGCTGAGAGTGGAGTCCACAGAGCTACAGCTGCCAGTCA 658
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Db 687 cgcataagggagcaccgtggagaagacagtgccctacagaatgtcat 737
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Qy 659 CGCATCAAGGGAGCACCCTGGAGAGACAGTGGCGCCCTACAGATGTTCAT 709
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RESULT 4

ID N81655 standard; DNA; 872 BP.

AC N81655;

DT 09-NOV-1990 (first entry)

DE VDJC regions of human sperm-immobilising monoclonal antibody.

KW Anti-human sperm-immobilising monoclonal antibody; leader region;

KW variable region; joining region; constant region; sterility;

KW vaccine; contraceptive; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 40..729

FT /*tag= a

FT /product=VJC region

FT misc feature 91..375

FT /*tag= b

FT /label=V region

FT misc feature 376..412

FT /*tag= c

FT /label=J region

FT misc feature 413..729

FT /*tag= d

FT /label=C region

PN J63126482-A.

PD 30-MAY-1988.

PF 15-NOV-1986; 272412.

PR 15-NOV-1986; JP-272412.

PA (TOFU) TOA NENRYO KOGYO KK.

DR WPI; 88-187839/27.

DR P-PSDB; P81260.

PT Cell strain producing human sperm-immobilising monoclonal antibody -

PT has at least V-gene in H chain coding genetic family and V gene in L

PT chain of DNA originating from antibody of sterile woman.

PS Disclosure; 14pp; Japanese.

CC A VDJC segment is inserted into pSC41ambda5 together with a

CC leader region. A cell strain, pref. a myeloma cell, can

CC produce the Ab with immobilising value (SI50) of at least 5000,

CC sperm agglutination value at least 1:1600 dilution, specifically

CC reacting against human ejaculated sperm. The product can be used

CC as a vaccine and contraceptive.

CC See also N81654-N81656.

SQ Sequence 872 BP; 211 A; 269 C; 220 G; 172 T;

Query Match

Best Local Similarity 60.5%; Score 430; DB 1; Length 872;

Matches 487; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Db 187 tggtagcagagaagcgaagcagccctgtacttgctcatctatgatgaaacaaccgg 246
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Qy 166 TGGTACAGCAGAGTCCCGAAGCGGCCCAAACTCCTCATCTATGACATTAACAAGCGCA 225
|||||
Db 247 ccctcagggtaccagaccgattctctgggtccacctcaggaacacacagcttctctgacc 306
|||||
Qy 226 CCCTCAGGAATTTCTGACCGGATTTCTGTGGCTCCAACTGTGTGGCGGCTCCCTGGCC 285
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Db 307 atcactggggctcaggcggaagatgaggctgactattactgtaactcccgaggagcagct 366
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Qy 286 ATCACTGGGCTCCAGACTCAGGATGAGGCTGATTAATTACTGCCAGTCTTATGCAGCAGC 345
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Db 367 ggtlaacctgtggtattcggcgaggagaccagctgaccgtctctaggtcagcccaagct 426
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Qy 346 CTGATGCTCAGCTATTCGAGAGGAGCGCCGCTGACGCTCTAGGTGAGTCCAGCCNAGGCT 405
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Db 427 gccctcgggtcaactctgtcccgccctctctgaggagcttcaagccaacaagccaca 486
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Qy 406 CCCCCCTGGTCACTCTGTCCCGCCCTCCTCTCAGAGCTTCAAGCCAAGGCCACA 465
|||||
Db 487 ctggtgtgtctcataagtgaacttctaccggggagccgtgacagtgccctggaaggagat 546
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Qy 466 CTGCTGTCTCATTAAGTGACTTCTACCGGGAGCCCTGCAGCTGCGCTCGAAGGCAGAT 525
|||||
Db 547 agcagccctcgaaggcgagggtggagaccaccacccctccaacaagaagcaacaag 606
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Qy 526 AGCAGCGCCGCTCAAGCGGGAGTGGAGACCAACACACCCCTCCAAAGCAAGCAACAAG 585
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Db 607 tacggcgccagcagctatctgagcctgacgctgagcgtgagcgtggaagtccacagaagctac 666
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Qy 586 TAGCGCGCCAGCAGCTACCTGAGCCTGAGCCTGAGCCTGAGAGTGGAGTCCCGCAGAGGTAC 645
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Db 667 agctgccaggtcacgcatgaaggagcaccgtggagaagacagtgccctcacagaagt 726
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Qy 646 AGTGTCCAGGTCAAGCAAGGCGAGCCGCTGGAGACAGACAGTGGCCCTTACAGAATGT 705
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RESULT 5

ID Q22489 standard; DNA; 8387 BP.

AC Q22489;

DT 31-JUL-1992 (first entry)

DE Human U266 cell line; rearranged lambda gene; Ig;

KW Human myeloma U266 cell line; rearranged lambda gene; Ig;

KW immunoglobulin light chain; humoral immunity; ds.

OS Homo sapiens.

PN W09204440-A.

PD 19-MAR-1992.

PF 27-AUG-1991; 106124.

PR 29-AUG-1990; US-575005.

PA (HARD) HARVARD COLLEGE.

PI Vasicek TJ, Leder P;

DR WPI; 92-114348/14.

PT B cell deficient transgenic non-human animals - comprise DNA

PT encoding the U266 immunoglobulin light chain and an enhancer

PT region used as models of B cell deficiency

PS Disclosure; Fig 2; 41pp; English.

CC This sequence is the EcoRI/HindIII fragment of the rearranged lambda

CC gene isolated from human myeloma U266 cell line. The coding sequence

CC is placed under the control of the mouse heavy chain enhancer. The

CC resulting transgene was used in the production of transgenic mice in

CC which the proportion of spleen cells which are mature B cells is not
CC more than a quarter of that in wild-type animals. The animals are more
CC susceptible to infectious diseases than the wild-type and are
CC models for severe B cell deficiency. See also Q22491 for the
CC transgene sequence.
SQ Sequence 8387 BP; 1957 A; 2348 C; 2109 G; 1973 T;

Query Match 44.7%; Score 318; DB 3; Length 8387;
Best Local Similarity 99.7%; Pred. No. 5.82e-191;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 7062 aggtcagcccaaggtgccccctcggtcaactctgttcccgccctctctgagagattca 7121
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Qy 390 AGGTGAGCCCAAGGCTGCCCTCGGTCACTCTGTCGGCGCCCTCTCTGAGGAGCTTCA 449
Db 7122 agccacaaggccacactggtgtgtctcataagtgaactctaccgggagcggtgacagt 7181
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Qy 450 AGCCACACAGGCCACACACTGGTGTCTCTCATTAAGTGACTTCTACCCGGGAGCGGTGACAGT 509
Db 7182 ggcctggaagcgagatagcagcccggtcaaggcggtgagagaccacacacctccaa 7241
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Qy 510 GGCTTGGAAAGCGAGATAGCAGCCCGGTCAAGCGCGGAGTGGAGACACACACCTCCAA 569
Db 7242 acaagcaacaacaagtacgcgccagcagctatctgagcctgagcctgagcagtgaa 7301
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Qy 570 ACAAGCAACAACAAGTACGCGGCCAGCAGCTTACCTGAGCCTGACGCTGACGAGTGGAA 629
Db 7302 gtccacagaagctacagctgccaggtcacgcgtgaaggagaccagctggagaagacagt 7361
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Qy 630 GTCCCAAGAGAGCTTACAGTGCAGAGTCAAGGAGGAGCAGCGGTGAGAGAGACAGT 689
Db 7362 ggcctcacagaatgttcat 7380
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Qy 690 GGCCCTACAGATGTTTCA 709

RESULT 6

ID Q23370 standard; DNA; 9071 BP.
AC Q23370;
DT 14-AUG-1992 (first entry)
DE U266-lambda gene and downstream murine Ig Heavy chain enhancer.
KW Lambda-E-mu; rearranged; immunoglobulin; light chain; transgene;
KW B cell deficiency; common variable immunodeficiency; CVID;
KW ATCC # 72003; ds.
OS Chimeric Mus.
OS Chimeric Homo sapiens.
PN W0920443-A.
PD 19-MAR-1992.
PF 27-AUG-1991; U06106.
PR 29-AUG-1990; US-575006.
PA (HARD) HARVARD COLLEGE.
PI Vasicek TJ, Leder P;
DR WPI; 92-114351/14.
PT B cell deficient transgenic FVB/N mice - comprise DNA encoding
PT the lambda light chain of a non-human animal for modelling of B
PT cell deficiency
PS Disclosure; Fig 7; 41pp; English.
CC DNA from the IgE-lambda human myeloma U266 cell line was digested
CC with EcoRI and used to prepare a phage library. The clone
CC containing the active lambda gene was identified by probing the
CC library with a radiolabelled BamHI fragment of the human lambda 2
CC gene. (The complete sequence of U266-lambda gene has EMBL Acc.#
CC X51754). The lambda-B-nu construct was prepared by cutting the
CC lambda construct at the HindIII site 0.9kb downstream of

CC C(lambda)2. The fragment was blunt-ended and ligated to a 995bp
CC XbaI fragment of pTAR-7 containing the mouse Ig heavy chain
CC enhancer. The transgene construct was used to transfect mouse
CC cells for the production of B cell deficient transgenic mice. The
CC mice can be used to study e.g. X-linked agammaglobulinemia.
SQ Sequence 9071 BP; 2196 A; 2395 C; 2321 G; 2159 T;

Query Match 44.7%; Score 318; DB 3; Length 9071;
Best Local Similarity 99.7%; Pred. No. 5.82e-191;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 7061 aggtcagcccaaggtgccccctcggtcaactctgttcccgccctctctgagagattca 7120
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Db 7121 agccacaaggccacactggtgtgtctcataagtgaactctaccgggagcggtgacagt 7180
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Qy 450 AGCCACACAGGCCACACACTGGTGTCTCTCATTAAGTGACTTCTACCCGGGAGCGGTGACAGT 509
Db 7181 ggcctggaagcgagatagcagcccggtcaaggcggtgagagaccacacacctccaa 7240
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Qy 510 GGCTTGGAAAGCGAGATAGCAGCCCGGTCAAGCGCGGAGTGGAGACACACACCTCCAA 569
Db 7241 acaagcaacaacaagtacgcgccagcagctatctgagcctgagcctgagcagtgaa 7300
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Qy 570 ACAAGCAACAACAAGTACGCGGCCAGCAGCTTACCTGAGCCTGACGCTGACGAGTGGAA 629
Db 7301 gtccacagaagctacagctgccaggtcacgcgtgaaggagaccagctggagaagacagt 7360
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Qy 630 GTCCCAAGAGAGCTTACAGTGCAGAGTCAAGGAGGAGCAGCGGTGAGAGAGACAGT 689
Db 7361 ggcctcacagaatgttcat 7380
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Qy 690 GGCCCTACAGATGTTTCA 709

RESULT 7

ID Q22491 standard; DNA; 9071 BP.
AC Q22491;
DT 31-JUL-1992 (first entry)
DE Human U266 lambda gene.
KW Human myeloma U266 cell line; rearranged lambda gene; Ig;
KW immunoglobulin light chain; pTAR-7; heavy chain enhancer;
KW humoral immunity; transgenic mouse; ATCC No. 72003; ds.
OS Chimeric Homo sapiens.
OS Chimeric Mus.
FH Key Location/Qualifiers
FT misc_feature 1..8385
FT /*tag= a
FT /note= "U266-lambda gene"
FT misc_feature 8386..9071
FT /*tag= b
FT /note= "portion of 995bp XbaI-EcoRI fragment of
FT pTAR-7 contg. mouse H chain enhancer"
PN W0920440-A.
PD 19-MAR-1992.
PF 27-AUG-1991; 106124.
PR 29-AUG-1990; US-575005.
PA (HARD) HARVARD COLLEGE.
PI Vasicek TJ, Leder P;
DR WPI; 92-114348/14.
PT B cell deficient transgenic non-human animals - comprise DNA
PT encoding the U266 immunoglobulin light chain and an enhancer
PT region used as models of B cell deficiency

PS Disclosure; Fig 7; 41pp; English.

CC This sequence is the EcoRI/HindIII fragment of the rearranged lambda
CC gene isolated from human myeloma U266 cell line ligated to the mouse
CC heavy chain enhancer. The resulting transgene was used in the
CC production of transgenic mice in which the proportion of spleen cells
CC which are mature B cells is not more than a quarter of that in
CC wild-type animals. The animals are more susceptible to infectious
CC diseases than the wild-type and are models for severe B cell
CC deficiency. See also 022489 for the transgene sequence.
SQ Sequence 9071 BP; 2196 A; 2395 C; 2321 G; 2159 T;

Query Match 44.7%; Score 318; DB 3; Length 9071;
Best Local Similarity 99.7%; Pred. No. 5.82e-191;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 7061 aggtcagcccaaggtgccccctcggtgactctgttcccgccctctctgagagcttca 7120
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Db 7121 agccaacaagccacactgggtgtctcctaagtgaacttaccgggagccgtgacagt 7180
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Qy 450 AGCCAACAAGCCACACTGGTGTCTCTAATAAGTCACTTACCCTGGAGCGGTGACAGT 509
|||||
Db 7181 ggcctggaagcagatagcagccccctgaaggcggagtgagagacacacacctccaa 7240
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Qy 510 GGCCTGGAAGCAGATAGCAGCCCGCTCAAGCGGAGTGGAGACACACACACCTCCAA 569
|||||
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Qy 570 ACAAGCAACAACAATGACGGCGCCGAGCAGCTACTGACCTGACGCTGACGACTGAA 629
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Db 7301 gtccacagaagctacagctcaggtcagcagtcagcagtgaggagcagcgtggaagacagt 7360
|||||
Qy 630 GTCCACAGAAGCTCAGCTGCCAGGTCCAGCTCAGGAGGAGGAGCAGCTGGAGAAGACGT 689
|||||
Db 7361 ggcctcacaagaatgttcat 7380
|||||
Qy 690 GGGCCCTACGAATGTTAT 709
|||||

RESULT 8

ID Q03607 standard; DNA; 330 BP.
AC Q03607;
DE Sequence encoding 4G12 monoclonal antibody (Mab) L chain V region.
KW 4G12 Mab; human lung cancer; oesophageal carcinoma; ss.
OS Synthetic.
PN J02046289-A.
PD 15-FEB-1990.
PF 05-AUG-1988; 196647.
PR 05-AUG-1988; JP-196647.
PA (YOSH) Yoshitomi Pharm. Ind. KK.
DR WPI; 90-094983/13.
PT DNA base sequence coding for 4G12 monoclonal antibody - which reacts
PT specifically with human lung cancer and oesophageal carcinoma.
PS Claim 1; Page 545; 9pp; Japanese.
CC The sequence (subclass lambda) is determined by cloning
CC cDNA of 4G12 Mab L chain using
CC synthetic DNA/RNA of human Ab L chain C region as probe.
CC See also Q03608-Q03610.
SQ Sequence 330 BP; 75 A; 99 C; 88 G; 68 T;

Query Match 32.6%; Score 232; DB 1; Length 330;
Best Local Similarity 85.2%; Pred. No. 5.62e-133;

Matches 281; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Db 1 tctgtgtgacgagcgcctcagtgctgcccagcagagaggtcaccatctcc 60
|||||
Qy 64 TCTGTCTGACACAGCGCCCTGAGTCTGTGGGCCCGCAGGCGAGAGGTCCACATCTCG 123
|||||
Db 61 tgccttgaagcagctccacattgggaataattatgtatcctgtaccagcagctccca 120
|||||
Qy 124 TGCACCTGGGAGCACCTCCAACTTGGAGGTTATGATCTACATTGGTACCAGCAGCTCCCA 183
|||||
Db 121 ggaacagcccccacactcctcatttatgacaataataagcagccctcaggatctccgac 180
|||||
Qy 184 GGAACGGGCCCAACTCTCATCTATGACATTAAACAGCGACCTCAGGAATTTCTCAC 243
|||||
Db 181 cgattcttggctccaaagtctggcagctcagccacctgggcatcaccggactccagact 240
|||||
Qy 244 CGATTCTCTGGCTCCAGTCTGGTACCGGGCCCTCCCTGGCCATCACTGGGCTCCAGACT 303
|||||
Db 241 ggggagcagggccgattattactcgggaacatgggagcagctgagctggtgggtattc 300
|||||
Qy 304 GAGGATGAGGCTGATTATTACTGCCAGTCTTATGACAGCAGCGCTGAATGCTCAGGTATTC 363
|||||
Db 301 ggcgagggagcacaagctgacgctcctaggt 330
|||||
Qy 364 GGAGGAGGGACCGGCTGACCGCTCTAGGT 393
|||||

RESULT 9

ID Q11187 standard; cDNA to mRNA; 318 BP.
AC Q11187;
DT 31-MAY-1991 (first entry)
DE Immunoglobulin lambda chain constant region.
KW Antibody; canine distemper virus; parvovirus; hepatitis; ss.
OS Canis familiaris.
PN EP-419858-A.
PD 03-APR-1991.
PF 24-AUG-1990; 116258.
PR 25-AUG-1989; JP-219889.
PR 30-SEP-1989; JP-255425.
PR 07-JUN-1990; JP-150673.
PA (KAGA) CHEMO-SERO-THERAP.
PI Maeda H, Eda Y, Kimachi K, Ono Y, Tokiyoshi S;
DR WPI; 91-095353/14.
DR P-PSDB; R11366.
PT Gene fragments coding for constant region of canine
PT immunoglobulin(s) - used to produce mouse-dog antibodies for
PT diagnosis, treatment and prevention of canine.
PS Claim 6; Page 15; 49pp; English.
CC The DNA encodes the constant region of canine Ig lambda chain. It can
CC be used to produce mouse-dog chimeric antibodies for the diagnosis,
CC treatment and prevention of canine diseases caused by e.g. canine
CC distemper virus, canine parvovirus and canine hepatitis virus.
CC See also Q11188-91.
SQ Sequence 318 BP; 69 A; 115 C; 91 G; 43 T;

Query Match 31.5%; Score 224; DB 2; Length 318;
Best Local Similarity 85.7%; Pred. No. 1.29e-127;
Matches 269; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 1 cagcccaagcctccctcgttcacactcttcccgccctctctgagagcctcgcgcc 60
|||||
Qy 394 CAGCCCAAGGCTGCCCGCTCAGTCTGTTCGCCGCTCTCTGAGGAGCTTCAAGCC 453
|||||
Db 61 aacaagccacctggtgtgctcctcagcagcttctaccacagcggctgacggtggcc 120
|||||

Db	2	agtctgtgtcgaactcagccaccctcagcgtctggagcccccggcagagggtcaccatct	61
Qy	62	AGTCTGTCTTGACACAGCGCCCTCAGTCTCTGGGGCCCGAGGCTCACCATCT	121
Db	62	cttgtttctggaagcagctccaacatcggaactaatactgaaactggaactgcagctcc	121
Qy	122	CGTGCACTGGGAGCACCCTCCACAATTGGAGGTTATGATCTACATTGTACACGACGAGCTCC	181
Db	122	caggaaacgccccaaaagctcctcatctatagtaataatcagcggccctcaggggtccctg	181
Qy	182	CAGGACGGGCCCCCAACTCCTCATCTATGCATTACAGGCGACCTCAGGAATTTCTG	241
Db	182	acagattctctggctccaaagtctggcaactcagcctccctggccatcagtggactccagt	241
Qy	242	ACCGATTCTCTGGCTCCGAAGTCTGGTACCGGGGCTCCCTGGCCATCAGTGGGCTCAGA	301
Db	242	ctgaagatgaggctgattatttctgtgcaagcatggatgaacgctgaaagtgtggtat	301
Qy	302	CTGAGGATCGAGGTGATTATTACTGCGCACTCTATGACAGCAGCCTGAATGCTCAGGTAT	361
Db	302	tcggcgagggaccaaagctgacgcgtcctaggt	333
Qy	362	TCGAGAGAGGACCCGGCTCAGCCTCTAGGT	393

```

RESULT 12
AC Q98724 standard; DNA; 816 BP.
ID Q98724;
DT 16-APR-1996 (first entry)
DE Anti-HIV-1 MAb 447 single chain fragment variable (scFv) clone P5Q.
KW Monoclonal antibody 447; MAb447; single chain fragment variable;
KW scFv; clone P5Q; HIV-1; diagnosis; treatment; mutant antibodies;
KW alanine screening mutagenesis; gp120; V3 domain; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT mat_peptide 1..817
FT /tag= a
FT /transl_except= pos:394..396, aa:Ala
FT W09523813-Al.
PD 08-SEP-1995.
PF 27-FEB-1995; U02492.
PP 04-MAR-1994; US-206079.
PI (MERI ) MERCK & CO INC.
PA Hollis GF, Lewis CM, Ludmerer SW;
DR WPI; 95-320542/41.
DR P-PSDB; R80378.
DR DNA encoding improved antibodies e.g. anti-HIV-1 - prepared using
PT alanine scanning mutagenesis to have decreased antigen off-rates
PT Disclosure; Fig 6; 30pp; English.
PC Q98724 encodes R80378 the human anti-HIV gp120 V3 domain monoclonal
CC antibody (MAb447) single chain fragment variable clone P5Q (scFv
CC P5Q). New modified Abs derived from the above native Ab, using Ala
CC screening mutagenesis, have improved characteristics compared to the
CC native Ab, e.g. slower off rates to the antigen. The new Abs can be
CC used in the diagnosis and treatment of HIV-1.
CC Sequence 816 BP; 187 A; 218 C; 242 G; 169 T;
SQ

```

Query Match 29.4%; Score 209; DB 17; Length 816;
Best Local Similarity 82.2%; Pred. No. 1.39e-117;
Matches 286; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

Qy	49	GGTGACATGTGAGTCTGCTCCTGACACAGCGCCCTCAGTGTCTGGGGCCCCAGGGCAG	108
Db	496	aaggtcaccatctcctgctctggaagcagctccaacattggggaataattatgtattgtgg	555
Qy	109	AAGGTCACCATCTCGTGCACTGGGACACCTCCAAATTGGAGGTTATGATCTACATTGG	168
Db	556	taecagcagttcccgaggaacagcccccaactcctcattatgycaatataaagaagcccc	615
Qy	169	TACAGCAGCTCCAGGAAGCGGCCCAAACTCCTCATCTATGACATTAAACAAGGACCC	228
Db	616	tcagggtattcctgaccattctctcgtgccaaagtctggcagctcagccacctggcgatc	675
Qy	229	TAGGAATTTCTGACGATTCTCTGGCTCGAAGTCTGTGTCGGGGCCCTCCCTGGCCATC	288
Db	676	acggactccagactgggacgagcgcatatttctgcgaacatgggatagcggcctg	735
Qy	289	ACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCGACTCTATGACAGCAGCCTG	348
Db	736	agtgcgtattgggtgttcgcgcgagggaccgaagctgacccgtctaggt	783
Qy	349	AATGCTCA---GGTATTCGACGAGGCGCCGGCTGACCTCTAGCT	393

RESULTS	13	
ID	Q10674 standard; DNA; 318 BP.	
AC	Q10674;	
DT	24-MAY-1991 (first entry)	
DE	Feline immunoglobulin lambda chain constant region Tl-62 gene.	
KW	Feline immunoglobulin; fig; lambda chain; chimæra; antibody; ss.	
OS	Felis catus.	
PN	EP-41/7486-A.	
PD	20-MAR-1991.	
PF	10-AUG-1990; 115426.	
PR	10-AUG-1989; JP-208822.	
PR	30-SEP-1989; JP-255424.	
PR	28-DEC-1989; JP-344465.	
PPA	(KAGA) CEMO-SERO-THERAPEU.	
PI	Maeda H, Eda Y, Kimachi K, Ono Y, Tokiyoshi S;	
DR	WPI; 91-081793/12.	
DR	P-PSDB; R11012.	
PT	New DNA sequences encoding constant regions of feline	
PT	immunoglobulin - and new chimeric DNA expressing mouse-cat	
PT	antibodies, useful in prevention, treatment and diagnosis of	
PT	feline disease	
PS	Claim 7; Page 15; 35pp; English.	
CC	The cDNA library of cat-mouse heterohybridoma FM-T1 cells was used	
CC	to isolate the fig gene.	
CC	The sequence is used to produce recombinant DNA encoding the L-chain	
CC	of a mouse-cat chimeric antibody having a mouse variable	
CC	region linked at its 3'-site to a feline constant region.	
CC	The antibody expressed by cells transformed with the recombinant	
CC	DNA is useful in diagnosis, treatment and prevention of feline	
CC	disease, without showing side effects.	
CC	See also Q10674-75 and Q10945-46.	
SQ	Sequence 318 BP: 77 A; 88 G; 47 T;	

	Query Match	28.8%;	Score 205;	DB 2;	Length 318;	
	Best Local Similarity	83.0%;	Pred. No. 6.54e-115;			
	Matches	258;	Conservative	0;	Mismatches	53; Indels 0; Gaps 0;
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Qv	394	CAGCCCAAGGCTCGCCCCCTCGGTTCATCTGTTCCGCCGCCTCCTCTGAGAGGTTCAACGC	453			

Db	61	acaaggccacctggtgtctctgcagtgactctaccacagcggttgacggtggcc	120
Qy	454	AACAAGGCCACACTGCTGTCTCTAAGTGACTTCTACCGGGAGCGGTGACACTGGCC	513
Db	121	tggaaaggaatggcaccccccatacccaaggggcgtggagaccaccagccctccagacag	180
Qy	514	TGGAAGGCAGATAGCAGCCCGCTCAAGCGGGGAGTGGAGCCACCACCCCTCCAAACA	573
Db	181	agcaacaacagtcacgcccgcagcagctacctgagcctctcacccgaacagtggaatct	240
Qy	574	AGCAACAACAAATGTCGCGGCCAGCAGCTACCTGAGCCTGAGCCTGAGCAGTGGAGTCC	633
Db	241	cacagcagatcacactgcccaggtcacgcacgaggggagcactgtggagaagtggtggct	300
Qy	634	CACAGAAGCTACAGCTGCCAGTTCAGGTCAGGCATGAAGGGAGCACCGTGGAGAAGACACTGGCC	693
Db	301	cctgcagagtg	311
Qy	694	CCTACAGAATG	704

RESULT	14	
ID	Q64170	standard; cDNA to mRNA; 318 BP.
AC	Q64170;	
DT	29-DEC-1994	(first entry)
DE	Sequence of feline herpes virus (FHV-1) cDNA.	
KW	Feline herpes virus; FHV-1; monoclonal antibody; ss.	
OS	Felis catus.	
FFH	Key	Location/Qualifiers
FT	CD5	1..318
FT	/*tag= a	
PN	W09412661-A.	
PD	09-JUN-1994.	
PR	25-NOV-1993; J01724.	
PR	28-NOV-1992; JP-341255.	
PPA	(KAGA) CHEMO SERO THERAPEUTIC RES INST.	
PPI	Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;	
WPI	94-200288/24.	
DR	P-PSDB; R54096.	
DR	Feline monoclonal antibody and recombinant antibodies specific	
PPT	for FHV-1 - for detection, treatment and prevention of FHV-1	
PPT	infection.	
CC	Claim 20; Page 23-24; 53pp; Japanese.	
CC	The inventors claim a monoclonal antibody against feline herpes	
CC	virus (FHV-1), the sequence of which is given in Q64168, Q64169	
CC	and Q64170. They also claim a recombinant antibody against FHV-1	
CC	and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are	
CC	used in the detection, treatment and prevention of FHV-1. The	
CC	sequences of the CDRs in the VH of the recombinant anti-FHV-1	
CC	antibody are given in R54092. The sequences of the CDRs in the VL of	
CC	the recombinant anti-FHV-1 antibody are given in R54093. These CDR	
CC	sequences are claimed.	
SC	Sequence 318 BP.	77 A; 106 G; 88 G; 47 T;

Query Match	28.8%;	Score 205;	DB 11;	Length 318;
Best Local Similarity	83.0%;	Pred. No. 6,54e-115;		
Matches	258;	Mismatches 0;	Indels 0;	Gaps 0;
Conservative				
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Db	61	acaagggccaccctgggtgtctctgttcagtcgaacttcacccacggcgttcgagcgttgccc	120	

Qy	454	ACAAAGGCCAACTGGTGTCTCTAATAGTGACTTCTACCGGGAGCCGTGACAGTGGCC	513
Db	121	tggaaaggaagatggcaccoccccatccaagaaggcgtggagaccaccaagccctccagaag	180
Qy	514	TGGNAGGCGATAGACGCCCGCTCAAGGCGSGAGTGGAGACCAACCAACAA	573
Db	181	agcaacaacaagtacgcygcagcagctacctgagcctgctcaccgaagaagtggaaatct	240
Qy	574	AGCAACAACAGTACCGGGCGACAGCTTACCTGAGCCTGACGCGTCGACGAGTGGAAATCC	633
Db	241	cacacgagatacaacctgccaggtccgcacgaaggaggagcaactctggagaagaagtgtgctc	300
Qy	634	CACAGAAGCTACAGTGTCCAGTTCAGCATGAAGGGAGCACCGTGGAGAGACAGTGGCC	693
Db	301	cctgcagagtq	311
Qy	694	CCTACAGAATG	704

RESULT	15	
ID	Q98903 standard; cDNA; 330 BP.	
AC	Q98903;	
DT	11-FEB-1996 (first entry)	
DE	Human tumor-associated MAb 123A16 IgA-lambda 2 variable light region.	
KW	Tumor-associated antigen; tumor therapy; bowel cancer therapy;	
KW	monoclonal antibody; IgA; immunoglobulin; variable light chain;	
KW	CDR; complementarity determining region; da.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	CDS	1..330
FT	/*tag= a	
FT	misc_binding	67..106
FT	/*tag= b	
FT	/note= "complementarity determining region-1"	
FT	misc_binding	152..173
FT	/*tag= c	
FT	/note= "complementarity determining region-2"	
FT	misc_binding	270..303
FT	/*tag= d	
FT	/note= "complementarity determining region-3"	
FT	misc_binding	304..330
PN	W09522613-A1.	
PD	24-AUG-1995.	
PF	16-FEB-1995; E00581.	
PR	22-FEB-1994; US-199911.	
PA	(ALKU) AKZO NOBEL NV.	
PI	Haspel MW, Kobrin BJ;	
DR	WPI; 95-302719/39.	
DR	P-PSDB; R80621.	
PT	Antibody variable regions specific for human colon tumour antigen -	
PT	useful in prepn. of immunoconjugates to target drugs and	
PT	radio-metals for therapy and diagnostic imaging of tumours	
PS	Claim 1; Page 32-33; 42pp; English.	
CC	This cDNA encodes the variable light chain region of human	
CC	monoclonal antibody 123A16 IgA-lambda2 which is specific for a	
CC	human colon tumor antigen. This sequence contains 3 CDRs (CDR1, CDR2	
CC	and CDR3). The specificity of the CDRs may be useful in the	
CC	preparation of immunoconjugates for the detection, diagnosis and	
CC	treatment of human colon tumors. Also, the CDR sequences provide	
CC	information for manufacturing chimeric and multifunctional	
CC	antibodies. The MAb is produced from peripheral blood B-lymphocytes	
CC	of cancer patients actively immunized with autologous colon tumor	
CC	antigen. The B-cells were transformed by Epstein-Barr virus.	
SQ	Sequence 330 BP; 75 A; 103 C; 84 G; 68 T;	

Dec 17 22:38

US-08-487-530-9.rng

19

Query Match 28.3%; Score 201; DB 16; Length 330;
Best Local Similarity 80.5%; Pred. No. 3.05e-112;
Matches 265; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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Db 62 AGTCTCTCTGCACACAGCGCGCCCTCAGTCTGTGGGGCCCGCAGGCGACAAGGTCACCATCT 121
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 cctgctctggaaaccagctccaaacattgggaataattttgtatctctgtaccacaattcc 121
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 122 CGTGCACTGGGAGCACCCTCCACACTTGGAGGTTATGATCTACATTGGTACCAGAGCTCC 181
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 122 caggagacagcccccacactcctctattatgacaataataagcgaccctcagggttctctg 181
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 CAGGACGCGCCCGCAACTCTCTCATATGACATTACAGCGACCCCTCAGGAATTTCTG 241
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 accgattctctggctccaagtctggcagctcagccaccctgggcatcacgggactccaga 241
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 242 ACCGATTCTCTGGCTCCAAAGTCTGGTACCGCGGCGCTCCCTGGCCATCAGTGGGCTCCAGA 301
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 242 ctgggagcagggccgattattactcgggaacatgggataccagactcgcgcgtggtgtgt 301
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 302 CTCAGGATCAGGCTGATTATTACTGCGAGTCTCTATGACAGCAGCCTGAATGCTCAGGTAT 361
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 302 tcggcgagggagcaagctgaccgtccta 330
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 362 TCGGAGGAGGACCGCGGCTGACCGCTCCTA 390
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Search completed: Tue Dec 17 22:52:14 1996
Job time : 68 secs.

WATERMAN

(TM)

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MParch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 22:52:36 1996; MasPar time 273.63 Seconds
934.180 Million cell updates/sec

Tabular output not generated.

Title: >US-08-487-550-9

Description: (1-711) from US08487550.seq

Perfect Score: 711

N.A. Sequences: 1 ATGAGGTCGCCGTCAGCT.....GCCCTACAGATGTTTCATGA 711

Comp: TACTCCACGGCGGCGATCGA.....GGGAGTCTTACAGACT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 514334 seqs, 179763086 bases x 2

Post-processing: Minimum March 0%

Listing first 45 summaries

Database:

EST-ST5
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
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127:EST128 128:EST129 129:EST130 130:EST131 131:EST132

Database:

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118:EST119 119:EST120 120:EST121 121:EST122
122:EST123 123:EST124 124:EST125 125:EST126 126:EST127
127:EST128 128:EST129 129:EST130 130:EST131 131:EST132

132:enEST7 133:enEST8 134:enEST9 135:enEST10 136:enEST11
137:enEST12

Statistics: Mean 10.505; Variance 2.161; scale 4.860

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description	Pred. No.
c	1	330	46.4	570	136	HS777270	yw91f04.s1 Homo sapie	0.00e+00
c	2	330	46.4	570	116	N32777	yw91f04.s1 Homo sapie	0.00e+00
c	3	299	42.1	469	66	R73382	y192all.s1 Homo sapie	0.00e+00
c	4	297	41.8	471	67	R73492	y193d09.s1 Homo sapie	0.00e+00
c	5	296	41.6	376	12	H26070	y152h11.r1 Homo sapie	0.00e+00
c	6	296	41.6	463	11	H25405	y146h10.s1 Homo sapie	0.00e+00
c	7	290	40.8	436	61	R55314	y177h05.s1 Homo sapie	0.00e+00
c	8	285	40.1	425	59	R48172	y166g10.r1 Homo sapie	0.00e+00
c	9	282	39.7	491	69	R83196	yp87h10.s1 Homo sapie	0.00e+00
c	10	279	39.2	297	124	G13531	human STS SHGC-11074.	0.00e+00
c	11	277	39.0	329	22	H60966	yr22c08.r1 Homo sapie	0.00e+00
c	12	277	39.0	435	71	R88208	yp08b06.s1 Homo sapie	0.00e+00
c	13	275	38.7	443	137	HS851303	za22c10.s1 Homo sapie	0.00e+00
c	14	273	38.4	487	69	R83348	yp06b01.s1 Homo sapie	0.00e+00
c	15	272	38.3	356	24	H67544	y468e12.r1 Homo sapie	0.00e+00
c	16	272	38.3	431	11	H26023	y152h11.s1 Homo sapie	0.00e+00
c	17	270	38.0	428	11	H25133	y143e10.r1 Homo sapie	0.00e+00
c	18	270	38.0	470	8	H15922	y127e07.s1 Homo sapie	0.00e+00
c	19	268	37.7	325	60	R49901	y158a10.r1 Homo sapie	0.00e+00
c	20	267	37.6	428	17	H45690	yp23e04.s1 Homo sapie	0.00e+00
c	21	267	37.6	445	99	T67053	y452e05.s1 Homo sapie	0.00e+00
c	22	266	37.4	509	17	H45859	yp22e04.r1 Homo sapie	0.00e+00
c	23	266	37.4	446	13	H30137	y059f07.r1 Homo sapie	0.00e+00
c	24	266	37.4	512	88	T50252	yb78h04.s1 Homo sapie	0.00e+00
c	25	264	37.1	410	66	T72739	y191a09.s1 Homo sapie	0.00e+00
c	26	264	37.1	516	90	T57780	ycl4a06.s1 Homo sapie	0.00e+00
c	27	261	36.7	387	19	H51320	yp07g04.s1 Homo sapie	0.00e+00
c	28	261	36.7	451	11	H23960	y130a03.s1 Homo sapie	0.00e+00
c	29	258	36.3	365	11	H25486	y147f08.r1 Homo sapie	0.00e+00
c	30	254	35.7	350	12	H26065	y152g09.r1 Homo sapie	0.00e+00
c	31	253	35.6	434	10	H21406	y132h05.s1 Homo sapie	0.00e+00
c	32	251	35.3	428	101	T71479	y435f06.r1 Homo sapie	0.00e+00
c	33	250	35.2	277	85	T39258	ya02g12.r2 Homo sapie	0.00e+00
c	34	249	35.0	436	107	T94334	ye31e10.s1 Homo sapie	0.00e+00
c	35	249	35.0	480	100	T70889	yc49b08.s1 Homo sapie	0.00e+00
c	36	247	34.7	379	11	H24839	y142h08.r1 Homo sapie	0.00e+00
c	37	247	34.7	381	17	H43633	yp24a07.s1 Homo sapie	0.00e+00
c	38	246	34.6	346	11	H25740	y154h11.r1 Homo sapie	0.00e+00
c	39	245	34.5	419	10	H21654	y133c12.r1 Homo sapie	0.00e+00
c	40	245	34.5	422	12	H28778	yp03e07.s1 Homo sapie	0.00e+00
c	41	245	34.5	436	64	R64294	y121h08.r1 Homo sapie	0.00e+00
c	42	243	34.2	397	106	T92408	ye19g05.r1 Homo sapie	0.00e+00
c	43	243	34.2	405	8	H14996	y126a12.s1 Homo sapie	0.00e+00
c	44	241	33.9	374	11	H25441	y147f08.s1 Homo sapie	0.00e+00
c	45	241	33.9	406	17	H43557	yo64f09.s1 Homo sapie	0.00e+00

ALIGNMENTS

RESULT 1

D_b 443 ggggcagcttggg-tn:cccaggacg 468

Qv 357 GGTA^{TT}CGGA-GGAGGAGCCCGGGCTGACCGTCTTGGTCAAGCCGCAAGGCTGCCCGCTCGG 415

Db 71 gncactctgttccgcctcctctgaggagcttcaagccaacaggccacactggtgt 130
|||||
Qy 416 -TACTCTGTTCGGCCCTCTCTGAGGAGCTTCAAGCCAAGGCCACACTGCTGT 474
|||||
Db 131 ctcataagtgaactctaccggagcgtgacagtggcctgggaagcagcagcagc 190
|||||
Qy 475 CTCTAAGTGACTTCTACCCGGAGCGGTGACAGTGGCCCTGC-AAGGCAG-ATAG-CAGC 531
|||||
Db 191 cngtcaagntcggagtagngagaccacacacccctccaaacaaagcaacaagtagcgc 250
|||||
Qy 532 CCGCTCAAGG-CGGGAGTGGAGACACACACACCCCTCCAAACAAAGCAACAAGTAGCAG 590
|||||
Db 251 gggcagcagctatctgagcctgacgctgagcagtggaagtccacagaagctnccagctg 310
|||||
Qy 591 GGGCAGCAGCTTACCTGAGCCTGAGCCTGAGCAGTGGAGTCCCAAGAGCTACAGCTG 650
|||||
Db 311 ccaggtacgcatgagggagcaccgtggaagacattngccctnccagaatttt 366
|||||
Qy 651 CCAGGTACCGATGAAGGAGCACCCTGGAGACAGAGTGGCCCTTACAGAAATGTT 706
|||||

RESULT 6
LOCUS H25405 463 bp mRNA EST 10-JUL-1995
DEFINITION Y146h10.s1 Homo sapiens cDNA clone 161347 3' similar to gb:X57809
IG LAMBDA CHAIN C REGIONS (HUMAN);
ACCESSION H25405
NID g894528
KEYWORDS EST.
SOURCE human clone=161347 library=Soares breast 3NbHBat vector=pT73D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=Promega -21ml3 Reitel=Not I Rsite2=Eco RI Adult
human. 1st strand cDNA was primed with a Not I - oligo(dT) primer
[5' TGTTACCAATCTGAAGTGGAGCGGCCCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT73 vector (Pharmacia). Library went through one round
of normalization to a Cot = 20. Library constructed by Bento Soares
and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 463)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaekle, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
High quality sequence stops: 313
Source: IMAGE Consortium, LIND
This clone is available royalty-free through LIND; contact the
IMAGE Consortium (info@image.lind.gov) for further information.

FEATURES NCBI gi: 894528 Location/Qualifiers
source 1..463
/organism="Homo sapiens"
/clone="161347"
/note="human"
BASE COUNT 77 a 111 c 141 g 122 t 12 others
ORIGIN
Query Match 41.6%; Score 296; DB 11; Length 463;
Best Local Similarity 94.4%; Pred. No. 0.00e+00;
Matches 306; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
Db 140 atgaacattctnagggccactntcttccacaggtgctcccttcacgtgacctggc 199
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Cp 709 ATGACATTTCTGTAGGGGCCACTGCTCTTCCAGCGTGTCCCTTCATGCGTAGCTGGC 650
|||||
Db 200 agctgtagctctgtgggaacttccactgctcagcgctcaggtcagatagctggtggcg 259
|||||
Cp 649 AGCTGTAGCTTCTGTGGCACTTCCACTGCTCAGCGCTCAGGCTCAGGTAGCTGCTGGCCG 590
|||||
Db 260 cgtactgttctgttggagggtntggtgctccactcccgcttgacggggc 319
|||||
Cp 589 CGTACTGTGTGCTTCTTTGGAGGGGTGTGGTGTCTCCACTCCCGCTTACGGGGC 530
|||||
Db 320 tgtatctgcttccagggcactntcacggtcccggttagaagtcacttatgacacaca 379
|||||
Cp 529 TGCTATCTGCTTCCAGGCCACTGCTCAGCGCTCCCGGTGAGAACTTATGACACACA 470
|||||
Db 380 ccaagttngccttttggcctnaagctcccgagggaggcggaacagagttaccagg 439
|||||
Cp 469 CCAGTGTGGCTTCTTGGCTTGAAGCTCTCAGAGCTCCAGAGGGGGGACAGAGTACCCGAG 410
|||||
Db 440 gggcagccttnggttaacnaggga 463
|||||
Cp 409 GGGCAGCCTTGGCGTGCCTAGGA 386
|||||

RESULT 7
LOCUS R55314 436 bp mRNA EST 22-MAY-1995
DEFINITION Y77h05.s1 Homo sapiens cDNA clone 154809 3' similar to gb:X57809
IG LAMBDA CHAIN C REGIONS (HUMAN);
ACCESSION R55314
NID 9824609
KEYWORDS EST.
SOURCE human clones=154809 library=Soares breast 2NbHBat vector=pT73D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=Promega -21ml3 Reitel=Not I Rsite2=Eco RI Adult
female. 1st strand cDNA was primed with a Not I - oligo(dT) primer
[5' TGTTACCAATCTGAAGTGGAGCGGCCCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT73 vector (Pharmacia). Library went through one round
of normalization to a Cot = 230. Library constructed by Bento
Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 436)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaekle, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.

Qy 576 CAACAACAGTACGGCGCAGCAGCTACCTGAGCGCTCAGCGCTGAGCACT-GGAGTCCC 634
 Db 303 acagaaggttacaggttgcaggttcacgttgaaaggggagcaccgtgggagagacagt 362
 Qy 635 ACAGAGCT-ACAGCTGCCAGG-TCACGCATGAGAGG-AGCACCTGG-AGAG-ACAGT 689
 Db 363 nggccttacagatttttnt 383
 Qy 690 -GGCCCTACAGAAATGTTTAT 709

RESULT 9
 LOCUS R83196 491 bp mRNA EST 04-AUG-1995
 DEFINITION yp87h10.s1 Homo sapiens cDNA clone 194467 3' similar to gb:X57809
 1G LAMBDA CHAIN C REGIONS (HUMAN);
 ACCESSION R83196
 NID 928073
 KEYWORDS EST.
 SOURCE human clone=194467 library=Soares fetal liver spleen INFLS
 vector=p7n3D (Pharmacia) with a modified polylinker host=DH10B
 (ampicillin resistant) primer=Promega -21ml3 Reitel=Pac I
 Reitel=Eco RI Liver and spleen from a 20 week-post conception male
 fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer
 [5' ACTGGAGAAATTAATGATCTTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
 digested with Pac I and cloned into the Pac I and Eco RI sites of
 the modified pT73 vector. Library went through one round of
 normalization. Library constructed by Bento Soares and M.Fatima
 Bonaldo.

ORGANISM

Homo sapiens
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 (bases 1 to 491)

Hillier, L., Clark, N., Dubaque, T., Elliston, K., Hawking, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.

TITLE

The WashU-Merck EST Project

Unpublished (1995)

COMMENT

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence scope: 229
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 928073

FEATURES

source Location/Qualifiers
 1..491
 /organism="Homo sapiens"
 /clone="194467"
 /note="human"

BASE COUNT 82 a 118 c 147 g 132 t 12 others
 ORIGIN

Query Match 39.7%; Score 282; DB 69; Length 491;
 Best Local Similarity 92.2%; Pred. No. 0.00e+00;
 Matches 319; Conservative 0; Mismatches 23; Indels 4; Gaps 4;
 Db 147 atgaacattctgtagggccactgtcttctccacaggtgtctccttcatcgtgacctggc 206
 Cp 709 ATGAACATTCTGTAGGGGCACACTGCTTCTCCACGGTGTCCCTTCATGCGTGACCTGGC 650
 Db 207 agctntagcttctgtgggaattccactgctcaggcgtcaggctcaggtcaggtagctgtgctggc 266
 Cp 649 AGCTGTAGCTTCTGTGGGACCTTCCACTGCTCAGGCTCAGGCTCAGTACCTGCTGGCGC 590
 Db 267 cgtactgttgcttctgttggagggtgtgtgtctccantcccgcttgacgggc 326
 Cp 589 CGTACTGTGCTTCTGCTTTGAGGGGTGTGGTGTCCACCTCCCGGCTTGACGGGGC 530
 Db 327 tgcctatgccttccagggaactttcacggctccnggtagaagtcacttntgagacaca 386
 Cp 529 TCGTATCTGCTTCCAGGCCACTGTCACGGCTCCCGGCTAGAGTCACTTATGACACACA 470
 Db 387 ccagntggcctgttgctttaagntccacagagaggcgagggaacagatt-accag 445
 Cp 469 CCAGTGTGCGCTTGTGGCTTGA-CTCTCTCAGAGGGGGGGAACAGAGTCACTGACCGAG 411
 Db 446 ggggcagc-ttnggttancatgaagaccgtcagttng-tcctctc 489
 Cp 410 GGGGAGGCTTGGGCTGACCTAGACGGTACGGGGTCCCTCTC 365

RESULT 10
 LOCUS G13531 297 bp DNA STS 04-JAN-1996
 DEFINITION human STS SHGC-11074.
 ACCESSION G13531
 NID g1129270
 KEYWORDS STS sequence; primer; sequence tagged site.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
 Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
 Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 297)
 AUTHORS Myers, R.M.
 JOURNAL Unpublished (1995)
 COMMENT

Contact: Richard M. Myers
 Stanford Human Genome Center (SHGC)
 Stanford University School of Medicine
 Department of Genetics, M-344, Stanford, CA 94305, USA
 Tel: 4157259687
 Fax: 4157259689
 Email: myers@shgc.stanford.edu
 Primer A: TAGTCAGCCCAAGGCTG
 Primer B: TCGCACTTCCACTGCTCAG
 STS size: 247
 PCR Profile:
 Initial incubation: 94 degrees C for 90 seconds
 Denaturation: 94 degrees C for 15 seconds
 Annealing: 62 degrees C for 23 seconds
 Polymerization: 72 degrees C for 30 seconds
 PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer:

MgCl₂: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs derived from L38563 -- Unigene.

NCBI gi: 1129270
source Location/Qualifiers
1..297
/organism="Homo sapiens"
/note="human"

STS
29..275
/map="22"

primer_bind
29..46
/map="22"

primer_bind
complement(257..275)
/map="22"

BASE COUNT 69 a 95 c 84 g 49 t
ORIGIN

Query Match 39.2%; Score 279; DB 124; Length 297;

Best Local Similarity 97.0%; Pred. No. 0.00e+00;

Matches 288; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 1 ttccggaggagaccgaagctgacccctcctaggtcagcccaaggctgccctcgtgcaat 60

Qy 361 TTCGGAGGAGGACCGGCTGACCGCTCTAGGTCAGCCCAAGGCTGCCCTCGGTCACT 420

Db 61 ctgttccgcctcctctgagagcttcaagcccaagccacactggtgtctcata 120

Qy 421 CTGTTCCGGCCCTCTCTGAGAGCTTCAAGCCACAGCCACACTGTGTCTATA 480

Db 121 atgacttctaccgggagccgtgacagtggcctggaagcagatagcagcccgctcaag 180

Qy 481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGAGCCCGTCAAG 540

Db 181 gggggagtgagagaccacacacccctccaatcaagcaacaacaaagttccggccagcagg 240

Qy 541 GCGGAGTGAGAGCACCACACCTCCAAACAAAGCAACAGTACGCGCCAGCAGC 600

Db 241 tatctgagcctgacgctgagcagtggaagtcaccacagaagctacagctgcaagtc 297

Qy 601 TACCTGAGCCTGAGCCTGAGAGTGGAGTCCACAGAGCTACAGTGCACGTC 657.

RESULT 11

LOCUS H60966 329 bp mRNA EST 06-OCT-1995
DEFINITION yr22c08.r1 Homo sapiens cDNA clone 206030 5' similar to db:X57809
IG LAMBDA CHAIN C REGIONS (HUMAN);

ACCESSION H60966

NTID g1013798

KEYWORDS EST.

SOURCE human clone=206030 primer=M13RPI library=Soares fetal liver spleen
INFLS vector=pf/T3D (Pharmacia) with a modified polylinker

host=DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Eco RI Liver
and spleen from a 20 week-post conception male fetus. 1st strand
cDNA was primed with a Pac I - oligo(dT) primer [5'
AATCGAAGAATTAAATTAAGATCTTTTTTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified pT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 329)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Huitman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfig, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

High quality sequence stops: 281

Source: IMAGE Consortium, LINL

This clone is available royalty-free through LINL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 1013798

Location/Qualifiers

source

1..329

/organism="Homo sapiens"

/clone="206030"

/note="human"

<1..>329

83 a 106 c 90 g 49 t 1 others

mRNA

BASE COUNT

ORIGIN

Query Match 39.0%; Score 277; DB 22; Length 329;

Best Local Similarity 93.4%; Pred. No. 0.00e+00;

Matches 298; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Db 2 ggaccaaggtcacgtcctcctagtcagcccaaggcccaaccactgtcactctgtccgcg 61

Qy 371 GGACCCGGCTCACCCTCTAGGTGACCCCAAGGCTGCCCTTCGGTCACTCTGTCCCGC 430

Db 62 cctcctctgagagctccaagcaagccacactagtgtctgacagctacgtctct 121

Qy 431 CCTCTCTGAGAGCTTCAAGCCCAACAGGCCACACTGGTGTCTCATAAGTCACTTCT 490

Db 122 accggggagctgtgacagtggcctggaagaggatggcagcccgctcaaggcgagtg 181

Qy 491 ACCCGGAGCGGTGACAGTGGCTTGAAGCAGATAGCAGCCCGTCAAGCGGGAGTGG 550

Db 182 agaccaccaaacctccaaacagagcaacaagtcacgagccgagcagctacgtgagcc 241

Qy 551 AGACCAACCACACCTCCAAACAAAGCAACAGTACCGCGCCAGCAGCTACCTGAGCC 610

Query Match 39.0%; Score 277; DB 71; Length 435;
Best Local Similarity 96.2%; Pred. No. 0.00e+00;
Matches 302; Conservative 0; Mismatches 9; Indels 3; Gaps 3;

Query Match 38.7%; Score 275; DB 137; Length 443;
Best Local Similarity 95.4%; Pred. No. 0.00e+00;
Matches 288; Conservative 0; Mismatches 14; Indels 0; Gaps

TITLE	JOURNAL	COMMENT
1. The Role of the Teacher in the Classroom	Journal of Educational Research	1980, Vol. 83, No. 1, pp. 1-10
2. The Impact of Technology on Education	Journal of Educational Technology	1985, Vol. 10, No. 2, pp. 1-15
3. The Importance of Parental Involvement	Journal of Educational Psychology	1990, Vol. 82, No. 3, pp. 1-12
4. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	1995, Vol. 98, No. 4, pp. 1-18
5. The Role of the School in the Community	Journal of Educational Research	2000, Vol. 103, No. 5, pp. 1-20
6. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2005, Vol. 108, No. 6, pp. 1-25
7. The Role of the Teacher in the 21st Century	Journal of Educational Research	2010, Vol. 113, No. 7, pp. 1-30
8. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2015, Vol. 118, No. 8, pp. 1-35
9. The Role of the Teacher in the 21st Century	Journal of Educational Research	2020, Vol. 123, No. 9, pp. 1-40
10. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2025, Vol. 128, No. 10, pp. 1-45

NCBI q1: 1026284

Location/Qualifiers

<1.>356

38.3%: Score 272: DB 24: Length 356:

Search completed: Tue Dec 17 22:57:19 1996
Job time : 283 secs.

variable region.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
REFERENCE 1 (bases 1 to 1599)
AUTHORS Lewis, A.P., Lemon, S.M., Barber, K.A., Murphy, P., Parry, N.R.,
Peakman, T.C., Sims, M.J., Worden, J., and Crowe, J.S.
TITLE Rescue, expression, and analysis of a neutralizing human
anti-hepatitis A virus monoclonal antibody
JOURNAL J. Immunol. 151 (5), 2829-2838 (1993)
MEDLINE 93367243
COMMENT NCBI gi: 185361
FEATURES
 location/Qualifiers
 source
 1..1599
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 /notes="Anti-hepatitis A; putative; NCBI gi: 185362"
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 /db_xref="PID:g185362"
 /translation="MDWTRFLFVAAATQSQMVQVQSGAEVKKPGSSVTVSKAS
GQTSFVATSWVRQAPCGLEWNGGIIPLEGPTYSQNFQGRVTITADKSTSTANWEL
ISLSEDAVYICATDRIQANFDRARVGFDPWQGLVTVSSASTKGPVFP LAP5
SKSTSGTAAACLVKDYFEPVTVSNWNGALTSVHTFPVAVIQSSGLYSLSVTVTP
SSSLGTOYICNVNHRPSNTHVKKVEPKSCDKTHCPCPAPPELLGSPVFLPPKP
KDTLMISRTPEVTVCVVDVSHEDPEVFNMYVDGVEVHNNAKTPREQINSTRVSV
LTVLHQDLNGKEIKCKVKNALPAP LKPTISKAKGPQRPQVYLPSPRDELTKNQV
SLTCLVKGTFPSDIAVWESNGQPPENNYKTPPVLDSGFFLYSLKLTVDKSRWQQGN
VFSSVNHAEALNHHTQKLSLSLPK"
 92..472
 /notes="variable region; putative"
 /codon_start=1
 /product="IgG"
 182..196
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 /notes="complementarity-determining region 1; putative"
 239..289
 /genes="CDR2"
 /notes="complementarity-determining region 2; putative"
 386..439
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 /notes="complementarity-determining region 3; putative"
 473..1462
 /notes="constant region; putative"
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Best Local Similarity 88.1%; Read No. 0.00e+00;
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RESULT 3 LOCUS 109303 1135 bp PAT 14-NOV-1994

DEFINITION Sequence 5 from patent WO 8902922.

ACCESSION 109303

NTD g587989

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1135)

AUTHORS Capon,D.J. and Gregory,T.J.

TITLE ADHESON VARIANTS

JOURNAL Patent: WO 8902922-A 5 06-APR-1989;

COMMENT NCBI gi: 587989

FEATURES Location/Qualifiers

source 1..1135

BASE COUNT 255 a 385 c 303 g 192 t

ORIGIN

Query Match

Best Local Similarity 71.6%; Score 1024; DB 37; Length 1135;

Matches 1079; Conservative 0; Mismatches 43; Indels 2; Gaps 2;

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TITLE Humanized monoclonal antibody CAMPATH-1H: myeloma cell expression of genomic constructs, nucleotide sequence of cDNA constructs and comparison of effector mechanisms of myeloma and Chinese hamster ovary cell-derived material

JOURNAL Clin. Exp. Immunol. 87 (1), 105-110 (1992)

MEDLINE 92127884

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 79307] from the original journal article. This sequence comes from Figure 2.a.

COMMENT**FEATURES**

source

NCBI gi: 243865

Location/Qualifiers

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/organism="Homo sapiens"

/note="human"

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RESULT 6

LOCUS A07562 1341 bp DNA PAT 28-JUN-1993

DEFINITION DNA sequence of chimeric monoclonal TSH antibody, gamma chain.

ACCESSION A07562

NID 9413075

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 1341)

AUTHORS Kalura,B. and Lenz,H.

TITLE Diagnostic method using chimeric antibodies

JOURNAL Patent: EP 0378175-A 13 18-JUL-1990;

COMMENT BOEHRINGER MANNHEIM GMBH

FEATURES NCBI gi: 413075

Location/Qualifiers

1..1341

/organism="Artificial sequences"

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LOCUS	HS1GG4FCA	768 bp
DEFINITION	H.sapiens mRNA for Immunoglobulin G1, Fc fragment.	PRI 21-JAN-1994
ACCESSION	X70421	
NID	q33068	
KEYWORDS	immunoglobulin; protein A binding.	
SOURCE	human.	
ORGANISM	Homo sapiens	
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	Catarrhini; Hominoidea; Homo.	

REFERENCE	1 (bases 1 to 768)	
AUTHORS	Filpula,D.	
TITLE	H. sapiens mRNA for immunoglobulin G1, Fc fragment	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 768)	
AUTHORS	Filpula,D.R.	
TITLE	Direct Submission	
JOURNAL	Submitted (10-FEB-1993) to the EMBL/GenBank/DBJ databases, D.R. Filpula, Enzon Labs, 16020 Industrial Drive, Gaithersburg, Maryland 20877, USA	
COMMENT	NCBI gi: 33068	
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DEFINITION	H.sapiens rearranged IgG VH-D-JH-Hinge-CH2-CH3 region.		
ACCESSION	X81695		
NID	g940515		
KEYWORDS	constant region; immunoglobulin heavy chain; variable region.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Osteichthyes; Sarcopterygii; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1163)		
TITLE	Khamlichi,A.A., Aouctourier,P., Preud'homme,J.L. and Cogne,M. Structure of abnormal heavy chains in human heavy-chain-deposition disease		
JOURNAL	Eur. J. Biochem. 229 (1), 54-60 (1995)		
MEDLINE	95262687		
REFERENCE	2 (bases 1 to 1163)		
AUTHORS	Khamlichi,A.A.		
TITLE	Direct Submission		
JOURNAL	Submitted (14-SEP-1994) to the EMBL/GenBank/DBJ databases. A.A. Khamlichi, CNRS URA 1172, LAB. IMMUN. AND GENETICS, IBMIG FACULTY OF SCIENCES, F-86022 POITIERS CEDEX, FRANCE		
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RESULT 11
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DEFINITION O-aries mRNA for immunoglobulin gamma1 chain secreted form.
ACCESSION X69797
NID g1268
KEYWORDS Ig heavy chain; immunoglobulin gamma-1.
SOURCE sheep.
ORGANISM Ovis aries
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Artiodactyla;
Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.
1 (bases 1 to 1594)
REFERENCE
AUTHORS Nau, F.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-1992) to the EMBL/GenBank/DBJ databases. F. Nau,
CNRS/Universite de Poitiers, IBMIG, Lab d'Immunologie Moleculaire,
Faculte des Sciences de Poitiers, 40 avenue du Recteur Pineau,
86022 Poitiers Cedex, FRANCE
REFERENCE 2 (bases 1 to 1594)
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AUTHORS Patri, S. and Nau, F.
JOURNAL Unpublished
COMMENT NCBI gi: 1268
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Db 235 tccagtccttaagtcgccgctcagcatcaccaagagacacacctccaagagtcagtgcgt 294
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QY 363 TTTTTCAGTTGTTGGAAGTGTTTACACAACACTGGTTGCACTGCTCTGGGGCGCGGAGTCT 422
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Qy 49 GTCTGTGTCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAG 108
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Db 81 ctgagactttctgtgcagctcttgattcaccttcag---taactacggctgagctgg 137
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Qy 169 ATCCGCCAGCCCCCAGGAGGAGGGGTGAGTGGATTGGGAGTTTCTATAGTAGTAGGG 228
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Qy 289 AACCAGTTCTCGCTCAAGCTGAACCTATATGACCGCGCGGACACGCGGTGTATTACTGT 348
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Db 318 acaactctacgtttctgtgcagctcgcctgttcactcagctcgtggactactgg 377
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Qy 349 GTGAGATGCTCTTTTTCAGTTGTTGGATGCTTTTACAACTGTTGTTGATGCTGCG 408
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Qy 409 GGGCCGGGAGTCTCGTACCGGTCTCTCAGCTAGCACCAAGGGGCCATCGGTCTTCCCC 468
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Db 438 ctggcccccagctggggggccaccaccacacagtgccctggcctggcctgggtgtcc 497
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Db 798 agggacacctctccatttccgaacccccagggtcacatgcattggtggtgacctg--- 854
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Qy 1423 GCTAAATGA 1431

RESULT 14
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DEFINITION S.domesticus immunoglobulin rearranged gamma chain mRNA, VJC
region, complete cds.
ACCESSION M81769
NID g164502
KEYWORDS C-region; D-region; J-region; V-region;
immunoglobulin gamma-chain; immunoglobulin heavy chain;
processed gene.
SOURCE Sus scrofa (individual isolate 5063-3, strain Minnesota miniature
swine, sub_species domesticus) adult spleen cDNA to mRNA.
ORGANISM Sus scrofa
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Artiodactyla; Suiformes; Suidae.
REFERENCE 1 (bases 1 to 1551)
AUTHORS Borch, B.L., Beaman, K.D. and Kim, Y.B.
JOURNAL Unpublished (1991)
COMMENT NCBI gi: 164502
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Qy 833 ACACCCTCATGATCTCCGGACCCCTGAGGTCACATGCGTCTGCTGGTGCAGCTGAGCCAGC 892
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Db 913 agaaccggaggtccagttctctggtcagtgagcggcgtagagtgacacgggcccaga 972
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Qy 893 AAGACCCTTGAGGTCGAAGTCAACTGCTAGCTGGAGCGGCTGGAGGTGCATAATGCCAAGA 952
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Db 973 cgaggccaaaggagcaggttcaacagcacctaccggtggtcagctcctaccatcc 1032
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Qy 1427 AATGA 1431
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```
RESULT 15
LOCUS RABIGHAD 1235 bp mRNA MAM 23-MAR-1995
DEFINITION Rabbit Ig active gamma H-chain (allotype Vha2 de12,14) mRNA.
ACCESSION K00752 M12187 M24226
NID g165127
KEYWORDS C-region; D-region; J-region; V-region;
heavy chain allotype Vha2; heavy chain allotype de12,14;
immunoglobulin gamma-chain; immunoglobulin heavy chain;
processed gene.
SOURCE Rabbit (haplotype F-I; Vha2 de12,14 allotype) spleen, cDNA to mRNA,
clone p-gamma-B1-12,14.
ORGANISM Oryctolagus cuniculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Lagomorpha; Leporidae.
REFERENCE 1 (bases 1 to 1235)
```

AUTHORS Bernstein,K.E., Alexander,C.B. and Mage,R.G.
TITLE Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplotype
JOURNAL Immunogenetics 18 (4), 387-397 (1983)
MEDLINE 84030930
COMMENT Original entry prepared by Dr. Rose Mage. The V-region is compared [1] with the Vha2 allotype p-mu-3 and the human genomic VH2 sequence. The two rabbit V-regions are 89.5% homologous, and this sequence is 77% homologous with the human segment. This sequence, as well as the p-mu-3 sequence, shows remarkable homology with the human CDR2 and D minigenes. The C-region is compared [1] with two rabbit C-regions, one of del1,15 allotype and the other of e15 and unknown d allotype.

NCBI gi: 165127 Location/Qualifiers
1..1235
/organism="Oryctolagus cuniculus"
<1..1209
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/codon_start=1
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/translation="MSWVRQAPGKLEWICYISGSAIYASWAKSRSTITRNTNENT
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TLGLVKGYLPEPVTWNSGLTNGVTFPPSRQSLGLSSVSVTSSQPVTCV
VAHPATNKTVDKTVAPSTCKPTPELLGGPSVFIFFPKPKDTLMISRTPEVTCV
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RYHNKALPAP IEXTISKARGPLEKPYTMGPPREELSSRSVSLTCMINGFYPSDI
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QKSLRSRSPK"
192..193
/organism="Oryctolagus cuniculus"
198..199
/organism="Oryctolagus cuniculus"
BASE COUNT 278 a 423 c 341 g 193 t
ORIGIN 9 bp upstream of AvalI site.

Query Match 34.0%; Score 487; DB 34; Length 1235;
Best Local Similarity 78.8%; Pred. No. 0.00e+00;
Matches 810; Conservative 0; Mismatches 197; Indels 21; Gaps 9;
Db 203 tctggggccaggcaccctgctcaccgtctcctcaggcaacctaaaggctccatcagctc 262
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Qy 404 TCTGGGGCCCGGAGTCTGTGCTCACCCTCTCTCTCAGCTAGCACCAAGGGCCCATCGGCTCT 463
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Db 323 tcaaaaggctacctccgggagcagtgacctgacctggaaactggggcaccctcaccatg 382
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Db 383 gggtagcaccttcccgctccggtccggtccctcaggtcctcaggtcctcagtgagcagctgg 442
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Qy 644 TGACCGCTGCCCTCCACAGAGCTTGGGCACCCAGACCTTACATCTCTCAACGCTGAATCA 703
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Db 494 ccaccaacacaaagtggagcaagacgcttgaccaccc---tc-----gacatg---cag-aa 542
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Qy 704 CCAGCAACACCAAGGTGCACACAGAAAGCAGAGGCCCAAAATCTTGTGCAAAACTCACACAT 763
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

[REDACTED]

(TM)

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MParch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 23:17:46 1996; MasPar time 117.29 Seconds
950.835 Million cell updates/sec

Tabular output not generated.

Title: >US-08-487-550-11

Description: (1-1431) from US08487550.seq

Perfect Score: 1431

N.A. Sequence: 1 ATGAACACCTGTGTTCTT.....CCTGTCTCGGGTAAATGA 1431

Comp: TACTTTCTGGACACCAAGAA.....GGCAGAGCCCCATTACT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 102519 seqs, 38967980 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-Geneseq24

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 9.440; Variance 6.351; scale 1.486

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1228	85.8	1431	19	Ti8059 Monoclonal antibody D	0.00e+00
2	1047	73.2	1549	3	Q20066 Encodes heavy chain o	0.00e+00
3	1048	73.2	1617	6	Q35099 Antibody D heavy chai	0.00e+00
4	1022	71.4	1135	1	N90736 DNA encoding linker	0.00e+00
5	1021	71.3	1136	1	N90779 Sequence of the linke	0.00e+00
6	1013	70.8	9208	11	Q65629 Vector contg. TCAE 8	0.00e+00
7	1008	70.4	1576	8	Q49944 Human anti-HBs heavy	0.00e+00
8	1003	70.1	1467	4	Q23570 Reshaped CD4 antibod	0.00e+00

9	1002	70.0	1386	8	Q49834 Anti-HIV-1 recombinan	0.00e+00
10	1001	70.0	1458	4	Q23571 Reshaped CD4 antibody	0.00e+00
11	999	69.8	1458	4	Q23581 Anti-IgE VH expressio	0.00e+00
12	999	69.8	6557	18	T15932 chiT84.12 H3 heavy ch	0.00e+00
13	995	69.5	1641	9	Q54655 Vector contg. TCAE 8	0.00e+00
14	987	69.0	8540	11	Q65628 Sequence of the chime	0.00e+00
15	983	68.7	1412	4	Q25692 Human kappa immunogl	0.00e+00
16	981	68.6	1174	9	Q51547 Synthetic IgG4 cDNA.	0.00e+00
17	824	57.6	1006	17	T12663 IgG1 hinge, CH2, CH3	0.00e+00
18	692	48.1	768	17	Q96101 Human IgG1 antibody F	0.00e+00
19	689	48.1	693	15	Q87592 IL4.Y124D/IgG1 gene f	0.00e+00
20	689	48.1	1164	17	T12658 Vector COSFLink.	0.00e+00
21	689	48.1	6367	17	T12661 IL-4.Y124D/IgG1 fusio	0.00e+00
22	689	48.1	6926	17	T12662 Human Fas/Fc fused OR	0.00e+00
23	687	48.0	1231	15	Q87593 cDNA sequence for a h	0.00e+00
24	685	47.9	699	9	Q53539 Immunoglobulin GI Fc	0.00e+00
25	685	47.9	705	18	Q74083 Polylinker/Fc fragmen	0.00e+00
26	686	47.9	745	9	Q55943 Fc cDNA.	0.00e+00
27	686	47.9	745	15	Q92273 Antibody Fc mutein co	0.00e+00
28	686	47.9	745	13	Q75425 Human IgG1 Fc-polylin	0.00e+00
29	686	47.9	745	9	Q58428 Human IgG1 Fc.	0.00e+00
30	684	47.8	740	6	Q41508 Human Fc polypeptide	0.00e+00
31	683	47.7	705	7	Q42589 LFA-3-Ig fusion gene	0.00e+00
32	682	47.7	1050	5	Q28684 VCAM 2D-IgG.	0.00e+00
33	682	47.7	1347	12	Q67347 tICAM(453)IgG immuno	0.00e+00
34	682	47.7	2043	9	Q55340 Plasmid pDC406/OX40/F	0.00e+00
35	681	47.6	1317	17	T00829 DNA sequence of LFA3T	0.00e+00
36	680	47.5	1050	6	Q40423 Sequence encoding a r	0.00e+00
37	675	47.2	1587	10	Q45225 P-selectin ligand-IgG	0.00e+00
38	675	47.2	1587	10	Q63958 P-selectin ligand/Fc	0.00e+00
39	675	47.2	1587	16	T02490 Portion of plasmid pp	0.00e+00
40	662	46.3	884	2	N70398 Part of the nucleotid	0.00e+00
41	658	46.0	765	1	N82142 Immunoglobulin G Fc d	0.00e+00
42	658	46.0	765	1	N82142 DHFR/intron (WTrasSD)	0.00e+00
43	645	45.1	6889	18	T15931 Human CD40-L/Fc fusio	0.00e+00
44	631	44.1	1425	6	Q41516 Sequence coding human	0.00e+00
45	631	44.1	1765	10	Q71873	0.00e+00

ALIGNMENTS

RESULT 1
ID Ti8059 standard; DNA; 1431 BP.
AC Ti8059;
DT 16-AUG-1996 (first entry)
DE Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.
KW Polymerase chain reaction; primer; amplify; PCR; light chain; Mab;
KW 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 1..1428
FT /*tag= a
FT sig_peptide 1..57
FT /*tag= b
FT mat_peptide 58..1425
FT /*tag= c
FT 3'UTR 1426..1431
FT /*tag= d
PN J08038178-A.
PD - 13-FEB-1996.
PF 20-FEB-1995; 030742.
PR 18-FEB-1994; JP-021628.
PA (NISN) NISSHINO IND INC.
PA (TANA/) TANAKA H.

DR	WPI; 96-154852/16.
DR	P-PSDB; R93553.
PT	Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -
PT	produced by primer amplification, used in the diagnosis of HCMV
PT	infection
PS	Claim #; Page 16-18; 22pp; Japanese.
CC	The sequences given in T18059-60 encode the heavy and light chains
CC	respectively of a monoclonal antibody against a 65 kD antigen of human
CC	cytomegalovirus (hCMV). These sequences were amplified using the
CC	sequences given in T18040-58. The monoclonal antibody may be used
CC	in the diagnosis of hCMV.
SQ	Sequence 1431 BP; 314 A; 475 C; 379 G; 263 T;
	Query Match 85.8%; Score 1228; DB 19; Length 1431;
	Best Local Similarity 94.7%; Pred. No. 0.00e+00;
	Matches 1359; Conservative 0; Mismatches 65; Indels 11; Gaps 8
D b	1 atgaacatctgtggtttcttcctcgtgtggcggtcccatgatgggtcgtgcaccag 60
Q y	1 ATGAACACCTGTGGTTCCTCCTCGTGCGGAGCTCCAGATGGGTCCTGCCACG 60
D b	61 ctgcagctgcaggagtgcgggccaggactggtgaagccttcggagacctgtccctcaac 120
Q y	61 GTCAAGCTGCAGAGTAGCGGGCCCCAGACTGGTCAAGCCCTCGGAGACCCTGTCCCTCAC 120
D b	121 tgcactgtctgtgtaicctcatcagcaggagtadtactcctggggctgcatccgcag 180
Q y	121 TGCGCGTGTCTGTGGTCCATCAGC--G-GTGGTTATGGCTGGGGCTGGATCCGCCAG 177
D b	181 cccccggggaagccttgagtgagtgagctgggaactatctat--ta-tagtggagacaactac 237
Q y	178 CCCCAGGCAAGGGCGCTGGAGTGGCATGGCAGTTTCTATTAGTAGTAGTGGGAACAACCTAC 237
D b	238 tacaaacogtccctcaagtgctgagtgcccacatatccgttagacgctgccacaacacagttc 297
Q y	238 TACAACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACAGCTCCAAGAACAGATTTC 297
D b	298 tcctgaagctgagctctgtgcacgcgcgcagacacgctgtgtattactgtgcaga-ac 356
Q y	298 TCCTCAAGCTGAACCTATGACCCCGCGGACACGGCCGCTGTTACTGTGTGAGAGAT 357
D b	357 c-tgcgcg--cagftattacgatacttttgactggttcctttccctcatactaatggggcaggg 413
Q y	358 CGTCTTTTTTCAGTGTGTGGAAATGTTTACAACATCGTTGCATGT-CTGGGGCGCGGG 416
D b	414 aaacctggtcacgctctctcaagctccaccaaggcccacatcggtcttccccctggcaacc 473
Q y	417 AGTCCTGGTCAACCGTCTCTCAGCTAGCAACAAAGGGCCCATCGGTCTTCCCTGTGCACC 476
D b	474 ctctccaagagacactctctgggggcacagcgcctggggtgcttgtgaaggactactt 533
Q y	477 CTCTCTCAAGAGCACCTCTGGGGGCACAGGGGCCCTGGGCTGGCTGGTGGTCAAGAGCTACTT 536
D b	534 ccccgaaacggtgacggtgtcgtggaaactcaggcgccctgaccagcggggtgcacacctt 593
Q y	537 CCCCGAACCGGTGAGGGTGTCTGGAACTCAGGGCCCTGACACAGCGGGCGTGCACACCTT 596
D b	594 ccggcgtgtcctacagtctcaggactctactccctcagcagcgtggtgacgctgccttc 653
Q y	597 CCGGGCTGTCTTACAGTCTCTAGAGACTCTTACTCCCTCAGACAGCGTGGTGAACCGTGCCTC 656
D b	654 cagcagcttgggcaccc-agaacctacatctgcaactgaatcacagccacagcaacaccaa 713
Q y	657 CACGACGTTGGGACCCCAACACCTACTCTCCACAGCTGAATCAAAGCCACACACACAA 716

Db	714	ggtggacaagaagtgtgacccaaatctttgtgacaaaactcacacatgccaccctgccc	773
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Db	774	agcaacctgaactcctgggggagaccgtcagttctctctcccccaaaacccaagacac	833
Qy	777	agcactcgaactcctggggggagccgtcagctagtcttcttcccccaaaacccaagacac	836
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Db	954	gccggggagagcagtagcaacagcagctacccgtggtcagcgtcctcaaccgtcctgca	1013
Qy	957	gccggggagagcagtagcaacagcagctacccgtggtcagcgtcctcaaccgtcctgca	1016
Db	1014	ccaggactggctgaatggcagaggtacaaagtgaaggtctccaaacaaagccctcccagc	1073
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Db	1074	ccccctcgaagaaacacatctccaaagccaaagggcagcccgagacacacaggtgtacac	1133
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Db	1134	cctgcccccaatcccgggatgagctgaccaagaaccaggtcagcgtgacctgacctgacaa	1193
Qy	1137	cctgcccccaatcccgggatgagctgaccaagaaccaggtcagcgtgacctgacctgacaa	1196
Db	1194	aggtctctatcccaggaactcgcggtggagtgggagagcaatgggcagccggagagacaa	1253
Qy	1197	aggtctctatcccaggaactcgcggtggagtggagagcaatgggcagccggagagacaa	1256
Db	1254	ctacaagaccacgcctcccgtgctgactccgacggtccttcttctctacagcaagct	1313
Qy	1257	ctacaaagacacgcctcccgtgctgactccgacggtccttcttctctacagcaagct	1316
Db	1314	caccgtggacaagagcaggtggcagcaggggaacgtctctcatgctccggtgatcatga	1373
Qy	1317	caccgtggacaagagcaggtggcagcaggggaacgtctctcatgctccggtgatcatga	1376
Db	1374	ggctctgcacaacacactacacgcaggaagagcctctccctgtctccgggtaaatga	1428
Qy	1377	ggctctgcacaacacactacacgcaggaagagcctctccctgtctccgggtaaatga	1431

RESULT	2	
ID	Q20066	standard; DNA; 1549 BP.
AC	Q20066;	
DC	Q20066;	
DT	25-MAR-1992	(first entry)
DE	Encodes heavy chain of 3D6 antibody.	
OS	Plasmid pUC26HC; human immunodeficiency virus; AIDS; ss.	
KW	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	sig_peptide	101..157
FT	/*tag= a	
FT	mat_peptide	158..1528
FT	/*tag= b	
FT	5'UTR	1..100
FT	/*tag= c	

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Q	y	717	ggtggacaagaacgacagcccaaaTCTTGTGCAAAATCTACATGCCACCGTGCC	776
D	b	774	agcaactgaactctgggggacgcgtcagttctctctcccccaaaaacccaagacac	833
Q	y	777	agcaactgaactctgggggacgcgtcagttctctctcccccaaaaacccaagacac	836
D	b	834	cctcatgatctcccgagccctgaggtcacatcgctgggtggagcgtgacacgaaga	893
Q	y	837	cctcatgatctcccgagccctgaggtcacatcgctgggtggagcgtgacacgaaga	896
D	b	894	ccctgaggtcaagtccaactggtcagcggtggaggtgcataatgccaaagacaaa	953
Q	y	897	ccctgaggtcaagtccaactggtcagcggtggaggtgcataatgccaaagacaaa	956
D	b	954	gcccggggagagcagtacaacagcagtcacgtggtcagcgtcctcacgcctgca	1011
Q	y	957	gcccggggagagcagtcacaacagcagtcacgtggtcagcgtcctcacgcctgca	1014
D	b	1014	ccagcactggtcgaatggcaaggagtcacaagtgcgaagttctccacaagaagccctccagc	1071
Q	y	1017	ccagcactggtcgaatggcaaggagtcacaagtgcgaagttctccacaagaagccctccagc	1074
D	b	1074	ccccatcgagaaaaccatctccaaagccaaaagccagcccgagaccacacaggtgtacac	1131
Q	y	1077	ccccatcgagaaaaccatctccaaagccaaaagccagcccgagaccacacaggtgtacac	1134
D	b	1134	ctgcccaccatcccgggatcgagctgaccaagaaccaggtcagcctgaactgctgtgtcaa	1191
Q	y	1137	ctgcccaccatcccgggatcgagctgaccaagaaccaggtcagcctgaactgctgtgtcaa	1194
D	b	1194	aggettctatcccagcgaactcgccgtggagtgaggagacaatgggcagccggagagaaa	1251
Q	y	1197	aggettctatcccagcgaactcgccgtggagtgaggagacaatgggcagccggagagaaa	1254
D	b	1254	ctacaagaccagcctccgtgctggactccgacggcgtcttctctctacagcaagct	1311
Q	y	1257	ctacaagaccagcctccgtgctggactccgacggcgtcttctctctacagcaagct	1314
D	b	1314	caccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgacga	1371
Q	y	1317	caccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgacga	1374
D	b	1374	ggctctgcaaaaaccatcacagcagaagagcctctccgtgctccgggttaaatga	1428
Q	y	1377	ggctctgcaaaaaccatcacagcagaagagcctctccgtgctccgggttaaatga	1431

RESULT	2	
ID	Q20066	standard; DNA; 1549 BP.
AC	Q20066;	
DC	Q20066;	
DT	25-MAR-1992	(first entry)
DE	Encodes heavy chain of 3D6 antibody.	
OS	Plasmid pUC26HC; human immunodeficiency virus; AIDS; ss.	
KW	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	sig_peptide	101..157
FT	/*tag= a	
FT	mat_peptide	158..1528
FT	/*tag= b	
FT	5'UTR	1..100
FT	/*tag= c	

FT misc feature 158..535
 FT /*tag= d
 FT /label= variable region
 FT misc feature 158..247
 FT /*tag= e
 FT /label= Framework 1
 FT misc feature 248..262
 FT /*tag= f
 FT /label= CDR_1
 FT misc feature 263..304
 FT /*tag= g
 FT /label= Framework 2
 FT misc feature 305..355
 FT /*tag= h
 FT /label= CDR_2
 FT misc feature 356..451
 FT /*tag= i
 FT /label= Framework 3
 FT misc feature 452..502
 FT /*tag= j
 FT /label= CDR_3
 FT misc feature 503..535
 FT /*tag= k
 FT /label= Framework 4
 FT misc feature 536..1528
 FT /*tag= l
 FT /label= Constant_region
 PN W09118983-A.
 PD 12-DEC-1991.
 PF 28-MAY-1991; 100067.
 PR 29-MAY-1990; AT-001178.
 PA (JUNG/) JUNGBAUER A.
 PI Felgenhauer M, Himmeler G, Kohl J, Steindl F;
 DR WPI; 92-007468/01.
 DR P-PDB; R20057.
 PT Recombinant protein which binds to complex viral antigen and
 PT HIV-1 - contains variable region of antibody derived from 3D6
 PT cell line, used for detecting HIV-1 antigen
 PS Claim 2; Page 24; 52pp; German.
 CC The 5'-UTR is 100 bases long although the specification numbers it
 CC at 98 bases. It is possible that two extra bases have been inserted
 CC as a typographical error in the specification (i.e. that the 5'-UTR
 CC sequence is incorrect as printed in the specification and reproduced
 CC here). The sequence comprises a human cDNA insert encoding the 3D6
 CC heavy chain flanked by short stretches of pUC19 DNA. The variable
 CC region of the heavy chain is used in a recombinant protein with the
 CC variable region from the kappa light chain of 3B6, the two V regions
 CC being joined by a linker. The recombinant protein binds to HIV gp160.
 CC See also Q20067 and Q20068.
 SQ Sequence 1549 BP; 362 A; 464 G; 416 C; 307 T;
 Query Match 73.2%; Score 1047; DB 3; Length 1549;
 Best Local Similarity 87.8%; Pred. No. 0.00e+00;
 Matches 1234; Conservative 0; Mismatches 169; Indels 3; Gaps 1;
 Db 126 tccttttgctattttaaaggtgtccagtgtaagtcagctgggtgagtcgtgggag 185
 |||| |||| | | |||| | | |||| |||| |||| |||| |||| |||| |||| ||||
 QY 26 TCCTGGTGGCAGCTCCACAGTCTCTGCCAGTGCAGCTGCAGAGTCGGGCCAG 85
 Db 186 gcttggtagcgcctggcaggttccctcgagactctctgtgcagcctgtggttcacctta 245
 | |||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
 QY 86 GACTGGTAGACCTTCGAGACCTCTCCCTACCTGCGCTGTCTGTGGTGGCTTCATCA 145
 Db 246 a---tgattatgcatgcaactgggttcggaagctccagggagggcctgagtggtgtct 302

QY 146 GCGGTGGTTATGGCTGGGGCTGATCCGCCAGGCCCGAGGGGCTGGAGTGGATTG 205
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 Db 303 caggtataagttgggagtagtagtgcggaactctgtgaaggggcgatgca 362
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 Db 483 tcacggttgctttgatctctggggccaaggagacaatggtcacctgtctcttcagctcca 542
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 QY 386 ACAACAACACTGGTTCCGATGCTGGGGCCGGGAGTCTGGTCACCGTCTCCTCAGCTAGCA 445
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 Db 543 ccaagggcccatcggtcttccccctggcacccctctccaagagcacctctctggggcacag 602
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 QY 446 CCAAGGGCCCATCGGTCTTCCCTTGGCACCCCTCTCCAACAGACCTCTTGGGGCACAG 505
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 Db 603 cagccttggtgctcctggtcaaggactactccccgaaccggtgacggtgtcgtggaact 662
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 QY 506 CCGCCTTGGCTGCTGCTCAAGGACTACTTCCCCCAACCGGTGACGGTGTCTGGTGAAT 565
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 Db 663 caggcgccctgaccagcgggtgcacacctccccggtgtcctacagtcctcaggactct 722
 |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 QY 566 CAGGCGCCTGACGACGGCGTGCACACTTCCGGCTGCTCTACAGTCTCCTCAGGACTCT 625
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 Db 723 actcctcagcagcgtggtgacgtgacctccagcagcttggccaccagacctacatct 782
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 QY 626 ACTCCTCAGCAGCGTGTGACGTGCCGTGCCAGCAGCTTGGCGACCCAGACCTTACATCT 585
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 Db 783 gcaactgtaatcacaagcccagcaacacaaggtcgacaagaagttagcccaaatctt 842
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 Db 843 gtgcaaaactcaacatgcccacgtgccacgacctgaactcctgtgggggaccgtcag 902
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 QY 986 ACCGTGTGTCAGCTCTCCCGTCTCCTGCACAGGACTGGCTGAATGGCAAGGAGTACA 1045
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 QY 1046 AGTGCAAGGTCTCCACAAAGCCCTCCCAAGCCCTCCGAGAAACCATCTCCAAAGCCA 1105
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 Db 1203 aagggcagccccgagaaccacaggtgtacacctgcccccatccccggatgagctgacca 1262

Qy	1106	AAGGGCAGCCCGGAAACACAGGTTACACCTTGCCTGCCCATCCGGGATGAGTGACCA	1165
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Qy	1166	AGAACAGGTGACGCTGACCTGCTGGTCAAGGCTTCTATCCACGGACATCCCGTGG	1225
Db	1323	agtggagagcaaatgggcagccgagagacaactacaagcacgcctccgtgtgtagct	1382
Qy	1226	AGTGGGAGAGCAATGGGCAGCCGGAGCAACACTACAAGACACGCCCTCCCGTGTGGACT	1285
Db	1383	ccgacggctccttctctctacagcaagctccacctggacaagagcaggtggcagcagg	1442
Qy	1286	CCGACGGCTCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGACAGGTGGCAGCAGG	1345
Db	1443	ggaacgtctttctatgtccgtgatgcatgcatgagggctctgcacaaccactacacacaga	1502
Qy	1346	GGAAAGCTTCTCAATGCTCCGTGATGCAATGAGGCTCTGCACACCACTACACGCAAGA	1405
Db	1503	gcctctccctgtctccgggtaaatga	1528
Qy	1406	GCCTCTCCCTGCTCCGGGGTAAATGA	1431

RESULT

ID Q35099 standard; DNA; 1617 BP.

Q35099;
AC Q35099;

DT 19-MAY-1993 (first entry)

DE Antibody D heavy chain.

KW Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;

KW Lymphocyte; hepatitis A virus; HAV; sero; positive; patient;

KW murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H; ss.

05 Synthetic.

FH	Key	Location/Qualifiers
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100	100	100

FT	CDS	
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FT /*tag= a

FT	sig_peptide	35..91
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IT = $\beta \tau a q = b$

FT	misc_RNA	92..181
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ET /*tag= c

FT /label= FR1

FT misc_RNA 182..196

FT /*tag= d

FT /label= CDR1

FT misc_RNA 197..238

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FT /label= FR2

FT misc_RNA 239..239

FT /*tag= f

FT /label= CDR2

FT misc_RNA 290..385

ET /*tag= g

FT /label= FR3

FT misc_RNA

$$E_T / \text{tag} = h$$

ET /label= CDR3

FT misc_RNA 440..472

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ET      / *tag= i
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FT /label= FR4

FT misc_RNA 473..763

FT /*tag= j

FT /label= CH1

ET misc_RNA 764..811

FT /*tag= k

FT	/label= HINGE	
FT	misc RNA	812..1141
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FT	/label= CH2	
FT	misc RNA	1142..1462
FT	/*tag= m	
FT	/label= CH3	
FT	TATA signal	1566..1571
FT	/*tag= n	
PN	EP-523949-A.	
PD	20-JAN-1993.	
PF	14-JUL-1992; 306420.	
PR	15-JUL-1991; GB-015284.	
PR	01-AUG-1991; GB-016594.	
PR	23-MAR-1992; GB-006284.	
PA	(WELL) WELLCOME FOUND LTD.	
PI	Crowe JS, Lewis AP;	
WPI	93-019951/03.	
DR	P-PSDB; R31024.	
PT	Prodn., of recombinant primate antibodies - useful for treating	
PT	infections caused by hepatitis A, B and C, herpes,	
PT	cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,	
PT	arthritis etc.	
PS	Disclosure; Fig 2; 35pp; English.	
CC	The sequences given in Q35099-100 encode the heavy and light chains	
CC	of Antibody D respectively. Antibody D is a monoclonal antibody which	
CC	was derived from peripheral blood lymphocytes from a hepatitis A virus	
CC	(HAV) sero positive patient. Antibody D is closely related in nature	
CC	to murine antibody B5B3. Total RNA was isolated from antibody D	
CC	expressing cells and polyadenylated RNA was extracted. These polyA	
CC	RNA's were used to prepare a cDNA library which was screened for human	
CC	kappa light (L) chains and two positive clones were detected.	
CC	Further heavy (H) chain clones were also isolated.	
SQ	Sequence 1617 BP 375 A; 526 C; 441 G; 275 T;	

QY 376 GGAAATGGTTTACAAACAATGCTTCCATGCTCTGGGGCCGGAGTCTCGTCAACGCTCTCC 435
DB 470 tcagctcccaagaaggccactcggtcttcccccctggacccctctcccaagagacactct 529
QY 436 TCAGCTAGCACACNAGGCGCATCGGTCTTCCCCCTGGACACCTCTCCCAAGACGACCTCT 495
DB 530 gggggcacacggccctgggtcgctgctcaaggactacttcccgaaccggtgacgggtg 589
QY 496 GGGGGCACAGCGCCCTGGGCTGCTTGGTCAAGGACTACTTCCCGCAACCGGTGACGGTG 555
DB 590 tcgtagactcaggcgccctgaccagcggtgtgacacacttcccggctgtctacagttcc 649
QY 556 TCGTGGAACTCAGGGCGCCTGACGACGGGCTGCACACCTTCCCGGCTGCTCTACAGTCC 615
DB 650 tcaggactctactccctcagcagctggtgacggtgcccctccagcagcttgggcaaccag 709
QY 616 TCAGGACTCTACTCTCCTGACGACGGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAG 675
DB 710 acctacatctgaacgtgaatcacaagccagcaacacaaaggtggacaagaagttag 769
QY 676 ACCTACATCTGCNAGCGTCAATCAAGGCCAGCAACCAAGGTGCAACAAGACGACAG 735
DB 770 cccaaatctgtgacaaactcaacatgccacagcggtgccagcactgaactcctcgggg 829
QY 736 CCCAAATCTTGTGACAAACTCACATGCCACCGTCCCGACGACCTGAACCTCTCGGG 795
DB 830 gaccgtcagcttctctcttcccccaaaacccaaggacacccctcatgatctcccgacc 889
QY 796 GGACGCTCAGCTCTCTCTTCCCGCCAAACCCAGGACACCTCATGATCTCCCGGACC 855
DB 890 cctgagctcacatgcgtggtggtgagctgagccacgaagacctgaggtcaagtcaac 949
QY 856 CTGAGGTCACATGGCTGGTGTGACGTGAGCGCAGCAGACCTGAGGTCAAGTTCAAC 915
DB 950 tggtagctggacggcgtgaggtgacatgccaagacaaagcgggagagcagtcac 1009
QY 916 TGTGACGTGGACGGGTGGAGGTGATTAATGCCAAGCAAAAGCCGGGAGGACGATC 975
DB 1010 aacagcagctacgctggtgagcgtcctcagcgtcctgacagagcagctgactgaatggc 1069
QY 976 AACAGCAGCTACCGTGTGTCAGCGTCTCAGCGTCTCAGCAGGACTGGCTGAATGCC 1035
DB 1070 aaggagtacaagtgaaggtctcccaaaagccctccagcccccatcgagaaaccatc 1129
QY 1036 AAGGAGTACAAGTGCAGGCTTCAACAAGCCCTCCAGCGCCCATGAGAAAACATC 1095
DB 1130 tccaaagccaaagggcagccccgagaacacaggtgtacacctgcccccatccccggat 1189
QY 1096 TCCAAAGCCAAAGGGACGCCCCGACGACAGGTGTACACCTGCCCCCATCCCGGAT 1155
DB 1190 gagctgaccaagaacacaggtcagcctgactgcctgggtcaaggcttctatcccagcagc 1249
QY 1156 GAGCTGACCAAGAACAGGTCAGCTGACCTGGCTGGTCAAGGCTTCTATCCGACGCAC 1215
DB 1250 atcgccgtggagtggagagcaatgggacggcgagaaactacaagaccagcctccc 1309
QY 1216 ATCGCCGTGGAGTGGGAGAGCAATGGGACGCGGAGAACTACAAGACCGCCTCCC 1275
DB 1310 gtgctgactccagcggctctctctctctctctctcagcaagctcaccgtggacaagcagg 1369
QY 1276 GTGCTGGACTCCGACGGTCTCTTCTTCTCTTACAGCAAGCTCACCGTGGACAGCAGG 1335
DB 1370 tggcagcaggggaacgtcttctctcgtcgtgatgcatgaggtctgcaacaactac 1429

QY 1336 TGGCAGAGGGGAAGCTCTCTCATGCTCCGTGATGCATGAGGCTCTGCACACCACTAC 1395
DB 1430 acqcaagaagcctctccctgtctccgggtaaatga 1465
QY 1396 AGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
RESULT 4
ID N90736 standard; DNA; 1135 BP.
AC N90736;
DT 06-JUN-1990 (first entry)
DE DNA encoding linked human IgG1 (gamma 1) chain fragment
KW Human IgG1; gamma 1; immunoglobulin; CD4; fusion protein.
OS Homo sapiens
FH Key Location/Qualifiers
FT CDS 8..1123
FT /tag= a
FT misc_feature 133..134
FT /tag= b
FT /note= "Insert site"
FT misc_feature 439..440
FT /tag= c
FT /note= "Insert site"
PN W08902922-A.
PD 06-APR-1989.
PE 03-OCT-1988; U03414.
PR 02-OCT-1987; US-104329.
PA (GETH) Genentech.
PI Capon DJ, Gregory TJ;
DR WPI; 89-114397/15.
DR P-PSDB; P93558.
PT New nucleic acid sequences encoding adhesion, esp. CD4, variants -
PT partic. with trans-membrane domain inactivated or fused to other
PT peptide, useful esp. for treating HIV infections
PS Figure 4A-4B2; pp. 10/13-12/13; 78pp; English.
CC It is employed in the prepn. of CD4 fusions. The insert sites are
CC given in the Features Table. CD4 fusion proteins can have antiviral and
CC immunomodulatory activity and are esp. useful for treating HIV infections,
CC regardless of genetic variation within the virus. They and antibodies
CC raised against them can also be used diagnostically for assaying adheosns
CC and their ligands.
SQ Sequence 1135 BP; 255 A; 386 C; 302 G; 192 T;
Query Match 71.4%; Score 1022; DB 1; Length 1135;
Best Local Similarity 95.9%; Pred. No. 0.00e+00;
Matches 1078; Conservative 0; Mismatches 44; Indels 2; Gaps 2;
DB 1 gaattctgtcaactccgcgacacacagcgctatattactgtgcagagc-caccttttgc 59
QY 309 GAACCTCTATGACCGCCGACACGCGCGGTATTACTGTGAGAGATCGTCTTTTTC 368
DB 60 tatgttaacagggagcgtccccccttgttgatcgaccccctggggcctgggaacccctggtca 119
QY 369 AGTTGTGGAATGTTTACAACAACCT-GTTTCGATGTCTGGGCGCGGAGTCTCTGTCA 427
DB 120 cagctctcctcggtctccaccaagcccccatcggtttcttccccctggcaacctctctccaaga 179
QY 428 CCGTCTCTCAGGTAGCACCAAGGCCCCATCGGTCTTCCCTCTGGACCCCTCTCCCAAG 487
DB 180 gcaactctgggggcacagcgccctgggctgcctggtcaaggactacttccccgaacgg 239
QY 488 GACCTCTGGGGGCGACAGCGCCCTGGGCTGGCTTGTGTCAAGGACTACTTCTCCCGAACCG 547

QY 1117 CGAGAACACAGGTGTACACCTTGGCCCATCCCGGATGAGTGCACCAACACAGGTC 1176
|||||
Db 3558 agcctgacctgctggtcaaggtcttatccagagacatcccggtggagtggagagc 3617
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QY 1177 AGCTGTACCTGCTGGTCAAGGCTTCTATCCACGGACATCCCGCTGAGTGGGAGAGC 1236
|||||
Db 3618 aatggcagcagagagaactacaagaccacgctcccgctgctgactccgacgctcc 3677
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QY 1237 AATGGCAGCCGAGAACTACAAGACACACGCTCCCGTGTGACTCCGACGGCTCC 1296
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Db 3678 ttcttctctacagcaggtcaacctggacaagagcaggtggcagcaggaggaacgtcttc 3737
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QY 1297 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGCAGCAGGTGGCAGCGGCAAGCTTTC 1356
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Db 3738 tcatgtccogtgcagtgaggtctctgcacaaccactacacgaggaagagctctccctg 3797
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QY 1357 TCATGCTCGTGTATCATGAGGCTCTGCACACCACTACACGAGAGAGGCTCTCCCTG 1416
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Db 3798 tctccgggttaata 3812
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QY 1417 TCTCGGCTAATGA 1431
|||||

RESULT 7

ID Q49944 standard; cDNA; 1576 BP.
AC Q49944;
DT 29-APR-1994 (first entry)
DE Human anti-HBs heavy chain.
KW Antibody; Ab; light; heavy; chain; hepatitis B;
KW HB; surface antigen; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 15..1394
FT /tag= a 15..41
FT sig_peptide
FT /*tag= b
FT mat_peptide 42..1391
FT /tag= c
FT /note= "claim 2, page 27"
PN W09320205-A.
PD 14-OCT-1993.
PF 30-MAR-1993; J00396.
PR 30-MAR-1992; JP-074678.
PA (SUNR) SUNTORY LTD.
PI Arima K, Kurihara T, Matsukura S, Nishihara T, Tsuruoka N;
DR WPI; 93-336913/42.
DR P-PSDB; R42066.
PT Human anti-hepatitis B surface antigen antibody gene - can be
PT used to produce L and H chains of the antibody in large quantity
PS Disclosure; Fig 6-8; 46pp; Japanese.
CC Polynucleotides encoding the L and H chains of human anti-HBs
CC Ab are given in Q49943-Q49944. The Ab can be easily produced in
CC large quantities for therapeutic use.
SQ Sequence 1576 BP; 394 A; 483 C; 426 G; 273 T;

Query Match 70.48; Score 1008; DB 8; Length 1576;
Best Local Similarity 98.5%; Pred. No. 0.00e+00;
Matches 1024; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Db 355 acagattgactctcgggcccaggaacacctggtcacgctctctcagcctccaccaagg 414
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QY 392 ACTGGTTCGATGCTCTGGGGCGGGAGTCTCTGTCACGCTCTCTCTAGCAGCACAGG 451
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Db 415 gccatcggtcttccccgtgcaacctctctccaagcaacctctggggcacagcgccc 474
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QY 452 GCCATCGGTCTTCCCGCTTGGACACCTCTCAAGAGACACCTTGGGGGCACACGGCGCC 511
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Db 475 tgggctgcctggtcaaggactacttccccgaaccggtgacggtgtcgtggaactcaggcg 534
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Qy 1424 GTAAATGA 1431

RESULT 10
ID Q23571 standard; DNA; 1458 BP.
AC Q23571;
DE 20-OCT-1992 (first entry)
DT Reshaped CD4 antibody heavy chain cDNA CD4VHNEW-Thr30
KW Antigen; CDR; complementarity determining region; graft rejection;
KW autoimmune diseases; rheumatoid arthritis; allergy; ss.
OS Rattus rattus.
EH Key Location/Qualifiers
FT CDS 36..1439
FT /tag= a
FT misc_feature 183..197
FT /tag= b
FT /note= "Complementarity determining region 1"
FT misc_feature 240..290
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PN W09205274-A.
PD 02-APR-1992.
PF 16-SEP-1991; G01578.
PR 17-SEP-1990; GB-020282.
PA (GORM/) GORMAN S D.
PI Clark M R, Cobbold S P, Gorman S D, Waldmann H.
DR WP1; 92-132139/16.
DR P-PSDB; R22758.
PT Humanisation of antibodies binding to human CD4 antigen - by
PT mutation of framework-encoding regions of DNA encoding variable
PT domain of rat or mouse antibody chain
PS Disclosure; Fig 6; 74pp; English.
CC CD4VHNEW-Thr30. Reshaped CD4 antibody can be used to induce tolerance
CC against an antigen. It can also be used to alleviate autoimmune diseases
CC such as rheumatoid arthritis, and to prevent graft rejection. Tolerance
CC to a graft, e.g. an organ graft or a bone marrow transplantation can
CC also be useful to alleviate allergies. Tolerance to allergens could
CC also be achieved. See also Q23566-Q23581.
SQ Sequence 1458 BP; 345 A; 467 C; 385 G; 261 T;

Query Match 70.0%; Score 1001; DB 4; Length 1458;
Best Local Similarity 98.7%; Pred. No. 0.00e+00;
Matches 1014; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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RESULT 15
ID Q25692 standard; cDNA; 1412 BP.
AC Q25692;
DT 28-DEC-1992 (first entry)
DE Sequence of the chimeric H chain cDNA contained in pBI373
KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;
KW antithrombotic agent; myocardial infarction therapy; ss.
OS Synthetic.

FH Key Location/Qualifiers
FT sig_peptide 13..69
FT /*tag= a
FT /product= Leader
FT CDS 70..414
FT /*tag= b
FT /product= VH 415..708
FT CDS
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FN EP-491351-A.
PD 24-JUN-1992.
PF 17-DEC-1991; 121591.
PR 18-DEC-1990; JP-413829.
PR 11-NOV-1991; JP-294464.
PI (TAKE) TAKEDA CHEM IND LTD.
PI Iwasa S, Taka H, Watanabe T, Tada H;
WIPI; 92-209528/26.
DR P-PSDB; R24812.
PT Chimeric monoclonal antibodies - contain anti-human fibrin
antibody light and heavy chain variable and constant for treating
thrombotic conditions e.g. myocardial infarction
PS Example; Figure 11; 8/pp; English.
CC Plasmid pBI373 contains the whole length of a mouse-human
chimeric anti-human fibrin heavy chain cDNA open reading
frame. It was prepd. using Poly(A)+ RNA from the anti-fibrin
chimeric Ab-producing transformant FIB1-H01/X63 as a template
to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as
a primer for first strand cDNA synthesis and the 5'CZH and 3'EH
primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding
cDNA was amplified. Similarly a human gamma-1 chain CH1 domain
encoding cDNA and an anti-fibrin antibody VH cDNA and a leader
peptide cDNA were amplified using the primers 3'EH, 3'CZH and 3'CIH
respectively as a primer for first strand cDNA synthesis and the
primer combination of 5'CIH and 3'CZH, of 5'LIH and 3'CIH and of
5'SH and 3'LIH respectively as primers for PCR. The amplified gene
products were isolated and used to produce plasmids. After
confirmation of the cDNA sequence of each plasmid, the cDNA
encoding LH, VH, CH1 and CH2CH3 were joined together to give
cDNA plasmid pBI373 contg. the whole length chimeric H chain
(LH, VH, CH1, CH2CH3), also abbreviated as Igh-FIB,
SQ Sequence 1412 BP; 325 A; 433 C; 381 G; 273 T;

Query Match 68.7%; Score 983; DB 4; Length 1412;
Best Local Similarity 97.9%; Pred. No. 0.00e+00;
Matches 1005; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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QY 405 CTGGGGCCGGGAGTCTCTGCTCAGCCTCTCTCTCAGTAGCACCAGGGCCCATCGGTCTT 464
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Db 441 cccctggcaccctctccaagagcacctctgggggacagcgccctggcgtgcctggt 500
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31

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Db 801 acccaaggacacctcatgatctcccgaccctcaggtcacatcggtgggtggtgagcgt 860
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Db 1341 cgtgatgatgaggtctgtgcacaacactacacgcagaagagcctctccctgtccccggg 1400
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Qy 1365 CGTGATGATGAGGCTCTGCACAACCACTACACGAGAGAGCCTCTCCCTGTCTCCGGG 1424

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IMAGE Consortium (info@image.llnl.gov) for further information.

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NID 9725078
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vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=M13RPL Rsite=EcoRI Reite2=XhoI Normal lung tissue from a 72
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
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5'-CTCAGATTTTTTTTTTTT-3'.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 415)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

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Parsons,J., Rifkin,L., Rohlifng,T., Tan,F., Trevaskie,E.,
Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
WashU-Merck EST Project
Unpublished (1995)

TITLE
JOURNAL
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

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  Matches 378; Conservative 0; Mismatches 2; Indels 10; Gaps 9;

Db 1 acaaaactcaacatgcccacngtgcacacacatgaactcctctggggggaccctcagtc 60
QY 749 ACAAAATCAACATGCCCCACC-GTCCCCAGCACCTGAATCTCTGGGGGAGCCGTGAGTC 807

Db 61 ttcttctcccccaaaacccaaggaacacctcatgatctcccgaccctcagggtcaca 120
QY 808 TTCTCTTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACA 867

Db 121 tgcgtggtggagcgtgagccacgaagaccctgaggtcgaagtccaacttggtacgtggac 180
QY 868 TGCCTGCTGCTGGAGCTGAGCCACGAGACCCCTGAGGTCAAGTCAAGTCAAGTCAAG 927

Db 181 ggcgtggaggtgcataatgccaaagcaaacgcgggagagcagtcacacagcacgtac 240
QY 928 GCGCTGGAGGTGCATAATGCCAAAGCAAAAGCCGGGAGGAGCAGTACACAGCAGCTAC 987

Db 241 cgtgtggtcagcgtcctcaccgtcctgcaccaggagactggtggtgaatggcaagagatc 300
QY 988 CGTGTGCTGAGCGTCTCTCAACGCTCTGCACAGG-ACT-GGCT-GAATGGCAAGGAGTAC 1044

Db 301 aagttgcaaggtttccacaagaagccctccagcccccttcgaaggaaaccatcttcca 360
QY 1045 AAGT-CCAGGTCT-CCACAAAGAGCCCTCCAGCCCCCATCGA--GAAACCATCT-CCA 1099

Db 361 aagccaagaagggcagcccgaggaaccacag 390
QY 1100 AAGCCAAAGGAGGCCCGCAG-AACCCAG 1128

RESULT 4
LOCUS R82750 484 bp mRNA EST 14-JUN-1995
DEFINITION yj25c07.r1 Homo sapiens cDNA clone 149772 5' similar to gb:M87789
IG GAMMA-1 CHAIN C REGION (HUMAN) .
ACCESSION R82750

```

NID 9862141
 KEYWORDS EST.
 SOURCE human clone=149772 library=Soares placenta Nb2HP vector=pf7T3D (Pharmacia) with a modified polylinker host=DHI0B (ampicillin resistant) primer=M13RPI Rsite1=Not I Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
 AACCTGCAAGATTGGGGCGCGAGCAATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pf7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaudo.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 484)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 290
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 862141
 Location/Qualifiers
 1..484
 /organism="Homo sapiens"
 /clone="149772"
 /note="human"
 BASE COUNT 122 a 143 c 129 g 88 t 2 others
 ORIGIN
 Query Match 21.7%; Score 310; DB 69; Length 484;
 Best Local Similarity 91.9%; Pred. No. 0.00e+00;
 Matches 442; Conservative 0; Mismatches 20; Indels 19; Gaps 19;
 Db 1 cacaagcccaagcaacacacaggtggacagagattgagccaaatctgtgacaaaact 60
 QY 697 CACAGCCGACGACACACAGGTGGACAGACAGAGCCCAATCTGTGCAAACT 756
 Db 61 cacacatgccaccgtgcccagcacctgaactcctgggggacccgacgtctctcttc 120
 QY 757 CACATGCCACCGTGGCCAGCACCTGAATCTGGGGGACCGTCATCTTCCTTC 816
 Db 121 ccccaaaacacaaagac 180
 QY 817 CCCCCAAACCAAGGACACCCCTCATGCTCCCGGACCCCTGAGGTGCATGCGGTG 876
 Db 181 gtggacgtgagccacgaagacacacacacacacacacacacacacacacacacac 240

QY 877 GTGAGCTGAGCCACGACGACCTGAGGTCAAGTTCAGTGTGACGTGACGGCGTGAG 936
 Db 241 gtccataatgccaaagacaaacccgagggagcagtcacaaacacgacgtacggtggtt 300
 QY 937 GTCCATAATCCAGACAAAGCCGGGAGGAGCAGGTACACACGACGACGTGCGT 995
 Db 301 cagcgttccacggttccctcctggcaccagagattgggtgaatgggcaaggaggttacaagt 360
 QY 996 CAGCGT-CCTACCGT-CCTG-CACCAGGACTGGCT-GAATGG-CAAGG-AGT-ACAAGT 1048
 Db 361 tgaaggtnttccaaagaagcctccagggcccttttttaggaaacacacacacacacac 420
 QY 1049 -GCAAGGTCT-CCAAAGACGCT-CCAG-CCCCATCG-AG-AAACCATCT-CCAAA 1101
 Db 421 gccaaagggcagcccgaggaacacacagtggttcaacttggcccttcccgaggagga 480
 QY 1102 GCCAAGGG-CAG-CCCCGAG-ACCACAGGTGTACACCTGCCCCCAT-CCCCGATGA 1157
 Db 481 g 481
 QY 1158 G 1158

RESULT 5
 LOCUS H67250 364 bp mRNA EST 27-OCT-1995
 DEFINITION yu65h03.r1 Homo sapiens cDNA clone 238709 5' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);.
 ACCESSION H67250
 NID g1025990
 KEYWORDS EST.
 SOURCE human clone=238709 primer=M13RPI library=Weizmann Olfactory Epithelium vector=pBluescript SK- host=SOLR cells (kanamycin resistant) Reitel-EcoRI Reite2=XhoI From 35 year old female. The cDNA was oligo (dT) primed with an XhoI restriction enzyme recognition site and an 18 base poly dT sequence. For the 5' end, the synthesized cDNA termini were treated with T4 DNA polymerase and EcoRI adaptors were ligated to the blunt ends.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 364)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
 TITLE WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 241
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source
1..364
/organism="Homo sapiens"
/clone="238709"
/note="human"
mRNA
79 a 117 c 101 g 65 t 2 others
ORIGIN

Query Match 21.2%; Score 304; DB 24; Length 364;
Best Local Similarity 98.4%; Pred. No. 0.00e+00;
Matches 312; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Db 1 ccgaagaacacagtgatataccctgcccccatcccggtgatgagtgaccagaaccaggt 60
|||||
Qy 1116 CCGAGACACAGGTGTACACCTGCCCCCATCCGGGATGAGTGCACAGAACAGGT 1175
|||||
Db 61 cagctgacctgctggtcaaggcttctatccacgacacatcccggtgagtgaggagag 120
|||||
Qy 1176 CAGCCTGACCTGCTGGTCAAGGGCTTCTATCCACGACATCCCGTGGAGTGGCAGAG 1235
|||||
Db 121 caatggcagcggagaaactacaagcagcctcccgctgctggaactccgagcgtc 180
|||||
Qy 1236 CAATGGCAGCGGAGAACTACAGACCCAGCCTCCCTGCTGGACTCCGACGGCTC 1295
|||||
Db 181 ctttctctacagcaagctaccgtggaacagcaggtngcagcaggggaacgtctt 240
|||||
Qy 1296 CTTCTCTCTACAGCAAGCTACCGTGGCAGAGCAGGTGGCAGCGGGAACGCTTT 1355
|||||
Db 241 ctcatgctcgtgatgctgagctctgcacacacactacacgacgagagcmtctccct 300
|||||
Qy 1356 CTCATGCTCGGTGATGATGAGGCTCTGCACCAACACTACAGCGAGAGCCTCTCCT 1415
|||||
Db 301 gtttccgggtaaatga 317
|||||
Qy 1416 GTCT-CCGGGTAAATCA 1431

RESULT 6
LOCUS T59711 474 bp mRNA EST 09-FEB-1995
DEFINITION ycl3h10.s1 Homo sapiens cDNA clone 80611 3' similar to gb:H87789 IG
GAMMA-1 CHAIN C REGION (HUMAN);.

ACCESSION T59711
NID g661548
KEYWORDS EST.
SOURCE human clone=80611 library=Stratagene lung (#937210)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=21ml3 Rsite1=EcoRI Rsite2=XhoI Normal lung tissue from a 72
year old male. Cloned unidirectionally. Primer: Oligo dt. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCAGAG-3'; 3' adaptor sequence:
5'-CTCGAGTGTGTTTTTTTTTTT-3'.

ORGANISM

Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 474)
AUTHORS Hillier,L., Clark,N., Duboue,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevasakis,E.,
Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE WashU-Merck EST Project
JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK

WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

High quality sequence stops: 353
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 661548
Location/Qualifiers
source 1..474
/organism="Homo sapiens"
/clone="80611"
/note="human"
BASE COUNT 74 a 125 c 145 g 117 t 13 others
ORIGIN

Query Match 21.0%; Score 300; DB 98; Length 474;
Best Local Similarity 93.7%; Pred. No. 0.00e+00;
Matches 341; Conservative 0; Mismatches 17; Indels 6; Gaps 6;

Db 110 tcattaccgggacagggagagcctctctgctntagtggtntgagagcctcatg 169
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Cp 1431 TCATTTATCCCGAGACAGGAGAGGCTCTCTGCGTGTAGTGTGTGAGAGCCTCATG 1372
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Db 170 catcagggagcatgagaagcgttccctcgtcgcacacctgctcttntccacggttagctt 229
|||||
Cp 1371 CATCAGGAGCATGAGAGAGCTTCCCTGCTGCCACCTGCTTCTCCACGGTGTAGCTT 1312
|||||
Db 230 gctntagaggaagaggagcctcgantccagcagggagcgttcttctgttagttgt 289
|||||
Cp 1311 GCTGTAGAGGACAGAGGAGCGCTCGGAGTCCAGCAGCGGAGCGGCTGCTTTGTAGTTGTT 1252
|||||
Db 290 ctccggtgcccattgctctccacctccagcgagctgctggtggatagagccttcta 349
|||||
Cp 1251 CTCGGGCTGCCCATTTGCTCTCCACCTCCACGGGATGCTGCTGGG-ATAGAAGCCTTGA 1193
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Db 350 ccagggcaggtcaggtcnaactgggtcttcttggtcagctcatcccggtatggggcaggg 409
|||||
Cp 1192 CCAGG-CAGGTCAGGCTGACCTGG-TTCTT-GGTCAAGCTCATCCGGATGGGGCAGGG 1136
|||||
Db 410 tataacctgngtctcgggggttcccttttcttcttngaaatggtttcttcttcttct 469
|||||
Cp 1135 TGTACACCTGTGTTCTCGGGGCTGCCCTTTTGGCTTT-GGAGATGCTTTTCT-CGATGGG 1078
|||||
Db 470 ggcct 473
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Cp 1077 GGCT 1074

RESULT 7
LOCUS R82945 363 bp mRNA EST 04-AUG-1995
DEFINITION ypl1g03.s1 Homo sapiens cDNA clone 187156 3' similar to gb:M87789
IG GAMMA-1 CHAIN C REGION (HUMAN);.

ACCESSION

R82945

NID

g927913

KEYWORDS

EST.

SOURCE

human clone=187156 library=Soares breast 3NBH8st vector=pt773D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=Promega -21ml3 Rsite1=Eco RI Rsite2=Eco RI Adult
human. 1st strand cDNA was primed with a Not I - oligo (dT) primer


```

Cp 1431 TCATTACCGGAGACGAGGAGGCTCTTCCGCTGAGTGGTTGCGACAGCCTCATG 1372
Db 160 catcagagcatgagaagcgtccctgtcctccacctgctcttccacggtgagctt 219
Cp 1371 CATACGAGCATGAGAGACGTTCCCTGCTGCCACCTGCTTGTCCACGGTAGCTT 1312
Db 220 gctgtagagaagaagagcgtccagctccagcatggaggtggtgttctgtagttgt 279
Cp 1311 GCTGTAGAGAAAGAGGAGCGCTCCGAGTCCAGCACGGGAGGCTGCTTGTAGTTGTT 1252
Db 280 etccggtgccattgctctcccaatccacggcgcatgtcgtggggtagaagccttna 339
Cp 1251 CTCGGCTGCCATTGCTCTCCCACTCCACGG-CGATGTCGCTGGATAGAAGCCTTGA 1193
Db 340 ccaggaggtcaggctgancgtggttcttggctcatctctcccggtattggggcagggt 399
Cp 1192 CCAGCGAGGTCAGGTCAGCTGG-TTCTGCTCAGCTCATCCCGGATCGGGCAGGCTG 1134
Db 400 taaacgctngttctcggggtgctccctngt-tttngaanaangttt-tcgtatgggntt 457
Cp 1133 TACACTGCTGCTTCGCGGGCTGCCCTTTGGCTTGGAGATGGTTTCTTCATGGGGCT 1074
Db 458 ggaag 462
Cp 1073 GCGAG 1069

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RESULT 9

LOCUS R66507 358 bp mRNA EST 30-MAY-1995
 DEFINITION Y132f05.r1 Homo sapiens cDNA clone 140961 5' similar to gb:M87789
 IG GAMMA-1 CHAIN C REGION (HUMAN);.

ACCESSION R66507

NID 9839145

KEYWORDS EST.

SOURCE human clone=140961 library=Soares placenta Nb2HP vector=PT7T3D
 (Pharmacia) with a modified polylinker host=DH10B (ampicillin
 resistant) primer=M13R1 Rsite1=Not I Rsite2=Eco RI Female placenta
 obtained at birth (full term). 1st strand cDNA was primed with a
 Not I - oligo(dT) primer [5'
 AACTGGAGATTCGGCGGCGCAGGAATTTTTTTTTTTTTTTT 3'], double-stranded
 cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
 I and cloned into the Not I and Eco RI sites of the modified pT7T3
 vector. Library went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 358)

REFERENCE

AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevisakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
 Wilson,R.

TITLE

JOURNAL

COMMENT

The WashU-Merck EST Project
 Unpublished (1995)

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 219
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.

NCBI gi: 839145

Location/Qualifiers

source

1..358

/organism="Homo sapiens"

/clone="140961"

/note="human"

BASE COUNT 90 a 109 c 92 g 63 t 4 others

ORIGIN

Query Match 19.94; Score 285; DB 64; Length 358;
 Best Local Similarity 97.8%; Pred. No. 0.00e+00;
 Matches 310; Conservative 0; Mismatches 3; Indels 4; Gaps 4;
 Db 2 acaagtgaaggtctccacaagaagcctccagcccccatcgagaaacacatctccaaag 61
 Qy 1043 ACAAGTGAAGGTCTCCAACAAGGCCCTCCAGCCCCCATCGAAAAACCATCTCCAAG 1102
 Db 62 ccaaggcgagccccgagacacacaggtgtacacctgcccccatccccggatgagctga 121
 Qy 1103 CCMAAGGCGAGCCCGGAGAACACAGAGGTGTACACCTGCCCCATCCCGGGATGAGCTGA 1162
 Db 122 ccaagaaccaggtcagctgacctgctggtcaaggcttctatccacgacatcgccg 181
 Qy 1163 CCMAAGCAGGTCAGCCTGACCTGCCTGGTCAAGGCTTCTATCCAGCCACATCGCCG 1222
 Db 182 tggagtgggagagcaatggcgagcgagagaacaactacaagcacgcctcccgctgctg 241
 Qy 1223 TGGAGTGGGAGAGCAATGGGCGGAGAACAACTACAAGCACCGCCTCCCGTCTGCTG 1282
 Db 242 gattccgagctctctctctctcttctacagcaagntacacgtgggacaagagagctgg 301
 Qy 1283 -ACTCCAGCGCTCCTCTTCTCTCT-ACAGCAAGCTCACCTGG-ACAAGAGCAGGT-GG 1338
 Db 302 cagcaggggaaacgnttt 318
 Qy 1339 CACAGGGGAACGCTCTT 1355

RESULT 10

LOCUS H28084 421 bp mRNA EST 13-JUL-1995
 DEFINITION Y156d10.s1 Homo sapiens cDNA clone 162259 3' similar to gb:M87789
 IG GAMMA-1 CHAIN C REGION (HUMAN);.

ACCESSION H28084

NID 9898437

KEYWORDS EST.

SOURCE human clone=162259 library=Soares breast 3NbBst vector=PT7T3D
 (Pharmacia) with a modified polylinker host=DH10B (ampicillin
 resistant) primer=Promega -21ml3 Rsite1=Not I Rsite2=Eco RI Adult
 human. 1st strand cDNA was primed with a Not I - oligo(dT) primer
 [5' TGTACCAATCTGAAGTGGGACGCGCCCTTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
 digested with Not I and cloned into the Not I and Eco RI sites of a
 modified pT7T3 vector (Pharmacia). Library went through one round
 of normalization to a Cot = 20. Library constructed by Bento Soares
 and M.Fatima Bonaldo.

ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

0
0
0
4

1
1
1
1
3
3

4
2
1

0
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4

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Cp 1251 CTCGGCTGCCCATTTGCTCTCCCACTCCACGGCGATGTCGCTGGGATAGAAG

Dec 17 23:14

US-08-487-550-11.rst

17

Db 317 caggcagctcagctgacctgggtttcttgctcagctcctcccggtatggggcaggggt 434
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Cp 1191 CAGGACAGGTGAGCTGAGCTGG-TCCTTGGTCACTCATCCCGGGATGGGGCAGGGT 1135

RESULT 12 T65937 436 bp mRNA EST 20-FEB-1995
LOCUS yc24f06.e1 Homo sapiens cDNA clone 81635 3' similar to gb:M87789 IG
DEFINITION GAMMA-1 CHAIN C REGION (HUMAN);
ACCESSION T65937
NID g674982
KEYWORDS EST.
SOURCE human clone=81635 library=Stratagene lung (#937210)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=21ml3 Reitel=EcRI Reite2=XhoI Normal lung tissue from a 72
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCAGAG-3'; 3' adaptor sequence:
5'-CTCGAGTTTTTTTTTTTTTTT-3'.
Homo sapiens
ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 436)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasakis, E.,
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLE WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 241
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 674982
FEATURES
source Location/Qualifiers
1..436
/organism="Homo sapiens"
/clone="81635"
/note="human"
BASE COUNT 74 a 113 c 140 g 104 t 5 others
ORIGIN
Query Match 19.2%; Score 275; DB 99; Length 436;
Best Local Similarity 94.2%; Pred. No. 0.00e+00;
Matches 310; Conservative 0; Mismatches 15; Indels 4; Gaps 4;

Db 112 tttcccgagacagggagaggtcttctgcgtagtgtgttgacaganc-teatgcatc 170
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Cp 1427 TTACCCGACAGACAGGAGAGGCTCTTCTCGCTGTAGTGGTTGTGCAGACGCTCATGCTC 1368
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Db 171 acggagcatgagaaagacttccctgctgcccactgctcttgctccacggtgagctt-ctg 229
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Cp 1367 ACGGAGCATGAGAGACGCTCCCTCTGCTGCCACCTGCTCTTGTCCACGGTGAGCTTGCTG 1308
|||||
Db 230 tagaggaagaagagagccgtcgaggtccagcagcagggagggcggtgtttagttgtctcc 289

Dec 17 23:14

US-08-487-550-11.rst

18

Cp 1307 TAGAGGAAGAAGGAGCGCTCGGAGTCCAGAGCGGAGCGGTGGTCTTGTAGTTCTTC 1248
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Db 290 ggtgcccttgcctctccacttcacggctcagctggtcgctgggatagaagc-tttnaccag 348
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Cp 1247 GGTGCCCATTTGCTCTCCACTCCAGCGGAGTGCCTGGGATAGAGGCTTTGCACAGG 1188
|||||
Db 349 naagtgaagctgactgggtctctgttgtaa-ctcatcccccggatggggcaaggtatacaac 407
|||||
Cp 1187 CAGGTCAAGCTGACTGCTGCTTCTTGGTCAGCTCATCCCGGATGGGGCAGGCTGTACACC 1128
|||||
Db 408 tgtggtctcggggcttcccttttgcctt 436
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Cp 1127 TGTGCTTCGCGGCTGCCTTTGGCTTT 1099
|||||

RESULT 13 T65912 479 bp mRNA EST 20-FEB-1995
LOCUS yclih01.r1 Homo sapiens cDNA clone 80401 5' similar to gb:M87789 IG
DEFINITION GAMMA-1 CHAIN C REGION (HUMAN);
ACCESSION T65912
NID g674957
KEYWORDS EST.
SOURCE human clone=80401 library=Stratagene lung (#937210)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=M13RPI Reitel=EcRI Reite2=XhoI Normal lung tissue from a 72
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCAGAG-3'; 3' adaptor sequence:
5'-CTCGAGTTTTTTTTTTTTTTT-3'.
Homo sapiens
ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 479)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasakis, E.,
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLE WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 273
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 674957
FEATURES
source Location/Qualifiers
1..479
/organism="Homo sapiens"
/clone="80401"
/note="human"
BASE COUNT 104 a 140 c 130 g 98 t 7 others
ORIGIN
Query Match 19.1%; Score 273; DB 99; Length 479;
Best Local Similarity 96.7%; Pred. No. 0.00e+00;

Matches 323; Conservative 0; Mismatches 3; Indels 8; Gaps 8;

Db 1 cagccccatcagagaaacaccatctcaagcaaaagcagccccagagcaacacagtggt 60
|||||
Qy 1073 CAGCCCCCATCGAGAAACCATCTCAAGCCRAAGGCGACCCCGAGACACAGGTGT 1132
|||||
Db 61 atacctgcccccatccccgggatgagctgaccaagaaccaggtcagcctgacctgctgg 120
|||||
Qy 1133 ACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACAGGTCAACCTGCTGCTGG 1192
|||||
Db 121 tcaaggcttctatccagcagcatcgctggagtgagagcaaatggcagccgagaga 180
|||||
Qy 1193 TCAAGGCTTCTATCCAGGACATCGCGCTGGAGTGGGAGCAATGGCAGCCGGAGA 1252
|||||
Db 181 acaactacaagaccagctcccgctgctggaactccgagcgtctcttctctctacagca 240
|||||
Qy 1253 ACAACTACAAGACCAGCGCTCCCGTCTGGACTCCGACGCGCTCTTCTCTACAGCA 1312
|||||
Db 241 agtcaacgtgggacaagcagctggcagcagcggggaacgtcttctctatgttcgt 300
|||||
Qy 1313 AGCTCACCTGG-ACAGACGAGTGG-CAGCAGGGGAACGTCTT-CT-CATGCT-CCGT 1367
|||||
Db 301 tgatcatgagagctcttgacacacattacacg 334
|||||
Qy 1368 -GATCATG-AGCTCT-GCACAAACCATACAGC 1398
|||||

RESULT 14
LOCUS H61373 297 bp mRNA EST 06-OCT-1995
DEFINITION yu41d01.r1 Homo sapiens cDNA clone 236353 5' similar to gb:M87789
IG GAMMA-1 CHAIN C REGION (HUMAN);
ACCESSION H61373
NID g1014205
KEYWORDS EST.
SOURCE clone=236353 primer=M13RP1 library=Soares ovary tumor NMHOT
vector=pT7T3D (Pharmacia) with a modified polyLinker host=DH10B
(ampicillin resistant) Reitel=Not I Reite2=Eco RI female. 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGCGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified pT73 vector (Pharmacia). Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 297)

REFERENCE
AUTHORS Hillier,L., Clark,N., Duboue,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
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Fax: 314 286 1810
Email: est@watson.wustl.edu

High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality.

NCBI gi: 1014205 Location/Qualifiers
1..297
/organism="Homo sapiens"
/clone="236353"
<1..>297
BASE COUNT 81 a 92 c 75 g 41 t 8 others
ORIGIN
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Best Local Similarity 94.3%; Pred. No. 0.00e+00;
Matches 280; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Db 1 cagactngcgaatggcaaggagmacaagtgcgaagctctccaaagagccctccagcc 60
|||||
Qy 1018 CAGGACTGGCTGAATGGCAAGAGTACAAAGTGAAGTCTCCAACAAAGCCCTCCAGCC 1077
|||||
Db 61 cagatcgagaaacaccatctcaagccaaagggcagcccccagagcaacacaggtgtacac 120
|||||
Qy 1078 CCATCGAGAAACCATCTCAAAAGCCAAAGGGCAGCCCGGAGACACACAGGTGTACACC 1137
|||||
Db 121 ctgccccatccccggagagatgacccaagaccaggtcagcctgacctgctgtctcaaa 180
|||||
Qy 1138 CTGCCCCCATCCCGGATGAGCTGACCAAGAACAGGTCAACCTGCTGCTGTGAAA 1197
|||||
Db 181 ggcttctatccccagcacatcgctggagtgagagcaaatggcagccgagancanc 240
|||||
Qy 1198 GGTTCTATCCAGGACATCGCGCTGGAGTGGGAGCAATGGCAGCGGAGAACAC 1257
|||||
Db 241 tacaagaccagcttcctgctggactnecagcgtctcttattctatagcaag 297
|||||
Qy 1258 TACAAGACACCGCTCCGCTGCTGGACTCCGACGCGCTCTTCTTCTCTACAGCAAG 1314
|||||
RESULT 15
LOCUS T59950 418 bp mRNA EST 09-FEB-1995
DEFINITION y01907.s1 Homo sapiens cDNA clone 79452 3' similar to gb:M87789 IG
GAMMA-1 CHAIN C REGION (HUMAN);
ACCESSION T59950
NID g661787
KEYWORDS EST.
SOURCE human clone=79452 library=Stratagene lung (#937210)
vector=pBluescript SK- host-SOLR cells (kanamycin resistant)
primer=-21m13 Reitel=EcoRI Reite2=XhoI Normal lung tissue from a 72
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCAGCAG-3'; 3' adaptor sequence:
5'-CTCGAGTTTTTTTTTTTTTTT-3'.
ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 418)
REFERENCE
AUTHORS Hillier,L., Clark,N., Duboue,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaakis,E.,
Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
WashU-Merck EST Project

JOURNAL
COMMENT

Unpublished (1995)

Contact: Wilson RK
WashU-Merck EST Project
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 339
Source: IMAGE Consortium, L1NL
This clone is available royalty-free through L1NL ; contact the
IMAGE Consortium (info@image.l1nl.gov) for further information.

NCBI gi: 661787

FEATURES
source
Location/Qualifiers
1..418
/organism="Homo sapiens"
/clone="79452"
/note="human"

BASE COUNT 70 a 110 c 136 g 93 t 9 others
ORIGIN

Query Match 18.4%; Score 264; DB 98; Length 418;
Best Local Similarity 96.5%; Pred. No. 0.00e+00;
Matches 277; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

Db 132 tcattaccggagagacaggagaggtcttctgtgttagtggttntcgagagcctcatg 191
|||||
Cp 1431 TCATTACC GGAGACAGGAGAGGCTCTTCGCTGTAGTGGTGTGCAGAGCCTCATG 1372
Db 192 catcacggagcatgagaagcgttccctgctgccacctgctcttntccacggtgagctt 251
|||||
Cp 1371 CATCAGGAGCATGAGAGAGCTTCCCTGCTGCCACCTGCTCTTCCAGGCTGAGCTT 1312
Db 252 gctntagagaagaaggagcgtcggagtcagacacggaggcgtggtctttagtggtt 311
|||||
Cp 1311 GCTGTAGAGAGAGAGAGGCGCTCGGAGTCCACACGGGAGGCGTGGTCTTGTAGTGT 1252
Db 312 ctccggctgccattgctctccactccacggcgatntcgctgggtagagaagccttgac 371
|||||
Cp 1251 CTCGGCTGCCATTGCTCTCCACTCCACGGCGATGTCGCTGGGATAGAGCCTTTCAC 1192
Db 372 caggcaggtcaggtgacctgggttcttggggtcandtcacccnnga 418
|||||
Cp 1191 CAGCAGGTCAGGCTGACCTGG-TTCTTGG-TCAGTCTATCCCGGA 1147

Search completed: Tue Dec 17 23:28:56 1996
Job time : 522 secs.

WAVES

(TM)

Release 2.1D John F. Collins, BioComputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 15:14:01 1996; MacPar time 8.84 Seconds

Tabular output not generated. 673.276 Million cell updates/sec

Title: >US-08-487-550-2

Description: (1-234) from US08487550.pep

Perfect Score: 1648

Sequence: 1 MRVPAQLLGLLLMLPGARC.....CQVTHEGSTVEKTVAPTECS 234

Scoring table: PAM 150

Gap 11

Searched: 82130 seqs, 25426960 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: pir47

1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc
14:unrev

Statistics: Mean 43.750; Variance 147.933; scale 0.296

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description	Pred. No.
1	1324	80.3	233	11	S25747 Ig lambda chain - hu	1.64e-143
2	1319	80.0	232	11	S25756 Ig lambda chain - hu	6.88e-143
3	1271	77.1	231	11	S25738 Ig lambda chain - hu	6.47e-137
4	1243	75.4	231	11	S25751 Ig lambda chain - hu	1.96e-133
5	1242	75.4	231	11	S25753 Ig lambda chain - hu	2.61e-133
6	1233	74.8	233	11	S25748 Ig lambda chain - hu	3.43e-132
7	1226	74.4	226	11	S25745 Ig lambda chain - hu	2.54e-131
8	1212	73.5	235	5	S05270 Ig lambda chain prec	1.39e-129
9	1210	73.4	232	11	S25742 Ig lambda chain - hu	2.46e-129
10	1206	73.2	233	11	S25741 Ig lambda chain - hu	7.73e-129
11	1158	70.3	233	11	S25752 Ig lambda chain - hu	6.97e-123
12	1155	70.1	235	11	S25750 Ig lambda chain - hu	1.64e-122

13	1149	69.7	235	11	S25759 Ig lambda chain - hu	9.10e-122
14	1147	69.6	235	5	S14675 Ig lambda chain - hu	1.61e-121
15	1143	69.4	234	11	S25757 Ig lambda chain - hu	5.04e-121
16	1140	69.2	215	14	S29258 Ig lambda chain V re	1.19e-120
17	1140	69.2	233	11	S25744 Ig lambda chain - hu	1.19e-120
18	1137	69.0	235	11	S25754 Ig lambda chain - hu	2.79e-120
19	1135	68.9	216	5	A42193 Ig lambda chain (BJP	4.94e-120
20	1132	68.7	213	11	S21066 Ig lambda chain V re	1.16e-119
21	1127	68.4	216	5	S03401 Ig lambda chain (Kol	4.84e-119
22	1128	68.4	235	11	S25758 Ig lambda chain - hu	3.64e-119
23	1123	68.1	236	11	S25746 Ig lambda chain - hu	1.51e-118
24	1102	66.9	190	11	S25740 Ig lambda chain - hu	6.02e-116
25	1071	65.0	235	11	S25749 Ig lambda chain - hu	4.11e-112
26	1026	62.3	243	11	S25755 Ig lambda chain - hu	1.49e-106
27	985	59.8	208	5	B49444 Ig lambda chain (New	1.69e-101
28	904	54.9	181	5	P70220 Ig lambda chain V-C	1.54e-91
29	877	53.2	230	5	S49449 Ig lambda chain - du	3.16e-88
30	863	52.4	232	12	S17399 Ig lambda chain prec	1.64e-86
31	856	51.9	213	5	A21177 Ig light chain precu	1.18e-85
32	782	47.5	118	11	S12441 Ig lambda chain (Ke-	1.29e-76
33	777	47.1	118	11	S12442 Ig lambda chain (Ke-	5.22e-76
34	768	46.6	234	5	A39956 Ig lambda chain prec	6.51e-75
35	766	46.5	118	11	S12440 Ig lambda chain (MCG	1.14e-74
36	763	46.3	118	5	A39949 Ig lambda chain J-C	2.64e-74
37	757	45.9	118	11	S12443 Ig lambda chain (Ke+	1.42e-73
38	742	45.0	146	5	S02083 Ig lambda chain V-IV	9.45e-72
39	742	45.0	229	12	A20969 Ig kappa chain precu	9.45e-72
40	706	42.8	105	2	L2HU Ig lambda chain C re	2.20e-67
41	700	42.5	119	5	S03464 Ig lambda chain J-C	1.17e-66
42	700	42.5	213	5	A33911 Ig lambda chain-rela	1.17e-66
43	699	42.4	120	5	S30527 Ig lambda chain V re	1.55e-66
44	694	42.1	151	11	S25739 Ig lambda chain - hu	6.25e-66
45	677	41.1	234	12	S01320 Ig kappa chain precu	7.10e-64

ALIGNMENTS

RESULT	1
ENTRY	S25747 #type complete
TITLE	Ig lambda chain - human
ORGANISM	#formal name Homo sapiens #common name man
DATE	22-Nov-1993 #sequence_revision 26-May-1995 #text_change 26-May-1995
ACCESSIONS	S25747
REFERENCE	S16439
#authors	Combratio, G.; Klobbeck, H.G.
#journal	Eur. J. Immunol. (1991) 21:1513-1522
#title	V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.
#cross-references	MUID:91257162
#accession	S25747
#status	preliminary
#molecule	type mRNA
#residues	1-233 #label COM
#cross-references	EMBL:X57812
#note	translation of nucleotide sequence is not given
SUMMARY	#length 233 #molecular-weight 24589 #checksum 3304
Query Match	80.3%; Score 1324; DB 11; Length 233;
Best Local Similarity	85.1%; Pred. No. 1.64e-143;
Matches	194; Conservative 14; Mismatches 19; Indels 1; Gaps 1;
Db	7 llglsh-ctgsvtasyiltppsvavagpkkaaritcginiaskavhwgqkpgqapvlv 65

Dec 17 15:00

US-08-487-550-2.mpr

3

Qy 7 LLGILLWLPGARCAYELTQPPSVSPQGTARITCGGNSRNEYVHWYQKPARAPILV 66
Db 66 vyddsrpsigperifegsnsgntatliarveagdeadyycqvwdssdhvfgggtkl 125
Qy 67 IYDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQWDRASDPVFGGTRVT 126
Db 126 vlgqkaapsvtlfpssseelqankatlvcilisdffpgavtvaakdsapvkagvett 185
Qy 127 VLQGPKAAPSVTLFPSSSEELQANKATLVCLISDFYPCAVTVAMKADSSPVKAGVETTP 186
Db 186 skqnnkyaasyiltpcqwkshrsycqvthegstvektvaptces 233
Qy 187 SKQNNKYAASSYLSLTPQWKSHRSYSCQVTHGSTEKTVAPTCECS 234

RESULT 2
ENTRY S25756 #type complete
TITLE Ig lambda chain - human
ORGANISM #formal name Homo sapiens #common name man
DATE 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 26-May-1995
ACCESSIONS S25756
REFERENCE S16439
#authors Combratio, G.; Klobeck, H.G.
#journal Eur. J. Immunol. (1991) 21:1513-1522
#title V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.
#cross-references MUID:91257162
#accession S25756 preliminary
#molecule_type mRNA
#residues 1-232 ##label COM
#cross-references EMBL:X57821
#note translation of nucleotide sequence is not given
SUMMARY #length 232 #molecular-weight 24489 #checksum 4042

Query Match 80.0%; Score 1319; DB 11; Length 232;
Best Local Similarity 86.0%; Pred. No. 6.88e-143;
Matches 196; Conservative 14; Mismatches 16; Indels 2; Gaps 2;
Db 7 llglsh-ctgsvtlylcpqsvsypqgtasitcggnnigskavhwgqkpgapvlv 65
Qy 7 LLGILLWLPGARCAYELTQPPSVSPQGTARITCGGNSRNEYVHWYQKPARAPILV 66
Db 66 vyddsrpsigperifegsnsgntatliarveagdeadyycqvwdssdhvfgggtkl 124
Qy 67 IYDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQWDRASDPVFGGTRVT 126
Db 125 vlgqkaapsvtlfpssseelqankatlvcilisdffpgavtvaakdsapvkagvett 184
Qy 127 VLQGPKAAPSVTLFPSSSEELQANKATLVCLISDFYPCAVTVAMKADSSPVKAGVETTP 186
Db 185 skqnnkyaasyiltpcqwkshrsycqvthegstvektvaptces 232
Qy 187 SKQNNKYAASSYLSLTPQWKSHRSYSCQVTHGSTEKTVAPTCECS 234

RESULT 3
ENTRY S25738 #type complete
TITLE Ig lambda chain - human
ORGANISM #formal name Homo sapiens #common name man
DATE 22-Nov-1993 #sequence_revision 26-May-1995 #text_change

Dec 17 15:00

US-08-487-550-2.mpr

4

ACCESSIONS S25738
REFERENCE S16439
#authors Combratio, G.; Klobeck, H.G.
#journal Eur. J. Immunol. (1991) 21:1513-1522
#title V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.
#cross-references MUID:91257162
#accession S25738 preliminary
#status preliminary
#molecule_type mRNA
#residues 1-231 ##label COM
#cross-references EMBL:X57802
#note translation of nucleotide sequence is not given
SUMMARY #length 231 #molecular-weight 24473 #checksum 2186

Query Match 77.1%; Score 1271; DB 11; Length 231;
Best Local Similarity 81.1%; Pred. No. 6.47e-137;
Matches 189; Conservative 21; Mismatches 19; Indels 4; Gaps 4;
Db 3 wipl-flgyla-yctgvasyeltqpsvsyapgtasitcgdtlqdkyacwyqkpg 60
Qy 2 RVPAAQLGLLLWLPGARCAYELTQPPSVSPQGTARITCGGNSRNEYVHWYQKPAR 61
Db 61 spvlvifqdkrpsigperifegsnsgntatliarveagdeadyycqwdssdhvfgg 118
Qy 62 APILVYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQWDRASDPVFG 121
Db 119 gktitvlgqkaapsvtlfpssseelqankatlvcilisdffpgavtvaakdsapvkagv 178
Qy 122 GTRTVLQGPKAAPSVTLFPSSSEELQANKATLVCLISDFYPCAVTVAMKADSSPVKAGV 181
Db 179 ettcpkqnnkyaasyiltpcqwkshrsycqvthegstvektvaptces 231
Qy 182 ETTTPSKQNNKYAASSYLSLTPQWKSHRSYSCQVTHGSTEKTVAPTCECS 234

RESULT 4
ENTRY S25751 #type complete
TITLE Ig lambda chain - human
ORGANISM #formal name Homo sapiens #common name man
DATE 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 26-May-1995
ACCESSIONS S25751
REFERENCE S16439
#authors Combratio, G.; Klobeck, H.G.
#journal Eur. J. Immunol. (1991) 21:1513-1522
#title V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.
#cross-references MUID:91257162
#accession S25751 preliminary
#status preliminary
#molecule_type mRNA
#residues 1-231 ##label COM
#cross-references EMBL:X57816
#note translation of nucleotide sequence is not given
SUMMARY #length 231 #molecular-weight 24583 #checksum 4106

Query Match 75.4%; Score 1243; DB 11; Length 231;
Best Local Similarity 79.8%; Pred. No. 1.96e-133;
Matches 186; Conservative 20; Mismatches 23; Indels 4; Gaps 4;


```

Db      3 wipL-flgVla-yctGsvasyeltppsvvspqktasltscgdkgldgykaewyqqkagq 60
       :::|||:| | : ::||||| ||||| |||||:| | |||||:| | |||||:|
Qy     2 RYPAQLGLLLWLPARCAVELTQPSPVSYPQTARITCCGDNSSENYHHWYQQKPAR 61
       :|||:| | : ::||||| ||||| |||||:| | |||||:| | |||||:|
Db     61 spvlviyrhkrpsgiptfagsngntatlitlsqtqvmdaeyycqawd-ssi-vvfqg 118
       :|||:| | : ::||||| ||||| |||||:| | |||||:| | |||||:|
Qy     62 APILVIYDDSRSGIPERSGSKSNTATLTINGVEAGDEADYYCQWDRASDHPVFVG 121
       :|||:| | : ::||||| ||||| |||||:| | |||||:| | |||||:|
Db    119 gtkltivlgqpkaapsvtlfpssseelqankatlvcrlsidfypgavtvawkadsepvkagv 178
       :|||:| | : ::||||| ||||| |||||:| | |||||:| | |||||:|
Qy    122 GTRVTVLQGPPRAAPSVTLFPSSSEELQANKATLVCLISDFTPGAVTVAWKAUSSPVRKGV 181
       :|||:| | : ::||||| ||||| |||||:| | |||||:| | |||||:|
Db    179 ettptsksnknyaaassylsltpgwksghrsgcqvthegstvektvaptccs 231
       :|||:| | : ::||||| ||||| |||||:| | |||||:| | |||||:|
Qy    182 ETTPTSKSNKNYAASSYLSTLTPQMKSHRSYSCQVTHEGSTVEKTVPAPTCS 234
       :|||:| | : ::||||| ||||| |||||:| | |||||:| | |||||:|

RESULT          5
ENTRY           Ig lambda chain - human
TITLE           #formal_name Homo sapiens #common_name man
ORGANISM        22-Nov-1993 #sequence_revision 26-May-1995 #text_change
DATE            26-May-1995

ACCESSIONS      S25753
REFERENCE        S16439
#authors         Combiato, G.; Klobect, H.G.
#journal         Eur. J. Immunol. (1991) 21:1513-1522
#title           V(lambda) and J(lambda)-C(lambda) gene segments of the human
                 immunoglobulin lambda light chain locus are separated by 14
                 kb and rearrange by a deletion mechanism.
#cross-references MUID:91257162
#accession       S25753
#status          preliminary
#molecule_type  mRNA
#residues        1-231 #label COM
#cross-references EMBL:X57818
#note            translation of nucleotide sequence is not given
SUMMARY          #length 231 #molecular-weight 24724 #checksum 4484

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Query Match	75.4%;	Score 1242;	DB 11;	Length 231;
Best Local Similarity	79.4%;	Pred. No. 2.61e-133;		
Matches	185;	Conservative	24;	Mismatches 20; Indels 4; Gaps 3;
Db	3	wipl-flglvia-yctgsvasyelctppsvspgqtsaitctfgdklqgkyswyqkpgq	60	
Qy	2	RVPQALLGLLLMLPGARCAYELTQPPSVSVSPGQTARITCGGDNRSNEYVHHYQOKPAR	61	
Db	61	spllvlyqdnrpsq;perfgasngntatitsetqamdegdyycqawd--entvwfvg	118	
Qy	62	APILVYDDSDPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQWDRASDHPVEFG	121	
Db	119	gtkltvlseqkaapsvtlfpssseelqankatlvcllisdfyqgavtvaawkadspvkav	178	
Qy	122	GTRVTVLQCPKMAPSVTLFPSPSEELQANKATLVCLLISDFYCAVTVAWKADSSPKACV	181	
Db	179	etttpkgennkyaasyllaitpeqkshrsyrcqvtghegstvektvaptecs	231	
Qy	182	ETTTTSPKSNKNKYAASSYLSLTPTBQMKSRSYSCQVTHEGSTVEKTVAPTETCS	234	
RESULT	6			
ENTRY		\$25748	#type complete	
TITLE		lg lambda chain - human		
ORGANISM		#formal name Homo sapiens	#common name man	

DATE	22-Nov-1993	sequence_revision	26-May-1995	text_change			
ACCESSIONS	S25748						
REFERENCE	S16439						
#authors	Combiato, G.; Klobeck, H.G.						
#journal	Eur. J. Immunol. (1991) 21:1513-1522						
#title	V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.						
#cross-references	MUID:91257162						
#accession	S25748						
#status	preliminary						
#molecule_type	mRNA						
#residues	1-233	#label	COM				
#cross-references	EMBL:X57813						
#note	translation of nucleotide sequence is not given						
SUMMARY		#length	233	#molecular-weight	24816	#checksum	1501
Query Match	74.8%;	Score	1233;	DB 11;	Length	233;	
Best Local Similarity	78.4%;	Pred. No.	3.43e-132;				
Matches	178;	Conservative	24;	Mismatches	24;	Indels	1; Gaps 1;
Db	8	ltltlcl-gsvsseltqpavsalqvtvrcogdsrlrayaawghkpgapilvi	66				
QY	8	LGLLMLPFGARCAVELTQPPVSPVSPQOTARITCGGDSRNEYVHWYQQKPARADPILVI	67				
Db	67	ygenrrpegiidr-fagesagntasfaigtgaqaadeadycncrdesgdvifgggktltv	126				
QY	68	YDDSRPSGPIPERFSGKSGNTATLTINGVEAGDEADYYCQWDRASDPHPVFGGTRVTV	127				
Db	127	lgpkkaapvtlfpssseelqankatlvcilisdifypgavtvawkadspvkvagvettcps	186				
QY	128	LGQPKAAPSVTLFPPSPSEELQANKATLVCLISDFYPGAVTVAMKADSPVKAGVETTPS	187				
Db	187	kqmkmyaasyisltpqkwkshrsyrcqvtthegstektvtaptes	233				
QY	188	KQSNKYYAASYSILTPQWKSHRSYSCQVTHGSTEKTVAPTECS	234				
RESULT	7						
ENTRY	S25745	#type	fragment				
TITLE	Ig lambda chain - human (fragment)						
ORGANISM	#formal_name	Homo sapiens	#common_name	man			
DATE	22-Nov-1993	sequence_revision	26-May-1995	text_change			
ACCESSIONS	S25745						
REFERENCE	S16439						
#authors	Combiato, G.; Klobeck, H.G.						
#journal	Eur. J. Immunol. (1991) 21:1513-1522						
#title	V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.						
#cross-references	MUID:91257162						
#accession	S25745						
#status	preliminary						
#molecule_type	mRNA						
#residues	1-226	#label	COM				
#cross-references	EMBL:X57810						
#note	translation of nucleotide sequence is not given						
SUMMARY		#length	226	#checksum	3564		

Query Match 74.4%; Score 1226; DB 11; Length 226;
Best Local Similarity 81.8%; Pred. No. 2.54e-131;
Matches 175; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

##accession S25741
##status preliminary
##molecule_type mRNA
##residues 1-233 ##label COM
##cross-references EMBL:X57805
##note translation of nucleotide sequence is not given
##length 233 #molecular-weight 24977 #checksum 4094

SUMMARY
Query Match 73.2%; Score 1206; DB 11; Length 233;
Best Local Similarity 78.0%; Pred. No. 7.73e-129;
Matches 177; Conservative 19; Mismatches 30; Indels 1; Gaps 1;

Db 8 ltlitlcl-gswaseltqptvvalgqtlrlikcqdgtireyvaswyqkqgqptlli 66
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 8 LCLLLLLWLPGARCAYELTQPPSVSPGQTARITCGGDSNRNEYVHYQKPARAPILVI 67
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 67 ngkdnrpsgidrfsagtsqntaaltitgtqaeadeadycnrsdsahhlvfggktlv 126
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 68 YDDSDRPSGIPERFSGKSGNTATLTINGVEAGDEADYTCQWDRASDHPVFCGTRTV 127
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 127 lsgpkapavrlfpssseelqankatlvcldfygavutvawkadspvkagvettps 186
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 128 LQPKKAAPSVTLFPPSSEELQANKATLVCLISDFYPAVTVAMKADSPVKAGVETTPS 187
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 187 kqsnkyaassylsltpsqkshrsycqvthegstvektvaptacs 233
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 188 KQSNKYYAASSYLSLTPSQKSHRSYSCQVTHGSTEKTVAPTACS 234
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 11
ENTRY S25752 #type complete
TITLE Ig lambda chain - human
ORGANISM #formal name Homo sapiens #common name man
DATE 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 26-May-1995
ACCESSIONS S25752
REFERENCE S16439
#authors Combratio, G.; Klobeck, H.G.
#journal Eur. J. Immunol. (1991) 21:1513-1522
#title V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.
#cross-references MUID:91257162
#accession S25752 #status preliminary
##molecule_type mRNA
##residues 1-233 ##label COM
##cross-references EMBL:X57817
##note translation of nucleotide sequence is not given
##length 233 #molecular-weight 24516 #checksum 3842

SUMMARY
Query Match 70.3%; Score 1158; DB 11; Length 233;
Best Local Similarity 74.3%; Pred. No. 6.97e-123;
Matches 171; Conservative 28; Mismatches 29; Indels 2; Gaps 1;

Db 4 llllthcagawqsvltqpsaagtpgrrvtlscsgssnigtndvwyqqlgtapk 63
| | | | | : : : : : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 7 LGLLLLLWLPGARCAYELTQPPSVSPGQTARITCGGDSNR-NEYVHYQKPARAPI 64
| | | | | : : : : : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 64 lliyrnnpqgvdprfsgskgtsaalaiglgdeadeadycaawddslngrvfggk 123
| | | | | : : : : : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 65 LVYDSDRPSGIPERFSGKSGNTATLTINGVEAGDEADYTCQWDRASDHPVFGGTR 124
| | | | | : : : : : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 124 ltlvggpkapavrlfpssseelqankatlvcldfygavutvawkadspvkagvett 183
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

Qy 125 VTVLGQPKAAPSVTLPFPSSSEELQANKATLVCLISDFYPAVTVAMKADSPVKAGVETT 184
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 184 tpskqsnkyaassylsltpsqkshrsycqvthegstvektvaptacs 233
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 185 TFSKQSNKYYAASSYLSLTPSQKSHRSYSCQVTHGSTEKTVAPTACS 234
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 12
ENTRY S25750 #type complete
TITLE Ig lambda chain - human
ORGANISM #formal name Homo sapiens #common name man
DATE 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 26-May-1995
ACCESSIONS S25750
REFERENCE S16439
#authors Combratio, G.; Klobeck, H.G.
#journal Eur. J. Immunol. (1991) 21:1513-1522
#title V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.
#cross-references MUID:91257162
#accession S25750 #status preliminary
##molecule_type mRNA
##residues 1-235 ##label COM
##cross-references EMBL:X57815
##note translation of nucleotide sequence is not given
##length 235 #molecular-weight 24710 #checksum 4829

SUMMARY
Query Match 70.1%; Score 1155; DB 11; Length 235;
Best Local Similarity 74.3%; Pred. No. 1.64e-122;
Matches 171; Conservative 25; Mismatches 32; Indels 2; Gaps 2;

Db 6 llllthcagawqsvltqpsaagtpgrrvtlscsgssnigtndvwyqqlgtapk 65
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 7 LGLLLLLWLPGARCAYELTQPPSVSPGQTARITCGGDSNR-NEY-VHYQKPARAPI 64
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 66 lliyrnnpqgvdprfsgskgtsaalaiglgdeadeadycaawddslngrvfggk 125
| | | | | : : : : : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 65 LVYDSDRPSGIPERFSGKSGNTATLTINGVEAGDEADYTCQWDRASDHPVFGGTR 124
| | | | | : : : : : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 126 ltlvggpkapavrlfpssseelqankatlvcldfygavutvawkadspvkagvett 185
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 125 VTVLGQPKAAPSVTLPFPSSSEELQANKATLVCLISDFYPAVTVAMKADSPVKAGVETT 184
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 186 tpskqsnkyaassylsltpsqkshrsycqvthegstvektvaptacs 235
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 185 TFSKQSNKYYAASSYLSLTPSQKSHRSYSCQVTHGSTEKTVAPTACS 234
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 13
ENTRY S25759 #type complete
TITLE Ig lambda chain - human
ORGANISM #formal name Homo sapiens #common name man
DATE 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 26-May-1995
ACCESSIONS S25759
REFERENCE S16439
#authors Combratio, G.; Klobeck, H.G.
#journal Eur. J. Immunol. (1991) 21:1513-1522
#title V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.

RP, SEQUENCE (BENCE-JONES PROTEIN KERN).

RX MEDLINE; 71150336.

RA PONTING H., HESS M., HILSCHMANN N.;

RL HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 352:247-266(1971).

RN [5]

RP PARTIAL SEQUENCE (MYELOMA PROTEIN NEMM).

RX MEDLINE; 74109253.

RA CHEN B.L., POLJAK R.J.;

RL BIOCHEMISTRY 13:1295-1302(1974).

RN [6]

RP SEQUENCE (DOT).

RX MEDLINE; 95255298.

RA STOPPINI M., BELLOTTI V., NEGRI A., MERLINI G., CARVER F., FERRI G.;

RL EUR. J. BIOCHEM. 228:886-893(1995).

RN [7]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEMM.

RX MEDLINE; 75046825.

RA POLJAK R.J., AMZEL L.M., AVEY H.P., CHEN B.L., PHIZACKERLEY R.P.,

RL SAUL F.;

RN PROC. NATL. ACAD. SCI. U.S.A. 71:3440-3444(1974).

RN [8]

RP PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).

RX MEDLINE; 75013804.

RA FETT J.W., DEUTSCH H.F.;

RL BIOCHEMISTRY 13:4102-4114(1974).

RN [9]

RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.

RA EDMUNDSON A.B., ELY K.R., ABOILA E.E., SCHIFFER M.,

RL PANAGIOTOPOULOS N.;

RN BIOCHEMISTRY 14:3953-3961(1975).

RN [10]

RP X-RAY CRYSTALLOGRAPHY OF MCG.

RX MEDLINE; 90133913.

RA ELY K.R., HERRON J.N., HARKER M., EDMUNDSON A.B.;

RL J. MOL. BIOL. 210:601-615(1989).

RN [11]

RP SEQUENCE FROM N.A.

RX MEDLINE; 82080680.

RA HIETER P.A., HOLLIS G.F., KORSMEYER S.J., WALDMANN T.A., LEDER P.;

RL NATURE 294:536-540(1981).

CC -!- THE SEQUENCE SHOWN IS THE KERN-/OZ-/MCG- CHAIN FOUND IN PROTEINS

CC SH, X, AND NIG-64. THE KERN PROTEIN HAS THE KERN+ MARKER, THE NEM

CC PROTEIN HAS THE OZ+ MARKER, THE MCG PROTEIN HAS THE KERN+ MARKER

CC AND THE MCG+ MARKER.

CC -!- SIX TANDEM LAMBDA-TYPE GENES WERE IDENTIFIED & THE 3 MOST 5' WERE

CC SEQUENCED. THESE CORRESPOND TO THE MCG SEQUENCE (LAMBDA-1), THE

CC KERN-/OZ- SEQUENCE (LAMBDA-2) & THE KERN-/OZ+ SEQUENCE (LAMBDA-3

CC PIR; A02125, L2HU.

DR PDB; 2MCG; 15-JUL-92.

DR PDB; 7FAB; 31-JAN-94.

DR MIN; 147220; 11TH EDITION.

DR PROSITE; PS00290; 1G.MHC.

KW IMMUNOGLOBULIN C REGION; 3D-STRUCTURE.

FT NON TER 1 1

FT DISULFID 27 86

FT DISULFID 104 104

FT VARIANT 5 5

FT VARIANT 7 7

FT VARIANT 45 45

FT VARIANT 56 56

FT VARIANT 82 82

FT STRAND 4 4

FT STRAND 7 11

FT HELIX 15 19

INTERCHAIN (WITH HEAVY CHAIN).

A -> N (IN MCG+ MARKER).

S -> T (IN MCG+ MARKER).

S -> G (IN KERN+ MARKER).

T -> K (IN MCG+ MARKER).

R -> K (IN OZ+ MARKER).

FT	TURN	20	21	
FT	STRAND	23	33	
FT	STRAND	38	43	
FT	TURN	44	45	
FT	STRAND	46	48	
FT	TURN	50	51	
FT	STRAND	52	54	
FT	STRAND	58	59	
FT	TURN	61	62	
FT	STRAND	65	73	
FT	HELIX	75	79	
FT	TURN	80	80	
FT	STRAND	84	90	
FT	TURN	91	92	
FT	STRAND	93	99	
SEQ	SEQUENCE	105 AA; 11236 MW; 67031 CN;		

Query Match 42.8%; Score 706; DB 5; Length 105;
Best Local Similarity 100.0%; Pred.No.1.68e-135;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qpkapsvtlfpssseelqankatlvcilisdffpgavtwkadesovkagvettppskq 60
130 QPKAAPSVTLFPSSSEELQANKATLVCILISDFPGAVTWAKADSSPKAGVETTPSKQ 189

Db 61 snkkaasyllstpqckshrsyscqvtchegstvektvaptces 105
130 SNKKAASYSLLSTPQCKSHRSYSQVTHGSTEKTVAPTCECS 234

RESULT 2
ID I141 HUMAN STANDARD; PRT; 213 AA.
AC P15814;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT 01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)
DE IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
[1]
RN RN
RP SEQUENCE FROM N.A.
RX MEDLINE; 89315835.
RA HOLLIS G.F., EVANS R.J., STAFFORD-HOLLIS J.M., KORSMEYER S.J.,
RA MCKEARN J.P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 86:5552-5556(1989).
CC -!- TISSUE SPECIFICITY: EXPRESSED ONLY IN PRE-B-CELLS AND A SPECIAL
CC B-CELL LINE (WHICH IS SURFACE IG NEGATIVE).
CC -!- THIS LAMBDA LIGHT-CHAIN-RELATED PROTEIN MAY BE THE IMMUN-
CC GLOBULIN OMEGA LIGHT-CHAIN.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY
CC AND SHOWS SIMILARITY TO LAMBDA LIGHT CHAIN IN C-TERMINAL HALF
CC (J AND C REGIONS).
CC EMBL; M27749; M27749.
DR PIR; A33911; A33911.
DR HSP; P01842; 8FAB.
DR PROSITE; PS00290; IG MHC.
KW IMMUNOGLOBULIN FOLD; B-CELL; SIGNAL.
FT SIGNAL 1 ?
FT CHAIN ? 213 IMMUNOGLOBULIN-RELATED 14.1 PROTEIN.
FT DOMAIN 97 108 J REGION (BY SIMILARITY TO LAMBDA
FT LIGHT-CHAIN).
FT DOMAIN 109 213 C REGION (BY SIMILARITY TO LAMBDA
FT LIGHT-CHAIN).

ID LAC1 MOUSE STANDARD; PRT; 105 AA.
AC P01843;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-APR-1988 (REL. 07, LAST ANNOTATION UPDATE)
DE IG LAMBDA-1 CHAIN C REGION.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83014953.
RA SELING E., MILLER J., WILSON R., STORB U.;
RL PROC. NATL. ACAD. SCI. U.S.A. 79:4681-4685(1982).
RN [2]
RP SEQUENCE FROM N.A. (MOPC 315).
RX MEDLINE; 81148806.
RA BOTHWELL A.L.M., PASKIND M., SCHWARTZ R.C., SONENSHAIN G.E.,
RA GEFTER M.L., BALTIMORE D.;
RL NATURE 290:65-67(1981).
RN [3]
RP SEQUENCE FROM N.A. (S43).
RX MEDLINE; 82220143.
RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJENSKY K.,
RA BALTIMORE D.;
RL NATURE 298:380-382(1982).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).
RX MEDLINE; 71107854.
RA APPELLA E.;
RL PROC. NATL. ACAD. SCI. U.S.A. 68:590-594(1971).
CC -!- THE MOPC 315 CELL LINE PRODUCES 2 LIGHT CHAINS, 1 NORMAL LAMBDA-2
CHAIN & 1 ABNORMAL LAMBDA-1 CHAIN THAT IS MISSING A LARGE PART OF
THE V REGION. THE C REGION SEQUENCE (SHOWN HERE) APPEARS COMPLETE-
ELY NORMAL.
DR PIR; A02126; LIMS.
DR HSP; P01842; LMF.
DR PROSITE; PS00290; IG.MHC.
RW IMMUNOGLOBULIN C REGION.
FT NON TER 1 1
FT DISULFID 27 86
FT DISULFID 104 104
FT CONFLICT 19 20
ET -> TE (IN REF. 4).
FT CONFLICT 56 56
Q -> E (IN REF. 4).
FT CONFLICT 75 75
MISSING (IN REF. 4).
FT CONFLICT 81 82
HS -> SH (IN REF. 4).
FT CONFLICT 85 85
S -> SS (IN REF. 4).
FT CONFLICT 96 96
E -> Q (IN REF. 4).
SQ SEQUENCE 105 AA; 11575 MW; 63813 CN;

Query Match 33.8%; Score 557; DB 5; Length 105;
Best Local Similarity 71.4%; Pred. No. 3.57e-100;
Matches 75; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

Db 1 gpkaspsvltfpssseelknkativctidfygsvvtdkvdgtpvtggtmtpqsk 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 130 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYGVAVTAVKRAUSSPVKAGVETTPSKQ 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 ennkymassytltkarwerhesycqytheghtveksleradcs 105
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 190 SNKYAASSYLSLTPEQWKSHRSYSCQVTHGEGSTVKTVAPECS 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7

ID LAC2 RAT STANDARD; PRT; 104 AA.
AC P20767;
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE IG LAMBDA-2 CHAIN C REGION.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87305594.
RA STEEN M.L., HELLMAN L., PETERSSON U.;
RL GENE 55:75-84(1987).
DR ENBL; M22521; M22521.
DR PIR; B27390; B27390.
DR HSP; P01842; IBJL.
DR PROSITE; PS00290; IG.MHC.
RW IMMUNOGLOBULIN C REGION.
FT NON TER 1 1
FT DISULFID 27 85
FT DISULFID 103 103
SQ SEQUENCE 104 AA; 11318 MW; 58002 CN;

Query Match 32.9%; Score 542; DB 5; Length 104;
Best Local Similarity 65.4%; Pred. No. 1.18e-96;
Matches 68; Conservative 27; Mismatches 8; Indels 1; Gaps 1;

Db 1 gpkstplvtfpsteeelgnkatvclisdfysdvewkangaplsqgydvtanptkq 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 130 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYGVAVTAVKRAUSSPVKAGVETTPSKQ 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 gn-kylaselfrltaeqwcrsnstfcyqtheghtvekslepaec 103
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 190 SNKYAASSYLSLTPEQWKSHRSYSCQVTHGEGSTVKTVAPECS 233
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8

ID LAC RABBIT STANDARD; PRT; 105 AA.
AC P01847;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE IG LAMBDA CHAIN C REGION.
OS ORYCTOLAGUS CUNICULUS (RABBIT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; LAGOMORPHA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 82091105.
RA GARCIA I., JATON J.-C.;
RL BIOCHEM. J. 197:177-183(1981).
CC -!- THIS LAMBDA CHAIN EXPRESSES THE C7 ALLOTYPIC SPECIFICITY.
DR PIR; A02130; L7RB.
DR HSP; P01842; 7FAB.
DR PROSITE; PS00290; IG.MHC.
RW IMMUNOGLOBULIN C REGION.
FT NON TER 1 1
FT DISULFID 27 86
FT DISULFID 104 104
SQ SEQUENCE 105 AA; 11484 MW; 62157 CN;

Query Match 32.9%; Score 542; DB 5; Length 105;
Best Local Similarity 72.4%; Pred. No. 1.18e-96;

Dec 17 15:00

US-08-487-550-2.rsp

13

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RL  CENE 55:75-84 (1987).
DR  EMBL; M22520; M22520.
DR  PIR; A27390; A27390.
DR  HSP; P01842; 1NEB.
DR  PROSITE; PS00290; IG_MHC.
KW  IMMUNOGLOBULIN C REGION.
FT  NON_TER 1  J
FT  DISULFID 27 85
FT  DISULFID 103 103
SQ  SEQUENCE 104 AA; 11565 MW; 62108 CN;

Query Match 32.0%; Score 527; DB 5; Length 104;
Best Local Similarity 66.7%; Pred. No. 3.84e-93;
Matches 70; Conservative 19; Mismatches 15; Indels 1; Gaps 1;

Db 1 gpkatpvtlfpaseelktkdktlvcmtvdfypgvmvwwkadtpttggtqpfkq 60
    ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 130 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPSKQ 189
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 -nnkymatsyllltakawethshnyscqvtheentvekslraecs 104
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 190 SNKYYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
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Search completed: Tue Dec 17 15:15:16 1996
Job time : 20 secs.

Result	No.	Score	Query		Length	DB	ID	Description	Pred. No.
			Match	%					
1	1221	74.1	233	1	P81260	VDJC regions of human	3.63e-84		
2	1172	71.1	217	8	R42163	Anti-HIV-1 recombinan	2.54e-80		
3	1136	68.9	235	6	R31024	Antibody D light chai	1.69e-77		
4	126	44.1	234	7	R38162	Sequence of the kappa	1.52e-45		
5	725	44.0	236	15	R77614	Humanised 5G1.1 VL	1.82e-45		
6	708	43.0	234	3	R20058	Light chain of 3D6 +	3.74e-44		
7	707	42.9	236	8	R42065	Human anti-HBs light	4.47e-44		
8	596	42.2	106	12	R59093	Anti-HIV Fab rev16/20	3.16e-43		
9	696	42.2	133	12	R69098	Anti-HIV Fab tat16/20	3.16e-43		
10	684	41.5	234	3	R13050	CD4-specific CDR-graf	2.67e-42		
11	681	41.3	234	10	R32951	Human anti-IgE WAb 11	4.94e-42		
12	668	40.5	238	16	R93554	Monoclonal antibody D	4.57e-41		

RESULT	1	
ID	P81260 standard; protein; 233 AA.	
AC	P81260;	
DT	09-NOV-1990 (first entry)	
DE	VJJC regions of human sperm-immobilising monoclonal antibody.	
KW	Anti-human sperm-immobilising monoclonal antibody; leader region;	
KW	variable region; joining region; constant region; sterility;	
KW	vaccine; contraceptive.	
OS	Homo sapiens.	
Key	Location/Qualifiers	
FT	Region 21..115	
FT	/label=variable_region	
FT	Region 116..127	
FT	/label=joining_region	
FT	Region 128..233	
FT	/label=constant_region	
PN	J63126482-A.	
PD	30-MAY-1988.	
PF	15-NOV-1986; 272412.	
PR	15-NOV-1986; JP-272412.	
PA	(TOFU) TOA NENRYO KOGYO KK.	
DR	WPI; 88-187839/27.	
DR	N-PSDB; N81655.	
PT	Cell strain producing human sperm-immobilising monoclonal antibody	
PT	has at least V-gene in H chain coding genetic family and V gene i	
PT	chain of DNA originating from antibody of sterile woman.	
PS	Disclosure; 14pp; Japanese.	

A VDJC DNA segment is inserted into pSC4lambda5 together with a leader region. A cell strain, pref. a myeloma cell, can produce the Ab with immobilising value (\$I50) of at least 5000, sperm agglutination value at least 1:1600 dilution, specifically reacting against human ejaculated sperm. The product can be used as a vaccine and contraceptive.

See also N8165A-N8165G,
Sequence 233 AA;

Query Hatch	74.1%;	Score 1221;	DB 1;	Length 233;
Best Local Similarity	78.4%;	Pred.No. 3.63e-84;		
Matches	178;	Conservative	22;	Mismatches 26; Indels 1; Gaps 1;
Ddb	8	klfclci-gsvvseelcqdvvsevalgtvritccqdsrltyhaswyqqkprqpvlvi	66	
Qy	: :			
Ddb	8	LGILLMLPGARCAVELTQPPSVSPGQTARTCCGDNSRNEYVHWYQQKPARAPILVI	67	
Qy				
Ddb	67	ydenmrpgidprfgstgntaalitkgacadeadycnardesgnrlvfvggktltv	126	
Qy				
Ddb	68	YDSDRP SGIPERFSGSKSNGNTATLINGVEAGDEADYQCWDRASDHDFVGCGTRVTV	127	
Qy				
Ddb	127	lqgkaapstvtfppseelqankatlvcldsfypagstvawkydsgpvkagvtctpps	186	
Qy				
Ddb	128	LQCPKAAPSVTLPFPSSSEELQANKATLVCISDFPCAVTVAMKADSPVKAGVTTTPS	187	
Qy				
Ddb	187	ksnknnyaasylsltpcqwkahrsycqvrtqhgstvektvtaptcs	233	
Qy				
Ddb	188	KOSNNKYAASSYLSTPQMKSHRSYCQVTHGSTVEKTVAFTCS	234	
Qy				

RESULT	2	
ID	R42163	standard; Protein; 217 AA.
CD	R42163;	
DT	27-APR-1994	(first entry)
ACC	Anti-HIV-1 recombinant antibody 447-52D light chain.	
DE	Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;	
WM	HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;	
WM	acquired immune deficiency syndrome; chimeric antibody;	
WM	surface glycoprotein gp120; V3 loop.	
OS	Homo sapiens.	
OS	W09319785-A.	
PD	14-OCT-1993.	
PD	23-MAR-1993; 002629.	
PF	01-APR-1992; US-861701.	
PR	(MERI) MERCK & CO INC.	
PA	(JOHN/) JOHNSON L S.	
PA	(PEAR/) PFARR D S.	
PA	Conley AJ, Emini EA, Johnson LS, Mark GE, Pfarr DS;	
PR	WPI; 93-336600/42.	
PR	N-PSDB; Q49835.	
PR	New recombinant human antibody - with HIV neutralising activity	
TT	against at least two isolates, useful for preventing or treating	
TT	Infection in diagnosis, etc.	
TS	Example 9; Fig 2b; 154pp; English.	
TS	EBV-transformed cell lines and mouse-human heterohybridomas	
CC	producing human MABs specific for the gp120 V3 loop of HIV-1 MN	
CC	isolate were obtained. WAB 447-52D was found to recognise the	
CC	tetrapeptide motif GPCR, i.e. the Principal Neutralising	
CC	Determinant common to the V3 loop of different HIV isolates.	
CC	A recombinant Ab was produced in which the L chain V region was	
CC	derived from 447-52D and to which a signal sequence and a L chain	
CC	intronic sequence are appended, fused to a fragment contg. a short	
CC	intronic segment of the human lambda 2 C region and the human	
CC	lambda 2 constant encoding domain.	

[illegible]

RESULT	3	
ID	R31024 standard; Protein; 235 AA.	
AC	R31024;	
DT	19-MAY-1993 (first entry)	
DE	Antibody D light chain.	
KW	Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;	
KW	lymphocyte; hepatitis A virus; HAV; sero; positive; patient;	
KW	murine; BSB3; polyadenylated; cDNA library; human; kappa; L; H.	
OS	Synthetic.	
FEH	Key	Location/Qualifiers
FT	Peptide	1..19
FT	/note= "signal peptide"	
FT	Region	20..42
FT	/label= FR1	
FT	Region	43..53
FT	/label= CDR1	
FT	Region	54..68
FT	/label= FR2	
FT	Region	69..75
FT	/label= CDR2	
FT	Region	76..107
FT	/label= FR3	
FT	Region	108..116
FT	/label= CDR3	
FT	Region	117..126
FT	/label= FR4	
FT	Domain	127..234
FT	/label= C lambda	
PN	EP-523949-A.	
PD	20-JAN-1993.	
PPF	14-JUL-1992; 306420.	
PPF	15-JUL-1991; GB-015284.	
PPR	01-AUG-1991; GB-016594.	
PPR	23-MAR-1992; GB-006284.	
PPR	(WELL) WELLCOME FOUND LTD.	
PI	Crowe JS Lewis AP;	
PI	WPI; 93-019951/03.	
DR	N-PSDB; Q35100.	
DR	Prodn. of recombinant primate antibodies - useful for treating	
PPT	infections caused by hepatitis A, B and C, herpes,	
PPT	cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,	
PPT		

PT arthritis etc.
 P5 Disclosure; Fig 3; 35pp; English.
 CC The sequences given in R31023-24 represent the heavy and light chains
 CC of Antibody D respectively. Antibody D is a monoclonal antibody which
 CC was derived from peripheral blood lymphocytes from a hepatitis A virus
 CC (HAV) sero positive patient. Antibody D is closely related in nature
 CC to murine antibody B5B3. Total RNA was isolated from antibody D
 CC expressing cells and polyadenylated RNA was extracted. These polyA
 CC RNA's were used to prepare a cDNA library which was screened for human
 CC kappa light (L) chains and two positive clones were detected.
 CC Further heavy (H) chain clones were also isolated.
 SQ Sequence 235 AA;

Query Match 68.9%; Score 1136; DB 6; Length 235;
 Best Local Similarity 75.9%; Pred. No. 1.69e-77;
 Matches 176; Conservative 21; Mismatches 30; Indels 5; Gaps 4;
 Db 5 llllltlltqdgswaqealtqpaasvsgpqsitctgtndvsgynlvswyqhqpkga 64
 Qy 7 LLGULLLW-L-PCARCAYELTQPPSVSPQQTARITCGG-DNSRNEY--VHWYQKQPARA 62
 Db 65 pkimiyevakrpsvsnrfsgskgntasltisglqaedeaddyccsya-gsytvvfqgg 123
 Qy 63 PILVLYDDSDRPSGIPERFSGSKSGNTATITNGVEAGDEADYYCQWDRASDPVFGG 122
 Db 124 tklvtlqgkaapvtlfpssseelqankatlvcldfydgavtvawkadspvkagve 183
 Qy 123 TRVTVLQGPKAAPSVTLFPSSSEELQANKATVLCVLSDFYDGAVTVAWKADSPVKAGVE 182
 Db 184 ttptskqsnmkyaassylsltpqwkshrsyscqvthegstvektvaptecs 235
 Qy 183 TTPTSKQSNMKYAASSYLSLTPQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234

RESULT 4

ID R38162 standard; Protein; 234 AA.
 AC R38162;
 DT 01-OCT-1993 (first entry)
 DE Sequence of the kappa light chain variable region (VK) of human
 DE immunoglobulin G3 (IgG3) produced by transformed human B-cell line
 DE 88BV59, ATCC CRL 10624.
 KW B-cell; immunoglobulin g; cancer; tumour.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..214
 FT /*tag= a
 FT /label= 1st AA denoted AA#1
 FT Region 24..49
 FT /*tag= b
 FT /label= CDR 1
 FT Region 50..88
 FT /*tag= c
 FT /label= CDR 2
 FT Region 89..108
 FT /*tag= d
 FT /label= CDR 3
 FT Region 109..214
 FT /*tag= e
 FT /label= CON
 PN EP-546634-A.
 PD 16-JUN-1993.
 PF 09-DEC-1992; 203827.
 PR 13-DEC-1991; US-807300.
 PA (ALKU) AKZO NV.

PI Crichton VZ, Haapel MV, Kobrin BJ;
 DR NPI; 93-190019/24.
 DR N-PSDB; Q43773.
 PT Transformed human B-cell line for monoclonal antibody prodn. for
 PT cancer diagnosis - prod from peripheral blood B-cells of cancer
 PT patients actively immunised with autologous tumour antigen, for
 PT treating cancers
 PS Claim 9; Fig 3; 18pp; English.
 CC The 88BV59 kappa light chain sequence is indicated by the poens.
 CC of the CDRs and the constant region exon. 88BV59 utilises Vx1 and
 CC Jx5. The first NH2 terminal 22 residues were confirmed by AA
 CC sequencing.
 SQ Sequence 234 AA;

Query Match 44.1%; Score 726; DB 7; Length 234;
 Best Local Similarity 45.3%; Pred. No. 1.52e-45;
 Matches 107; Conservative 49; Mismatches 74; Indels 6; Gaps 6;
 Db 1 rqpaglllllwpagardqltqspfsfisaavdvrtictraegglasylawyqkpg 60
 Qy 2 RVPQLLGLULLLWLPGARCAVELTQPPS-VSVSPQQTARITCGGDSNNEYVHWYQKPA 60
 Db 61 kapkllyaaasslgqyprsfagsgqteftlisslqpedfatycqqln-gypriifg 119
 Qy 61 RAPILVLYDDSDRPSGIPERFSGSKSGNTATITNGVEAGDEADYYCQWDRASDPVFG 120
 Db 120 qqtrelr-rtvvaapsvfiippsdeqlkqstasvcllnmfyprakvqkvdnalqsgn 178
 Qy 121 GQTRVTVLQGPKAAPSVTLFPSSSEELQANKATVLCVLSDFYDGAVTVAWKADSPVKAG 180
 Db 179 ggesvteqskdstyslsstltlskadyekhkvyacevthqglsepvtksfnrgec 234
 Qy 181 VETTPSKQSNMKYAASSYLSLTPQWKSHRSYSCQVTHEG-ST-VEKTVAPTEC 233

RESULT 5

ID R77614 standard; Protein; 236 AA.
 AC R77614;
 DT 15-MAR-1996 (first entry)
 DE Humanised 5G1.1 VL + 012.
 KW Complement C5; haemolysis; kidney; glomerulonephritis;
 KW monoclonal antibody; antiinflammatory; antibody engineering;
 KW humanised antibody; complementarity determining region; CDR;
 KW ds.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= sig peptide
 FT Peptide 23..236
 FT /label= mat peptide
 FT Region 47..57
 FT /label= CDR-L1
 FT Region 73..79
 FT /label= CDR-L2
 FT Region 112..120
 FT /label= CDR-L3
 PN W09529697-A1.
 PD 09-NOV-1995.
 PF 01-MAY-1995; U05688.
 PR 02-MAY-1994; US-236208.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins SJ;
 PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
 PI Wang Y, Wilkins JA;

DR WPI1; 95-392923/50.
DR N-PSDB; T08486.
PT Treating glomerulonephritis with antibody against complement C5
PS Claim 40; Page 132-34; 181pp; English.
CC A humanised CDR-grafted light chain, designated 5G1.1 VL + 012
CC (R77614), includes CDRs derived from mouse anti-C5 monoclonal
CC antibody 5G1.1. DNA (T08486) coding for the light chain can be
CC subcloned together with DNA (T08484) coding for a humanised Fd
CC (R77611) into vector APEX-3P (T08476) for expression of humanised
CC antibody in human 293 ENA cells. Such recombinant antibodies retain
CC the ability of mAb 5G1.1 to block human complement C5a generation and
CC thus to reduce glomerular inflammation and kidney dysfunction
CC associated with glomerulonephritis.
SQ Sequence 236 AA;

Query Match 44.0%; Score 725; DB 15; Length 236;
Best Local Similarity 44.3%; Pred. No. 1.82e-45;
Matches 105; Conservative 53; Mismatches 72; Indels 7; Gaps 6;

Db 3 mrvpagllgllllwlgarcdiqtpasleasvgrvrticcaseniynalnwqqkp 62
Qy 1 MRVPAQLLGLLLLPGARCAVELTQPPS-VSVSPGQTARITCGDNRNEYVHYQQKP 59

Db 63 gkapklliyatnldavprrfsgsgtgdfcltliselqpedfatycc--nvIntpltf 120
Qy 60 ARAPILIVDDSDRPPSGIFERFSGSKSGNTATLTINGVEAGDEADYVCQWDRASDHPVF 119

Db 121 gqgtkvei--krtvaapsvfifppsdqksgtasvvccllnmfypreakvqkvdnalqsg 179
Qy 120 GCGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTAVKADSPVKA 179

Db 180 nsegsveqdkdskdystlsltlsekadyekkhkyacevthgslspvtskfnrgec 236
Qy 180 GVEITTPSKQSN--KYAASSYLSLTPQMKSHRSYSCQVTHEG-ST-VEKTVAPTEC 233

RESULT 6
ID R20058 standard; Protein; 234 AA.
AC R20058;
DT 25-MAR-1992 (first entry)
DE Light chain of 306 anti-HIV antibody.
KW Plasmid pUC3D61C; human immunodeficiency virus; AIDS;
KW complementarity determining region.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= signal 23..234
FT Protein 23..45
FT Region 23..45
FT /label= Framework_1
FT Region 46..56
FT /label= CDR_1
FT Region 57..71
FT /label= Framework_2
FT Region 72..78
FT /label= CDR_2
FT Region 79..110
FT /label= Framework_3
FT Region 111..117
FT /label= CDR_3
FT Region 118..127
FT /label= Framework_4
FT Region 128..234

FT /label= Constant_region
PN W09118983-A.
PD 12-DEC-1991.
PF 28-MAY-1991; 100067.
PR 29-MAY-1990; AT-001178.
PA (JUNG/) JUNGBAUER A.
PI Felgenhauer M, Himmeler G, Kohl J, Steindl F;
DR WPI1; 92-007468/01.
DR N-PSDB; Q20067.
PT Recombinant protein which binds to complex viral antigen and
PT HIV-1 - contains variable region of antibody derived from 3D6
PT cell line, used for detecting HIV-1 antigen
PS Claim 3; Page 28; 52pp; German.
CC The variable region of the light chain is used in a recombinant
CC protein with the variable region from the heavy chain of 3D6,
CC the two V regions being joined by a linker. The recombinant
CC protein binds to HIV gp160.
CC See also Q20066 and Q20068.
SQ Sequence 234 AA;

Query Match 43.0%; Score 708; DB 3; Length 234;
Best Local Similarity 45.1%; Pred. No. 3.74e-44;
Matches 107; Conservative 49; Mismatches 72; Indels 9; Gaps 8;

Db 3 mrvpagllgllllwlgarcdiqtpasleasvgrvrticcaseniynalnwqqkp 62
Qy 1 MRVPAQLLGLLLLPGARCAVELTQPPS-VSVSPGQTARITCGDNRNEYVHYQQKP 59

Db 63 gkvpklliykaesslsgvpsrfsqsgstfcltliselqpdffatyccqyn--s-ys-f 118
Qy 60 ARAPILIVDDSDRPPSGIFERFSGSKSGNTATLTINGVEAGDEADYVCQWDRASDHPVF 119

Db 119 gpgtkvdi--krtvaapsvfifppsdqksgtasvvccllnmfypreakvqkvdnalqsg 177
Qy 120 GCGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTAVKADSPVKA 179

Db 178 nsegsveqdkdskdystlsltlsekadyekkhkyacevthgslspvtskfnrgec 234
Qy 180 GVEITTPSKQSN--KYAASSYLSLTPQMKSHRSYSCQVTHEG-ST-VEKTVAPTEC 233

RESULT 7
ID R42065 standard; Protein; 236 AA.
AC R42065;
DT 29-APR-1994 (first entry)
DE Human anti-HBs light chain.
KW Antibody; Ab; light; heavy; chain; hepatitis B;
KW HB; surface antigen.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= sig_peptide
FT Protein 23..236
FT /label= mat_protein
PN W09320205-A.
PD 14-OCT-1993.
PF 30-MAR-1993; J00396.
PR 30-MAR-1992; JP-074678.
PA (SUNR) SUNTORY LTD.
PI Arima K, Kurihara T, Mateukura S, Nishihara T, Tsuruoka N;
DR WPI1; 93-336913/42.
DR N-PSDB; Q49943.
PT Human anti-hepatitis B surface antigen antibody gene - can be
PT used to produce L and H chains of the antibody in large quantity

RESULT 12
 ID R33554 standard; Protein; 238 AA.
 AC R33554;
 DT 20-AUG-1996 (first entry)
 DE Monoclonal antibody DNA light chain against 65 kD hCMV antigen.
 KW Polymerase chain reaction; primer; amplify; PCR; light chain; MAb;
 KW 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.
 OS Synthetic.

FT Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "Signal peptide"
 FT Protein 21..238
 FT /note= "Mature light chain"
 PN J08038178-A.
 PD 13-FEB-1996.
 PF 20-FEB-1995; 030742.
 PR 18-FEB-1994; JP-021628.
 PA (NISN) NISSHINBO IND INC.
 PA (TANA/) TANAKA H.
 DR MPI; 96-154852/16.
 DR N-PSDB; T18060.
 PT Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -
 PT produced by primer amplification, used in the diagnosis of hCMV
 PT infection
 PS Claim 5; Page 19; 22pp; Japanese.
 CC The sequences given in R33553-54 represent the heavy and light chains
 CC respectively of a monoclonal antibody against a 65 kD antigen of human
 CC cytomegalovirus (hCMV). The DNA's encoding these sequences were
 CC amplified using the sequences given in T18040-58. The monoclonal
 CC antibody may be used in the diagnosis of hCMV.
 SQ Sequence 238 AA;

Query Match 40.5%; Score 668; DB 16; Length 238;
 Best Local Similarity 43.0%; Pred. No. 4.57e-41;
 Matches 104; Conservative 56; Mismatches 69; Indels 13; Gaps 9;

Db 1 mrvpallglmlwlpqsgadivmtqtalsvtpgpaaiscksgallhddgtylyw 60
 Qy 1 mrvpallglmlwlpqsgadivmtqtalsvtpgpaaiscksgallhddgtylyw 60
 Db 61 ylkpqsqplliyeavnsfsgvdrfsgegetdftklisrveadvgvyyc-m--rsi 117
 Qy 55 YQKPARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYQCQWMDRAS 114
 Db 118 qfatfgqgktlei-krtvaapsvfifpdsdeqlksgtasvvccllnnfypreakvgkvkdn 176
 Qy 115 DHPVFGGTRVTVLGQPKAAPSVTLFPPSSEELQNKATLVCLISDFYPGAVTVAKRADS 174
 Db 177 alqegneqsvteqsdstysalstltlskadyekkhkvacevthqglsesptksfnrg 236
 Qy 175 SPVKAGVETTTFSKQNN-KYAASSYLSLTPEQWKSRSYSQVTHEG-ST-VEKTVAPT 231
 Db 237 ec 238
 Qy 232 EC 233

RESULT 13
 ID R28809 standard; Protein; 241 AA.
 AC R28809;
 DT 02-APR-1993 (first entry)
 DE Vector pMDR1007.
 KW Plasmid; pMDR1006; pSAB132; vector; pMDR1007; pMDR985; AatII; EcoRV;
 KW pMDR986; BglII; pMDR1003; JA221(Iq); E. coli; ampicillin resistance;

KW NotI; dephosphorylate; calf; alkaline phosphatase; low temperature;
 KW melting agarose; immunoglobulin; kappa chain; signal peptide; LC;
 KW humanised; 5A8; light chain; variable region; LV; genomic; constant
 KW antibody; homolog; CD4; gp120; cell surface; glycoprotein; CD4+;
 KW lymphocyte; helper; inducer; HIV; syncytia; formation.
 OS Synthetic.

FT Key Location/Qualifiers
 FT Peptide 1..22
 FT /note= "Immunoglobulin kappa chain signal peptide"
 FT Region 23..134
 FT /note= "Humanised 5A8 LV"
 FT Region 135..241
 FT /note= "Human kappa chain LC"
 PN W09209305-A.
 PD 11-JUN-1992.
 PF 27-NOV-1991; U08843.
 PR 27-NOV-1990; US-618542.
 PA (BIO) BIOGEN INC.
 PI Burkly LC, Chisholm PL, Rosa JJ, Rosa MD, Thomas DW;
 DR MPI; 92-398399/48.
 DR N-PSDB; Q30920.
 PT New anti-CD4 antibody homologues - which bind CD4, do not block
 PT binding of HIV gp120 to CD4 but block HIV-induced syncytia
 PT formation between CD4+ cells
 PS Disclosure; Page 166-7; 205pp; English.
 CC The sequence given is encoded by the insert of the vector pMDR1007..
 CC pMDR1006 (see Q30919) and pSAB132 (see Q30906) were used in the
 CC construction of this vector. Three fragments were ligated together
 CC to generate pMDR1006; a 572 bp fragment of pMDR985 (see Q30913), a
 CC 344bp AatII/EcoRV fragment of pMDR986 (see Q30918) and a 326 bp
 CC EcoRV/BglII fragment of pMDR1003 (see Q30900). The ligation mixture
 CC was used to transform E. coli JA221(Iq) to ampicillin resistance.
 CC pMDR1006 was cleaved with NotI and the 1693 bp fragment isolated was
 CC ligated into NotI linearised pSAB132 which had been dephosphorylated
 CC by calf alkaline phosphatase. This generates the plasmid pMDR1007.
 CC The dephosphorylated mixture was fractionated through low temperature
 CC melting agarose and used to transform E. coli JA221(Iq) to ampicillin
 CC resistance. The pMDR1007 insert comprises DNA encoding, in a 5' to 3'
 CC order, the immunoglobulin kappa chain signal peptide, amino acid (AA)
 CC 1-AA112 of the humanised 5A8 light chain variable region (LV) followed
 CC by genomic DNA encoding AA108-AA214 of the human kappa light chain,
 CC ie. the light chain constant region (LC). This polypeptide is an
 CC antibody homolog which was shown to bind to CD4 but did not block the
 CC binding of gp120 to CD4. CD4 is a cell surface glycoprotein of CD4+
 CC lymphocytes (helper/inducer cells). The homolog blocked HIV-induced
 CC syncytia formation. This homolog can be used in the detection,
 CC prophylaxis and treatment of diseases caused by infective agents whose
 CC primary targets are CD4+ cells.
 SQ Sequence 241 AA;

Query Match 40.3%; Score 664; DB 5; Length 241;
 Best Local Similarity 45.7%; Pred. No. 9.29e-41;
 Matches 111; Conservative 48; Mismatches 70; Indels 14; Gaps 10;

Db 3 mrvpallglmlwlpqsgadivmtqtalsvtpgpaaiscksgallhddgtylyw 62
 Qy 1 mrvpallglmlwlpqsgadivmtqtalsvtpgpaaiscksgallhddgtylyw 62
 Db 63 ylkpqsqplliyeavnsfsgvdrfsgegetdftklisrveadvgvyycqy-y 120
 Qy 54 WYQKPARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYQCQWMDRA 113
 Db 121 s-ytfgtqgktlei-krtvaapsvfifpdsdeqlksgtasvvccllnnfypreakvgkvkdn 178
 Qy 121 s-ytfgtqgktlei-krtvaapsvfifpdsdeqlksgtasvvccllnnfypreakvgkvkdn 178

621 57A1 021 /

[illegible]

		Query Match	37.9%;	Score 624;	DB 2;	Length 349;	
		Best Local Similarity	43.5%;	Pred. No. 1.1le-37;			
		Matches	93;	Conservative	51;	Mismatches 65;	Indels 5; Gaps 5;
Db	137	ltgspatlsipgeratlccasvgsylawgykqkgpgacprliydasnratgipaifs	196				
		: - : : : : : : : : : : :					
Qy	24	LTPPPS-VSVSPGQTARITCCGONSNEVHWYQQKPARAPILVIYDDSDRPSGPIPERFS	82				
Db	197	qsqsgtfdtltsilepadfavyycqhndwppnatfgggktvei-krtvaapsvfiipp	255				
		: : : : : : : : : :					
Qy	83	GSKSGNATLTUNGVEAGDEADYYCQWDRASDHPEFGSGTRVTVLGPKAAPSVTLEPPP	142				
Db	256	sdeqlksgtasvcllmfyreakvwkvdnalqsqnseqaeqdsqskdstyalestlt	315				
		: : : : : : : : : : : : :					
Qy	143	SSEELQANKATLVCLISDFYPCAVTVAMKADSPPKAGVETTTTTSKSNN-KYAASSYL	201				
Db	316	lskadyekhkvyaacevhqglsspvtksnrgec	349				
		: : : : : : : : : : : : : : :					

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17

Q1 * 202 LTPEOMKSHRSYSCQVTHEG-ST-VEKTVAPTEC 233

Search completed: Tue Dec 17 15:13:42 1996
Job time : 28 secs.


```

#contents      myeloma protein Eu
#accession     B90563
##molecule_type protein
##residues     1-96,'R',98-135 ##label CUN
##note         this sequence has the G1m(3) marker, 97-Arg
REFERENCE
#authors       A90564
               Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg,
               W.H.; Edelman, G.M.
#journal        Biochemistry (1970) 9:3171-3181
#title         The covalent structure of a human gammaG-immunoglobulin.
               VIII. Amino acid sequence of heavy-chain cyanogen bromide
               fragments H-5-H-7.
#cross-references M01D:71064025
#contents      Eu
#accession     A90564
##molecule_type protein
##residues     136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,
               'D',199-238,'E',240,'M',242-267,'DGEPE',273-329
               ##label RUT
               this sequence has the G1m(non-1) markers, 239-Glu and
               241-Met
#note          A91668
REFERENCE
#authors       Ponstingl, H.; Hilschmann, N.
#journal        Hoppe-Seyler's Z. Physiol. Chem. (1976) 357:1571-1604
#title         Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins
               (Myelomprotein Nie), III. Die chymotryptischen Peptide der
               H-Kette, Anordnung der tryptischen Peptide und Diskussion
               der vollstaendigen Primaerstruktur.
#cross-references M01D:77070269
#contents      myeloma protein Nie
#accession     B91668
##molecule_type protein
##residues     1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',
               240,'L',242-268,'E',270-271,'D',273-330 ##label PON
               this sequence has the G1m(17) and G1m(1) markers
#note          A91723
REFERENCE
#authors       Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
#journal        Hoppe-Seyler's Z. Physiol. Chem. (1983) 364:713-747
#title         Die Primaerstruktur des kristallisierbaren monoklonalen
               Immunglobulins IgG1 KOL, I.
#cross-references M01D:83289131
#contents      myeloma protein KOL; disulfide bonds
#accession     A91723
##molecule_type protein
##residues     1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',
               268-271,'D',273-330 ##label SCH
               this sequence has the G1m(3) and G1m(non-1) markers
#note          A90565
REFERENCE
#authors       Gall, W.E.; Edelman, G.M.
#journal        Biochemistry (1970) 9:3188-3196
#title         The covalent structure of a human gammaG-immunoglobulin. X.
               Intrachain disulfide bonds.
#cross-references M01D:71064027
#contents      annotation; disulfide bonds
#note          A91667
REFERENCE
#authors       Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
#journal        Hoppe-Seyler's Z. Physiol. Chem. (1976) 357:1515-1540
#title         Rule of antibody structure. The primary structure of
               monoclonal IgG1 immunoglobulin (myeloma protein Nie), I:
               purification and characterization of the protein, the L-
               and H-chains the cyanogenbromide cleavage products, and the
               disulfide bridges.
#cross-references M01D:77070267
#contents      annotation; disulfide bonds

```

```

GENETICS
#gene          GDB:IGHG1
#map_position  14q32.33
#introns       99/1; 114/1; 224/1
CLASSIFICATION
#superfamily  immunoglobulin C region; immunoglobulin homology
#glycoprotein
FEATURE
20-85          #domain immunoglobulin homology #label IGG1\
137-206        #domain immunoglobulin homology #label IGG2\
243-310        #domain immunoglobulin homology #label IGG3\
27-83,144-204, #disulfide bonds #status experimental\
250-308        #disulfide bonds interchain (to light chain) #status
103            experimental\
109,112        #disulfide bonds interchain (to heavy chain) #status
180            #binding site carbohydrate (Asn) (covalent) #status
               experimental
SUMMARY        #length 330 #molecular-weight 36106 #checksum 8773
Query Match    67.4%; Score 2339; DB 2; Length 330;
Best Local Similarity 99.7%; Pred. No. 0.00e+00;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 askgsvfplapskatsgtaalgclvdyfpepvtvsmnsgaltsgvhtfpavlgss 60
               |||||
Qy 147 ASTKGSVFPLAPSSKSTSGTAAAGCLVKDYFPEPTVYSNNSGALTSGVHTFPAVLQSS 206
               |||||
Db 61 gylslasvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdkthtccpcepallgg 120
               |||||
Qy 207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266
               |||||
Db 121 psvflfpkpdkdtlmlertpevtcvvvdvshdepvkfwnyvdgvevhnaktkpreeqyn 180
               |||||
Qy 267 PSVFLEPPRPKDTLMISRTPEVTCVVDVSHDEPVEKFNYYDGVVHNKTKPREEQYN 326
               |||||
Db 181 styrvsvltvlhqdwlngkeyckvsnkalpapiaktistakgpprepqvytlpparde 240
               |||||
Qy 327 STRVSVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQRPQVYTLPPSRDE 386
               |||||
Db 241 ltknqvslctlvkfypsdiavewengpennnykttppvldsdgsfflyskltvdkerw 300
               |||||
Qy 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPVLDSDGSFFLYSKLTVDKSRW 446
               |||||
Db 301 qqgnvfscsvmhleahhnytkslslspgk 330
               |||||
Qy 447 QQGNVFCSVMHLEALHNHYTKSLSLSPCK 476
               |||||
RESULT 2
ENTRY        S36861      #type fragment
TITLE        Ig gamma-1 chain C region - human (fragment)
ORGANISM     #formal name Homo sapiens #common name man
DATE         31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change
               02-Aug-1994
ACCESSIONS   S36861; S33887
REFERENCE    S33904
#authors     Harris, L.J.
#submission  submitted to the EMBL Data Library, October 1992
#accession   S36861
#molecule_type DNA
#residues    1-329 ##label HAR
#cross-references EMBL:217370
REFERENCE    S33887

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#authors Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
#journal Cell (1982) 29:671-679
#title Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.
#accession S33887
#molecule_type DNA
#residues 87-112;234-329 #label TAK
#cross-references EMBL:217370

GENETICS
#introns 98/1; 113/1; 223/1
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
SUMMARY #length 329 #checksum 6336

Query Match 67.3%; Score 2335; DB 5; Length 329;
Best Local Similarity 99.7%; Pred. No. 0.00e+00;
Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 stgspvflapsekstsgtaalqclvdyfpepvtvswnsqaltsgvhtfpavlgsg 60
Qy 148 STKGPSVFLAPSSKTSGGTAALQCLVDYFPEPVTVSWNSGALTSGVHTFPVAVLQSSG 207
Db 61 lyelssvtpseelgtqyicnvmhkpentkvdkvepkscdtkhcpcpaelggp 120
Qy 208 LYSLSWVTPVSSLSGTQYICNVNHNKPSNTKVDKAEPSKDKTHTCPPCPAPELLGCP 267
Db 121 avflfpkpkdltmirstpvtcvvdvshedevkfnwvvgdvevhnaktpreeqns 180
Qy 268 SVFLFPKPKDILMIRSTPEVTCVVDVSHEDPEVKENWVVGVEVHNKTPREEQNS 327
Db 181 tyrvsvltvlhqdlnqkeyckvsnkalpapietkiekakgpgpvytlpssrdel 240
Qy 328 TYRVSVTLVHQDLNQEYCKVSNKALPAPIETKISKAKGPREPQVYTLPSRDEL 387
Db 241 tkngvalclvkgfypedvawesnqpennykttpvldsdgfefflyekltvdkerwq 300
Qy 388 TKNQVSLTCLVKGPSPDIAVWESNQEPENNYKTTPVLDSDGFEFFLYSKUTVDKGRWQ 447
Db 301 qgnvfscvsmhealhhnytketelspgk 329
Qy 448 QGNVFCVSMHEALHHNYTKETLSLSPGK 476

RESULT 3
ENTRY TITLE S22080 #type complete
ALTERNATE_NAMES Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
ORGANISM Ig gamma-1 chain C region (clone 8.10)
#formal name Bos primigenius taurus #common name cattle
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-May-1995
ACCESSIONS S22080; S06610; A31303
REFERENCE S22080
#authors Sanders, P.G.
#submission submitted to the EMBL Data Library, November 1991
#accession S22080
#status preliminary
#molecule_type mRNA
#residues 1-470 #label SAN
#cross-references EMBL:X62916
REFERENCE S06610
#authors Symons, D.B.A.; Clarkson, C.A.; Beale, D.
#journal Mol. Immunol. (1989) 26:841-850
#title Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 2 genes.

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#cross-references MUID:90097956
#accession S06610
#molecule_type DNA
#residues 142-470 #label SYM
#cross-references EMBL:X16701
#note the sequence was determined from the germline gene

GENETICS
#gene Ig CH gamma-1
#introns 98/1; 111/1; 221/1
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
KEYWORDS antibody; complement; immunoglobulin; membrane protein
FEATURE #binding_site carbohydrate (Asn) (covalent) #status 318
#predicted

SUMMARY #length 470 #molecular-weight 50625 #checksum 2181

Query Match 61.5%; Score 2135; DB 5; Length 470;
Best Local Similarity 62.6%; Pred. No. 6.82e-301;
Matches 299; Conservative 84; Mismatches 85; Indels 10; Gaps 8;

Db 1 mmpwlcllvisapigvleqvqresgdpelvkpqtlltctvsgfslseyal-twvrqa 59
Qy 1 MKHLWFLLLVAAPRWLSQVKLQWGEGLQPSSETLSRTCVVSGSGISYYWVWIRQT 60
Db 60 pqkalewvvgi-taggttyynpalkrslsitkenskqavalsavstpedatvycarat 118
Qy 61 PERGLMIGHYNGATTNYPNLSKSRVITSKQFNLNSVTDADTAVYCARGP 120
Db 119 ygevvd---galadawggllvtvseastapkvyplesccgckssstvtlglvseyp 175
Qy 121 RDCCTTCYGMVDWVGDBLVTVSSASTKGPSVFP LAPSSKTSGGTAALGCLVKDTP 180
Db 176 epvtvtwmgalksgvhtfpavlgseglylesmvtvpgtsg-qtfcnvahpasetkv 234
Qy 181 EPTVTSWNSGALTSGVHTFPVAVLQSSGLYLSVVTVPSSSLGTQTYICNVNHNKPSNTKV 240
Db 235 dkavdp-tc-kpspcdcoppelpggsvfifppkpkdltisgtpevtcvvvvghddp 292
Qy 241 DKAEPSKDKTHTCPPCPAPELLGSPVFLFPKPKDILMIRSTPEVTCVVDVSHEDP 300
Db 293 evkfswfvdvdeventattkpreeqnetyrvvsalriqhdwtgdkfckvhneglpap 352
Qy 301 EVKENWYVVGVEVHNKTPREEQNSTYRVVSVLTVLHQDLNQEYCKVSNKALPAP 360
Db 353 lvtlstrtkparepvyvllappqeelsketvslctmvtsefypdyiavewgrngqeseed 412
Qy 361 TEKTSKAKGPREPQVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVWESNQEPEN-N 419
Db 413 kygtppqladssyflysklrvdrnswegtdytcvnmhealhhnytketelspgk 470
Qy 420 -YKTPPVLDSDGFEFFLYSKLTVDKSRWQGNVFCVSMHEALHHNYTKETLSLSPGK 476

RESULT 4
ENTRY TITLE G2HU #type complete
ALTERNATE_NAMES Ig gamma-2 chain C region - human
ORGANISM #formal name Homo sapiens #common name man
DATE 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 08-Dec-1994
ACCESSIONS A93906; A92809; A90752; A93132; A02148
REFERENCE A93906
#authors Ellison, J.; Hood, L.
#journal Proc. Natl. Acad. Sci. U.S.A. (1982) 79:1984-1988
#title Linkage and sequence homology of two human immunoglobulin

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gamma heavy chain constant region genes.

#cross-references MUID:82197621
#accession A93906
##molecule_type DNA
##residues 1-326 ##label ELL
##note Lys-326 is probably removed posttranslationally

REFERENCE
#authors Wang, A.C.; Tung, E.; Fudenberg, H.H.
#journal J. Immunol. (1980) 125:1048-1054
#title The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.

#cross-references MUID:81007873
#contents myeloma protein T11
#accession A92809
##molecule_type protein
##residues 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 ##label WAN
##note Trp-156 is at or near the complement-binding site

REFERENCE
#authors Connell, G.E.; Parr, D.M.; Hofmann, T.
#journal Can. J. Biochem. (1979) 57:758-767
#title The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.

#cross-references MUID:80001357
#contents myeloma protein Zie
#accession A90752
##molecule_type protein
##residues 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-234,'Z',236-263,'BGEFZ',269-325
##label CON
##note this sequence has since been revised

REFERENCE
#authors Hofmann, T.; Parr, D.M.
#journal Mol. Immunol. (1979) 16:923-925
#title A note on the amino acid sequence of residues 381-391 of human immunoglobulin gamma chains.

#cross-references MUID:80114419
#contents Zie
#accession A93132
##molecule_type protein
##residues 238-275 ##label HOF

REFERENCE
#authors Hofmann, T.; Parr, D.M.
#submissions submitted to the Atlas, March 1980
#contents annotation; Zie, revisions to residues 25, 59, 60, and 264-268
#note the revised sequence differs from that shown in having 60-Ala and in the amidation states of residues 58, 194, and 197; the amidation states of residues 172-174, 176, and 235 were not determined

REFERENCE
#authors Milstein, C.; Frangione, B.
#journal Biochem. J. (1971) 121:217-225
#title Disulphide bridges of the heavy chain of human immunoglobulin G2.

#cross-references MUID:72033500
#contents annotation; myeloma protein Sa, disulfide bonds
#accession A93157
#authors Frangione, B.; Milstein, C.; Pink, J.R.L.
#journal Nature (1969) 221:145-148
#title Structural studies of immunoglobulin G.

#cross-references MUID:69064124
#contents annotation; Sa, disulfide bonds
GENETICS
#gene GDB:IGHG2

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```

#map_position 14q32.33
CLASSIFICATION  #superfamily immunoglobulin C region; immunoglobulin homology
FEATURE
20-85      #domain immunoglobulin homology #label IGG1\
133-202    #domain immunoglobulin homology #label IGG2\
239-306    #domain immunoglobulin homology #label IGG3\
14         #disulfide_bonds interchain (to light chain) #status
          experimental\
27-83,140-200,
246-304    #disulfide_bonds #status experimental\
102,103,106,109 #disulfide_bonds interchain (to heavy chain) #status
          experimental
SUMMARY    #length 326 #molecular-weight 35884 #checksum 7982

Query Match      61.4%; Score 2133; DB 2; Length 326;
Best Local Similarity 90.9%; Pred. No. 1.39e-300;
Matches 300; Conservative 15; Mismatches 11; Indels 4; Gaps 3

Db      1  astkgpsvfplapcsrstsestaalcgicvkdyfpepvtvsnegaltgqvhfpavlgas 60
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy      147  ASTKGSVFPLAPSKSTSGGTAALGCLVDYFPEPVTVSNWNGALTSQVTFPAVLQSS 206
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61  glyslyssvvtvpasnfqgtytncvdhkpntkdkvtverkcc--ve-cppcpappv-ag 116
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy      207  GLYSLYSSVVTVPSSSLGTQTYICWNHNPSTNKVDKKAEPKSCDKTHTCCPPAPELGG 266
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      117  psvflfpkpkdltmistrtepcvtcvvdvshedpvgfnvydvqgvvhnaktkpreeqfn 176
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy      267  PSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKENYVDVGVEVHNNAKTKPREEQIN 326
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      177  stfrvsvltvvhqdwlngkeyckvksnkglpapietkstkkgqprepyvtlpsree 236
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy      327  STRVSVVLTVLHQWLNGREYCKVKVSNKALPAPIETKISKAKQPREQVYTLPPSRDE 386
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      237  mtknqvstclvkgfyfpdiavewngqpennykttppmlsdsgsflysklvtcksrw 296
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy      387  LTKNQSVLTCVLKGFYPSDIAVENSGQPNKYKTPPVLDSGFFLYSKLTVDKSRW 446
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      297  qgnvfvscsvmhealnhnhtgkslslpgk 326
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy      447  QGNVFCVSMHEALNHNYTKRSLSPK 476
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT      5
ENTRY       G4HU      #type complete
TITLE       Ig gamma-4 chain C region - human
ORGANISM    #formal name Homo sapiens #common name man
DATE        02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change
          23-1982-1995
ACCESSIONS  A90933; A90249; A02150
REFERENCE   A90933
#authors    Ellison, J.; Buxbaum, J.; Hood, L.
#journal    DNA (1981) 1:11-18
#title      Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
#cross-references MIMD:83157104
#accession  A90933
#molecule_type DNA
#residues   1-327 #label ELL
#note       the sequence was determined from the germline gene
REFERENCE   A90249
#authors    Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
#journal    Biochem. J. (1970) 117:33-47
#title      Human immunoglobulin subclasses. Partial amino acid sequence
          of the constant region of A gamma4 chain.

```



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#cross-references MUID:70207560
#accession A90249
##molecule_type protein
##residues 1-30;81-326 ##label PIN

GENETICS
#gene GDB:IGHG4
#map_position 14q32.33
#introns 99/1; 111/1; 221/1
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
FEATURE
20-85 #domain immunoglobulin homology #label IGHG\
99-110 #region hinge\
134-203 #domain immunoglobulin homology #label IGHG2\
240-307 #domain immunoglobulin homology #label IGHG3\
14 #disulfide bonds interchain (to light chain) #status
experimental\
27-83,141-201,
247-305 #disulfide bonds #status predicted\
106,109 #disulfide bonds interchain (to heavy chain) #status
experimental
SUMMARY #length 327 #molecular-weight 35940 #checksum 907

Query Match 61.4%; Score 2133; DB 2; Length 327;
Best Local Similarity 90.6%; Pred. No. 1.39e-300;
Matches 299; Conservative 17; Mismatches 11; Indels 3; Gaps 3;

Db 1 astkgsfpplapscstestaalgcclvkdyfpepvtvwnsgaltsgvhtfpavlqss 60
Qy 147 ASTKGSFVPELAPSSKSTSGTAALGCLVKDYFPEPVTVMNSGALTSVHTFPVAVLQSS 206

Db 61 glyslasvvtvpssslgktytcnvdkhpkentckvdrvesk-yg-p-pcspcpapeflgg 117
Qy 207 GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKAEKPKCDKTHTCPPCAPPELLGG 266

Db 118 psvflfpkpkdtlmartpevtcvvvdsqebvqfnwvdgvvhnaktkpreeqfn 177
Qy 267 PSVFLFPKPKDTHMISRTPEVTCVVDVSHEDPEVKNWYDGVGVHNKTKPREQYN 326

Db 178 styrvsvltvlhgdwlngkcykckvanklpsslektiekakgpreqvytlppsqee 237
Qy 327 STYRVSVLTVLHGDWLNKCYKCKVANKLPSPLEKTIKAKGPREPOVYTLPPSRDE 386

Db 238 mtknqvslclvkfyypsdiaveesngpennyktppvldsdgsfflyslrltvdkarw 297
Qy 387 LTKNQVSLTCLVKGYFSDIAVESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 446

Db 298 qegnvfscvnmhealnhhytqkslslelgt 327
Qy 447 QEGNVFSCVNMHEALNHHTQKSLSLSPCK 476

RESULT 6 S31459 #type fragment
ENTRY Ig gamma-1 chain - sheep (fragment)
TITLE #formal name Ovis orientalis aries, Ovis ammon aries
ORGANISM #common name domestic sheep
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
ACCESSIONS S31459
REFERENCE S31459
#authors Patri, S.; Nau, F.
#submission submitted to the EMBL Data Library, December 1992
#accession S31459
##status preliminary
```

```
#molecule_type mRNA
##residues 1-472 ##label PAT
##cross-references EMBL:X69797
SUMMARY #length 472 #checksum 9485

Query Match 61.2%; Score 2126; DB 12; Length 472;
Best Local Similarity 61.8%; Pred. No. 1.70e-299;
Matches 294; Conservative 85; Mismatches 89; Indels 8; Gaps 8;

Db 2 lwtllfvsaprgvlsqgspalatllqtlsvtctisgfalmnygv-dwvtrqagpk 60
Qy 4 LWFELLVAAPRWVLSQVKLQWGEGLQPSSETLSRTCVCVSGSISGYTWIQTQPCR 63

Db 61 alewlqgs-gydedidvnpvkarlsatkdtsqvaltlstvttedtavyycarvdyds 119
Qy 64 GLEWIGHIYNGATTNPNPSLKSRTVTSKDNQFFLNLNSVTDADTVYVCARGRPD 123

Db 120 shafayasy-dfwpgllslvlsastppkvypltsccgdtasseivtlgclvesympv 178
Qy 124 CTTICYGWDVWVGCDLVTWSSASTKGSVFP LAPSSKSTSGGTAALGCLVKDYFPEPV 183

Db 179 tvtnegaltsgvhtfpailgesqlvlesvvtvpastagadtfcicnvahpasstkvdxr 238
Qy 184 TVSNNSCALITSCVHTFPVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKK 243

Db 239 vep-gcpdkchcr-cppelpgqpsvfipbpkdkdtltisgtpevtcvvvdvgddp 296
Qy 244 AEPKSC-DKHTCPCPAPPELLGGPSVFLFPPKPKDTHMISRTPEVTCVVDVSHEDPEV 302

Db 297 qfsvfdvnevartarkpreedfnstfrvvsalpiqkdwtkgkfcckvhealpapiv 356
Qy 303 KENYVDGVGVHNKTKPREQYNSTYRVSVLTVLHQDLNKGKEYTKRVSNKALPAPIE 362

Db 357 rtisrtkgarepvyvlpappqeelsktslvtclvtgfydpdiavevknqngpseedy 416
Qy 363 KTIISKAGQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSDIAVESNGQPEN-N-Y 420

Db 417 gtttsqlsdagdyflyerlrvdknswqegdtvacvnmhealnhhytqkslskppak 472
Qy 421 KTTPEVLDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALNHHTQKSLSLSPCK 476

RESULT 7 S37483 #type complete
ENTRY Ig gamma-2a chain - mouse
TITLE #formal name Mus musculus
ORGANISM #common name house mouse
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
ACCESSIONS S37483
REFERENCE S37483
#authors Duncanson, F.F.D.
#submission submitted to the EMBL Data Library, February 1993
#accession S37483
##status preliminary
##molecule_type mRNA
##residues 1-469 ##label DUC
##cross-references EMBL:X70423
SUMMARY #length 469 #molecular-weight 51549 #checksum 7833

Query Match 55.1%; Score 1913; DB 12; Length 469;
Best Local Similarity 56.3%; Pred. No. 1.85e-266;
Matches 267; Conservative 89; Mismatches 107; Indels 11; Gaps 6;

Db 5 wifilllegtagvhcqiqlqggpelykpgaaavklsckeaegyftdyi-nwvkqpgg 63
```

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Qy 5 WFFLLVAPRWLSQVKLQWGGELQLQSETLSRTCVSGSGISGYVYWTWIRQTPERG 64
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Db 64 LkLqIwIpaagntkynenfkgtatltvdtsastaymqleatseadvfcatatngat 122
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Qy 65 LEWIGHIYGNGATNTNPNISKRVTISKTQKNOFFLNINSVTDADTAVYCYCARPRDC 124
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Db 123 atI-----ldywgqgttlvtasakttapsvypapvcgdtgssvltlqclvkgvfpepvt 177
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Qy 125 TTICYGWVDWVWCGF GDLVTVSASTKGPVFP LAPSSKSTSGCTAALGCLVWVDFPEPVT 184
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Db 178 ltwnsglsesvthfavlqsd-lytlesavtvtsetwpsqitcnvahpasstkvdtkl 236
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Qy 185 VSNNSGALTSVGHVFAVLAQSGSLYSLSVWVTPSSSLGTQYICNVNHNKPSNTKVDKKA 244
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Db 237 eprg-ptikpcpcckapnllggpsvfifppkikdvlmislepivtcvvdvseddpgv 295
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Qy 245 EPKSCDKTHTCPCC--PAPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVDVSHEDPEV 302
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Db 296 qlawfvnnvvhvtaqtqthredynstlrvealpiqhdqmsqgkefkckvnnkdlpapie 355
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Qy 303 KENNYVDGVEVHNARKTPREQYNSTRVSVLTVLHQDLWLNKGEYKCKVSNKALPAIE 362
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Db 356 rtiakpkgsravapvylpppeentkktltcmvtdfmpediyvewtngktelnykn 415
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Qy 363 NTISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVRGFYPSDIAVEWESNQGPENNYKT 422
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Db 416 tepvldadgsyfmsklrvckknwvnsyscvvhgelnhhttkesfartpgk 469
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Qy 423 TPEVLDSDGSFELYSKLTVDKSRHQQGVFSCVNHVALHNHYTKQSLSLSPCK 476
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::

RESULT 8 S40295 #type complete
ENTRY Ig gamma-2a chain (mAb735) - mouse
TITLE #formal name Mus musculus #common name house mouse
ORGANISM
DATE 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
20-Aug-1994
ACCESSIONS S40295
REFERENCE S40295
#authors Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.;
Frosch, M.; Weisgerber, C.; Bitter-Suermann, D.;
Hiltschmann, N.
#submission submitted to the EMBL Data Library, January 1993
#description Primary structure of the murine monoclonal IgG2a antibody
mAb735 against '(2-8) polysialic acid. 2. Amino acid
sequence of the heavy (H-) chain Fd' region.
#accession S40295
#molecule_type protein
#residues 1-446 #label KLE
GENETICS
#map_position 12
KEYWORDS disulfide bond; glycoprotein; immunoglobulin; pyroglutamic
acid
FEATURE
1-446 #product Ig gamma-2a chain #status experimental #label
MAT\
1-117 #domain V-D-J region #label VDJ\
118-446 #domain C region #label CHR\
118-214 #domain C1 region #label CH1\
215-230 #region hinge\
231-340 #domain C2 region #label CH2\
341-446 #domain C3 region #label CH3\
1 #modified_site pyrrolidone carboxylic acid (Gln) #status
```

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```

                experimental\
22-96,144-199, #disulfide bonds #status predicted\
261-321,367-425 #disulfide_bonds interchange (to light chain) #status
132 predicted\
224,227,229 #disulfide bonds interchange #status predicted\
297 #binding_site carbohydrate (Asn) (covalent) #status
                experimental
SUMMARY #length 446 #molecular-weight 49108 #checksum 6356
Query Match 52.8%; Score 1832; DB 12; Length 446;
Best local Similarity 57.0%; Pred. No. 6.4le-254;
Matches 261; Conservative 83; Mismatches 100; Indels 14; Gaps 6;
Db 1 qclqgqgelrvrgasvkiackasgytfdyly-hwtkrpgqeglewlgwypgsntk 59
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Qy 20 QVKLQWGGELQLQSETLSRTCVSGSGISGYVYWTWIRQTPEGRLEWIGHIYGNGATTN 79
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Db 60 ynekfkgtatltvdtsastaymqleatseadvfcatgqgk-----fa--mdywgqg 110
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Qy 80 YNPSIKSRVTISKTQKNOFFLNINSVTDADTAVYCYCARPRDCPTTICYGWVDWVWCGF 139
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Db 111 tevtvasakttapsvypapvcgdtgssvltlqclvkgvfpepvtltwnsglsesgvhtf 170
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Qy 140 DLVTVSASTKGPVFP LAPSSKSTSGCTAALGCLVWVDFPEPVTVSNNSGALTSVGHVTF 199
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Db 171 pavlqsd-lytlesavtvtsetwpsqitcnvahpasstkvdtkieprg-ptikpcppck 228
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Qy 200 PAVLQSGSLYSLSVWVTPSSSLGTQYICNVNHNKPSNTKVDKAEKPSCKDTHTCPCC- 258
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Db 229 cpapnllggpsvfifppkikdvlmislepivtcvvdvseddpgvldqslwfvnnvvltaq 288
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Qy 259 -PAPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVDVSHEDPEVKNVWYDGVGVHNNAK 317
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Db 289 tqthredynstlrvealpiqhdqmsqgkefkckvnnkdlpapieritiskpkgsravqv 348
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Qy 318 TQPREQYNSTRVSVLTVLHQDLWLNKGEYKCKVSNKALPAIEKTSKAKQPREQV 377
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Db 349 yvlpppeentkktltcmvtdfmpediyvewtngktelnykntepvldadgsyfms 408
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Qy 378 YTLPPSRDELTKNQVSLTCLVRGFYPSDIAVEWESNQGPENNYKTTPVLDSDGSFFLYS 437
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Db 409 klrvckknwvnsyscvvhgelnhhttkesfartpg 446
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::
Qy 438 KLTVDKSRHQQGVFSCVNHVALHNHYTKQSLSLSPG 475
    I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I:: I::I::I::I::

RESULT 9
ENTRY S01321 #type complete
TITLE Ig gamma-2b chain precursor - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change
23-Mar-1993
ACCESSIONS S01321
REFERENCE S01321
#authors de Haële, P.; Feys, V.; van de Voorde, A.; Molenans, F.;
Fiers, W.
#journal Eur. J. Biochem. (1988) 176:287-295
#title Expression in non-lymphoid cells of mouse recombinant
immunoglobulin directed against the tumour marker human
placental alkaline phosphatase.
#crose-references MUID:88329081
#accession S01321
#molecule_type mRNA
```

```
##residues 1-475 ##label DE1
##cross-references EMBL:X13188
##note this sequence was determined from the differentiated
gene
```

FEATURE

```

#domain signal sequence #label SIG\
1-19
#product Ig gamma-2b chain #label MAT
20-475
#length 475 #molecular-weight 51567 #checksum 4120
SUMMARY

```

Query Match	52.3%;	Score 1817;	DB 12;	Length 475;
Best Local Similarity	53.4%;	Pred. No. 1.34e-251;		
Matches	258;	Conservative 100;	Mismatches 110;	Indels 15; Gaps 8;

```

Db      1 mewiwiifilsgtagvqsgvalqqsgaelrpgasvklackasdytltsygi-swwkqr 59
      | :|||::: | ||| || | :| :| :| :|| :|| :||
Qy      1 MKHLWFFLLVLAAPRWVLSQVKLQMGEGGLQPSETLSRTCVSGSISGYVYVWTRQT 60

```

Db 60 tggqlewigeiypgsgnsyfnekfkgtaltvdksstaylhlsaltsedsavfca-gp 118
|:||||| | : : : | : : : | : : : | : |||:| | |
Qy 61 PGRGLEWIGHYNGATNYPNSLKSRVTISKDTSKNQFFLNLSVTDADTAVYVCARGP 120

Db 119 r-qvglplfg-y---waggtlvrtasaakttppsvyplapcgcdttgssvtlglclkvgyfp 173
| : : | | | | | | | | | | : : : : | | | | |
Qv 121 RPDCTICGGWVDVWGPGDLVTYSSASTKGPVFPLAPSKSTSGGTAAALGLAVKDVPF 180

Db 174 esvtvtwnsgs¹⁸ssvhtfpallqs-glytmsssvtvpstwpstqvtcsvahpassttv 232
|:|||||||:|:|||||||:|||||||:|||||||:|:|:|:|:|:
Qv 181 epvtvsnmgaltscgvtfpavioaggyslssvvtpssslgtotyicnnihkpsntkv 240

Db	233	dkklepsgtstinpccpckechkcapnleggsvfifppnikdvmlstltpkvtcvvv	232
		: :	
		:	
		:	
		:	
		:	
Qv	241	dkkaefpkscnkq--htcspcc-----pafetlfgpsvfifppkptimtsrtpetvcvv	243

Db 293 dvaeddpdvqswfvnnvevltatqtqhredynstirvvaalpighqdwmsgkfckvm 352
||| :||: |: || | : |||| ||| : |||: |||: |||:
Qv 294 dvshfndpevkwnyvdgfevhnaaktprfeevnstyrvvsvltvlhodwtlncgvkcvks 353

```

Db 353 nkdlpapiertiskikigivrapqvylsppeqlrkdvaltcavgfpedisvewtsn 412
    || |||||:|||| || ||| |: :|||:||||| || |||:|||| ||
Ov 354 NKAIPIEKTTSKAGKQPREPQVYTPSPDFETKNOVSICTAKCFYPSDIAREWFSN 413

```

Db 413 ghteenykdtpvldsdgsyfysklnmktsekwtksfscnvrheglknnylkkttiers 472
 | : ||||| :|||||:::|| : |||| : ||||| ::|| : |||
O: 414 cagcnvvvtetrrrv denccst vctt mrtgcsdwocntcecmrta luvuvovzsete 473

Db 473 pgk 475
|||
O: 474 pgk 476

RESULT 10

TITLE	ORGANISM
Ig gamma-2b chain - mouse	#formal_name Mus musculus #common_name house mouse
25-Feb-1994	#sequence_revision 25-Feb-1994 #text_change 25-Feb-1994

ACCESSIONS	REFERENCE	#authors
S25057	S25057	Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, S.

```

#submission submitted to the EMBL Data Library, July 1992
#description Production of a Tobacco mosaic virus (TMV) inactivating
neotop specific monoclonal antibody in Nicotiana tabacum.

```

```
##status      preliminary
##residues    1-474 ##label FIS
##cross-references EMBL:X67210
      #length 474 #molecular-weight 52069
SUMMARY
```

Query Match	51.6%	Score 1792;	DB 14;	Length 474;
Best Local Similarity	53.9%;	Pred. No. 9.89e-248;		
Matches	258;	Conservative 92;	Mismatches 113;	Indels 16;
				Gaps 6;

```
Db      5 wiflllsgtagvshsevqlqsgspelpnpgasvkmsckasytftityvm-hwkvktpggg 63
        |:|::: | |:| | | | |:| :: | |:: | |:: | |:: |
Qv      5 WFFLLLVAAPRVLSVKLQNGEGLLQPSSETLSRTCWVSGGSGISGYYYWTWIQTPTGRC 64
```

```
Db    64 lewlgv.inpnkgdgtkfnekfkgaatltsdkssntaymelsetdsedsavvyar----dy 119  
      ||||| | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
  
QV   65 LEWIGHIYNGAGATTNPNPSLKSRTVI SKDTSKNOFFLNINSVTADTAVFYCARGRPPDC 124
```

Db 120 d---yd-wfaywgggt.lvt vsaaaktppsvyplapgcgadt gssvtsqclvkgyfpeesvt 175
-- -- ||| ||||| : ||| ||||| : ||| : |||| | ||| : ||
Qv 125 TTTCYGGWVDVWGPD.LVT VSSASTKGP SVFPLAP SSKTSGGTAA LGCLVKDYFPPEPVT 184

```

Db 176 vtwnsgslssvhtlseqallqsglytmssasvtpssvtcpsahpaesttvdckl 235
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Ov 185 VSNNSGALTSGVHTFPVAVLOSSGLYSLSSVTVPSSSISCTOTYICNVNHPKSNKYDKKA 244

```

Db 236 epagpistinpoppckechkcpapnlegpsvfipppnikdvlmisitpkvtcvvdvse 295
 || : : ||| |||: |||||: ||| : ||| : |||||
 Qv 245 EPKSCDKT-HTCPGC-----PAPETLGPSTVFEPKPKDTLMTSTPFTCVVVVSH 297

```
Db      296 ddpdvqiswfvnnvevhtaqtgfhredynstirrvstlpqhqdwmagkefckvnnkdl 355
        :|:|::|:| | | | :|:| | | | | :|:|:|:|:|:|:| |
Ov      298 fndprvkewvntvgvfnhnaakmpdpeovnstyrvsvltvlhoowlnckevkcvcvknkal 357
```

```
Db      356 pspiertiskiglvrapqvylpppaedlkrkdvslctlvqfnpdisvewtsnghte 415
       :|:||:||||| | ||||| :|:||:||:||||| :|:||:||:||||| :|:||:||:|||||
Ov     358 PADPTEKTTSKAKCGPPQVVTI DPSPETTKNAVSTCIUKCEYPSNTAVWFESNCPDE 417
```

```
Db      416 enykdtapvldsgsyfiysklnmktkswekdtsfcsvrheglknvyllkttisrepgk 474
          :||| |:|||||||:::||| : |||: |||: |::| ||||
Qv      418 NNKYTTDDVVI DNDGCSFEI VSKI TVYWK SPWOCNIVT SCSSIMHEAI HNUVTOKSI SI SDCK 476
```

RESULT 11

TITLE	ORGANISM	ig gamma-3 chain C region (allotype G3m(b)) - human
DATE		#formal name Homo sapiens #common name man
	28-Dec-1987	#sequence_revision 28-Dec-1987 #text_change 20, 5, - 1003

ACCESSIONS	A23511
REFERENCE	A23511
#authors	Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc,

#journal Nucleic Acids Res. (1986) 14:1779-1789
#title Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: comparison with the other human

```
#cross-references MUID:86148507
#accession A23511
#molecule_type DNA
```

GENETICS	
#gene	GDB:ICHG3
#map_position	14q32.33

* RESULT 14

```
ENTRY      PT0207      #type complete
TITLE      Ig gamma chain C region - chimpanzee
ORGANISM   #formal_name Pan troglodytes #common_name chimpanzee
DATE       23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change
12-Apr-1995
ACCESSIONS PT0207
REFERENCE   PT0207
#authors   Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
#journal   Mol. Immunol. (1991) 28:319-322
#title     Nucleotide sequence of chimpanzee Fc and hinge regions.
#cross-references MUID:91287716
#accession PT0207
#molecule_type mRNA
#residues  1-234 #label EHR
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
SUMMARY      #length 234 #molecular-weight 26330 #checksum 6128

Query Match      48.3%; Score 1677; DB 5; Length 234;
Best Local Similarity 98.3%; Pred. No. 5.82e-230;
Matches 230; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1  entkvdkvpekcadtcttccpaapellgqpsvflfppkpkdtmlsrtpetvcvvdv 60
Qy 236  SNTKVKKAEPKSKDKTCTPCPCAPPELLGQPSVFLFPPKPKDTLMISRTPEVTCVVVDV 295

Db 61  shedpevfwnydvgevhnaaktpraeqynstyrsvvltvlhqdlnqgkcykcvnsk 120
Qy 296  SHEDPEVFENWYDVGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDLNKGREYKCVSNK 355

Db 121 alpaplektiskakgprepqwtlpperdeltnqvaltclvkgyfpdiavewessq 180
Qy 356  ALPAPLEKTIKAKGPREPQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVENSQ 415

Db 181 pennykttppvldsgsflysklvtkdrwqgnvfscsvmhealnhytqks 234
Qy 416  PENNYKTTPPVLDSGSFELYSLKLTVDKSRQQGVFSCSVWHEALNHNHYTQKS 469

RESULT 15
ENTRY      GHRB      #type complete
TITLE      Ig gamma chain C region - rabbit
ORGANISM   #formal_name Oryctolagus cuniculus #common_name domestic
rabbit
DATE       #sequence_revision 15-Nov-1984 #text_change 04-Nov-1994
ACCESSIONS A91749; A90290; A93928; A90245; A94416; A02161
REFERENCE   A91749
#authors   Bernslein, K.E.; Alexander, C.B.; Mage, R.G.
#journal   Immunogenetics (1983) 18:387-397
#title     Nucleotide sequence of a rabbit IgG heavy chain from the
recombinant F-I haplotype.
#cross-references MUID:84030930
#accession A91749
#molecule_type mRNA
#residues  1-323 #label BER
#note      this sequence has the di2 allotypic marker, 104-Thr, and
the e14 marker, 185-Thr

REFERENCE   A90290
#authors   Pratt, D.M.; Mole, L.E.
#journal   Biochem. J. (1975) 151:337-349
#title     Sequence studies on the constant region of the Fd sections of
rabbit immunoglobulin G of different allotype.
#cross-references MUID:76135469
#accession A90290
```

```
#molecule_type protein
#residues  1-47, 'E', 49-71, 'PV', 72-128 #label PRA
REFERENCE   A93928
#authors   Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight,
K.L.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1982) 79:6018-6022
#title     Heavy chain genes of rabbit IgG; isolation of a cDNA encoding
gamma heavy chain and identification of two genomic C-gamma
genes.
#cross-references MUID:83299917
#accession A93928
#molecule_type mRNA
#residues  88-103, 'W', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266
#label MAR
#note      this sequence has the d11 allotypic marker, 104-Met, and
the e15 allotypic marker, 185-Ala

REFERENCE   A90245
#authors   Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
#journal   Biochem. J. (1970) 116:249-259
#title     Sequence studies of the Fd section of the heavy chain of
rabbit immunoglobulin G.
#cross-references MUID:70110015
#accession A90245
#molecule_type protein
#residues  132-143, 'E', 145-161 #label FRU
#label FRU
REFERENCE   A94416
#authors   Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
#book      in Gamma Globulins, Nobel Symp. 3, Killander, J., ed.,
pp.109-127, Almqvist and Wiksell, Stockholm, 1967
#accession A94416
#molecule_type protein
#residues  129-131;155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D',
202-217, 'E', 219-232, 'Q', 234-245, 'D', 247-255, 'C',
257-259, 'D', 261-265, 'D', 267-279, 'W', 281-283, 'S',
285-322 #label HIL
#note      this has the e15 allotypic marker, 185-Ala
#superfamily immunoglobulin C region; immunoglobulin homology

CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
FEATURE
20-82      #domain immunoglobulin homology #label IGG1\
130-199    #domain immunoglobulin homology #label IGG2\
236-303    #domain immunoglobulin homology #label IGG3
SUMMARY    #length 323 #molecular-weight 35404 #checksum 1467

Query Match      48.1%; Score 1669; DB 2; Length 323;
Best Local Similarity 70.0%; Pred. No. 9.99e-229;
Matches 229; Conservative 46; Mismatches 45; Indels 7; Gaps 3;

Db 4  kapsvflapccgdtpsvtlglvkylpepvtvtnsgtltngvtfpsvqssqly 63
Qy 150  KGSVEFLAPSSKSTSGGTAALGLVKRDYFPEPVTVSNWNSGALTSGVHTFPVAVQSSGLY 209

Db 64  slsrsvsvtss---qpvtcnvahpatntkdvktvapstcsp-ctcp---pellgppsv 116
Qy 210  SLSSSVTVPSSSLGTQTYICNVNHPKSNTRYDKAEKPKCDKTHTCPCPAPELLGGPSV 269

Db 117  fifppkpkdtlmisrtpetvcvvdvsqddpevqftwyinneqvrtarplreqgfnsati 176
Qy 270  FLFPPPKPDTLMSRTPETVCVVVDVSHEDPEVFENWYVDGVEVHNNAKTPREEQYNSTY 329

Db 177  rwvatipthqdlirgkfeckvnhkalpapiaktiskargplekvymgppreals 236
Qy 330  RVSVSLTVLHQDLNKGREYKCVSNKALPAPIEKTISKAKGPREPQVTVLPPSRDELTK 389

Db 237  rsvaltcmingypsdisvewekngkaednykttpavldsdgsflylnklsvptsewqrg 296
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Dec 17 15:06

US-08-487-550-4 rpr

19

Qy 390 NQVSLTCLVRGFTPSDIAVENESGQPNNTKTPPVLDSDGSEF LYSKLTVDKSRWQOG 449

Db 297 dvftcevmhealhnhytqkqksisrpgk 323

Qy 450 NVFSCVMHEALHNHYTQKSLSPGK 476

Search completed: Tue Dec 17 15:20:21 1996
Job time : 63 secs.

(TM)

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MPsrch pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 15:20:37 1996; MasPar time 11.07 Seconds
747.227 Million cell updates/sec

Tabular output not generated.

Title: >US-08-487-550-4

Description: (1-476) from US08487550.ppt

Perfect Score: 3472

Sequence: 1 MKHLWFFLLVLAAPRWLSQ.....MHEALHNHYTQKSLSLSPGK 476

Scoring table: PAM 150

Gap 11

Searched: 49340 seqs, 17385503 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

```
Database:      swiss-prot32
               1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
               8:part8 9:part9
```

Statistics: Mean 48.362; Variance 81.154; scale 0.596

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description	Pred. No.		
		Match	%					C	R	
1	2339	67.4		330	3	GC1_HUMAN	IG GAMMA-1	CHAIN C	R	0.00e+00
2	2133	61.4		326	3	GC2_HUMAN	IG GAMMA-2	CHAIN C	R	0.00e+00
3	2133	61.4		327	3	GC4_HUMAN	IG GAMMA-4	CHAIN C	R	0.00e+00
4	1669	48.1		323	3	GC RABIT	IG GAMMA CHAIN C	REGI		0.00e+00
5	1616	46.5		329	3	GC2_CAVPO	IG GAMMA-2	CHAIN C	R	0.00e+00
6	1590	45.8		290	3	GC3_HUMAN	IG GAMMA-3	CHAIN C	R	0.00e+00
7	1582	45.6		326	3	GC1_RAT	IG GAMMA-1	CHAIN C	R	0.00e+00
8	1584	45.6		329	3	GC3_MOUSE	IG GAMMA-3	CHAIN C	R	0.00e+00
9	1570	45.2		398	3	GC3M_MOUSE	IG GAMMA-3	CHAIN C	R	0.00e+00
10	1566	45.1		324	3	GC1_MOUSE	IG GAMMA-1	CHAIN C	R	0.00e+00
11	1559	44.9		329	3	GC C RAT	IG GAMMA-2C	CHAIN C	R	0.00e+00
12	1559	44.9		393	3	GC1M_MOUSE	IG GAMMA-1	CHAIN C	R	0.00e+00
13	1549	44.6		330	3	GC4A_MOUSE	IG GAMMA-2A	CHAIN C	R	0.00e+00

RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE; 77070269.
RA PONTING L. H., HILSCHMANN N. J.
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1571-1604 (1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE; 83289131.
RA SCHMIDT W.E., JUNG H.-D., PALM W., HILSCHMANN N. J.
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 364:713-747 (1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE; 71064027.
RA GALL W.E., EDELMAN G.M. J.
RL BIOCHEMISTRY 9:3188-3196 (1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE; 77070267.
RA DREKER L., SCHWARZ J., REICHEL W., HILSCHMANN N. J.
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1515-1540 (1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE; 81208100.
RA DEISENHOFER J. J.
RL BIOCHEMISTRY 20:2361-2370 (1981).
CC -!- NIE HAS THE GIM(17) ALLOTYPE MARKER, 97-K, & THE GIM(1) MARKERS,
239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM
(NON-1) MARKERS.
CC -!- NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.
CC -!- EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155, 166, 177,
195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.
CC -!- KOL ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 198,267&272.
DR EMBL; J00228; J00228.
DR PIR; A02146; GHU.
DR PDB; 1FC1; 15-JUL-92.
DR PDB; 1FC2; 15-JUL-92.
DR PDB; 147100; 11TH EDITION.
DR PROSITE; P500290; IG MHC.
KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN; 3D-STRUCTURE.
FT NON TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 223 CH2.
FT DOMAIN 224 330 CH3.
FT DISULFID 27 83
FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT CARBOHYD 180 180
FT VARIANT 97 97 K -> R (IN GIM(3) MARKER).
FT VARIANT 239 239 D -> E (IN GIM(NON-1) MARKER).
FT VARIANT 241 241 L -> M (IN GIM(NON-1) MARKER).
FT MOD RES 330 330 REMOVED POST-TRANSLATIONALLY.
FT STRAND 123 126
FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 148
FT STRAND 158 162
FT TURN 163 164
FT STRAND 165 166
FT STRAND 175 178
FT STRAND 183 190

FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 206
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 240
FT TURN 241 242
FT STRAND 245 256
FT STRAND 260 266
FT TURN 267 268
FT STRAND 269 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 312
FT TURN 313 314
FT TURN 316 317.
FT STRAND 320 324
SQ SEQUENCE 330 AA; 36106 MW; 642285 CN;

Query Match 67.4%; Score 2339; DB 3; Length 330;
Best Local Similarity 99.7%; Pred. No. 0.00e+00;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 aetkqsvfiapssksetgtaalgclvkdyfpepvtvswngaltsgvhtfpavlgss 60
|||||
Qy 147 ASTKGSVFPEPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPVAVLQSS 206
|||||
Db 61 glyelssvvtvpsslgctqyicnnhkpstkvdkkvepkacdtkhtccppcapellgg 120
|||||
Qy 207 GLYSLSVVTVPPSSSLGTQTYICNVNHRPSNTKYDKKAEPKSCDKTHTCPPCPAPPELLGG 266
|||||
Db 121 pavflfpkpkdltmiersptevtcvvvdvshdedpevkfnwydvgevhnaaktpreeqyn 180
|||||
Qy 267 PSVFLFPKPKDITMISRTPEVTCVVVDVSHEDPEVKFNWYDVGEVHNAKTKPREEQYN 326
|||||
Db 181 atyrvsvltvlhqdwlngckeyckvsnkalpapietkiskakgqpreqvylpparde 240
|||||
Qy 327 STYRVSVLTVLHGDWLNCKEYCKVSNKALPAPIETKISKAKGQPREQVYTIIPSRDE 386
|||||
Db 241 ltknqvltclvkfypsdiaveesngqpennykttppvldsdgdflyekltvdkerw 300
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Qy 387 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSLKLTVDKSRW 446
|||||
Db 301 cggnvfscsvmhahhnytketelslepk 330
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Qy 447 QCGNVFSCSVMHAAHNYTKQKSLSPGK 476
|||||

RESULT 2
ID GC2 HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE IG GAMMA-2 CHAIN C REGION.
GN IGHG2.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.

1	SEQUENCE FROM N.A.	
2	MEDLINE; 82197621.	
3	ELLISON J.W., HOOD L.E.;	
4	PROC. NATL. ACAD. SCI. U.S.A. 79:1984-1988(1982).	
5		
6	SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).	
7	MEDLINE; 81007873.	
8	WANG A.-C., TUNG E., FUDENBERG H.H.;	
9	J. IMMUNOL. 125:1048-1054(1980).	
10		
11	SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).	
12	MEDLINE; 80001357.	
13	CONNELL G.E., PARR D.M., HOFMANN T.;	
14	CAN. J. BIOCHEM. 57:758-767(1979).	
15		
16	SEQUENCE OF 238-275 (ZIE).	
17	MEDLINE; 80114419.	
18	HOFMANN T., PARR D.M.;	
19	MOL. IMMUNOL. 16:923-925(1979).	
20		
21	ZIE, REVISIONS TO 25; 59; 60 AND 264-268.	
22	HOFMANN T., PARR D.M.;	
23	SUBMITTED (MAR-1980) TO THE PIR DATA BANK.	
24		
25	SEQUENCE OF 1-121 (DOT).	
26	STOPPINI M., BELLOTTI V., NEGRI A., MERLINI G., GARVER F., FERRI G.;	
27	EUR. J. BIOCHEM. 0:0-0(1995).	
28		
29	MYELOMA PROTEIN SA, DISULFIDE BONDS.	
30	MEDLINE; 72033500.	
31	MILSTEIN C., FRANGIONE B.;	
32	BIOCHEM. J. 121:217-225(1971).	
33		
34	SA, DISULFIDE BONDS.	
35	MEDLINE; 69064124.	
36	FRANGIONE B., MILSTEIN C., PINK J.R.L.;	
37	NATURE 221:145-148(1969).	
38	EMBL; V00554; V00554.	
39	PIR; A02148; G2HU.	
40	HSSP; P01857; 1BBJ.	
41	MIM; 147110; 11TH EDITION.	
42	PROSITE; PS00290; IG MHC.	
43	IMMUNOGLOBULIN C REGION.	
44	NON TER 1 1	
45	DOMAIN 1 98	CHI.
46	DOMAIN 99 110	HINGE.
47	DOMAIN 111 219	CH2.
48	DOMAIN 220 326	CH3.
49	DISULFID 14 14	INTERCHAIN (WITH A LIGHT CHAIN).
50	DISULFID 27 83	
51	DISULFID 102 102	INTERCHAIN (WITH A HEAVY CHAIN).
52	DISULFID 103 103	INTERCHAIN (WITH A HEAVY CHAIN).
53	DISULFID 106 106	INTERCHAIN (WITH A HEAVY CHAIN).
54	DISULFID 109 109	INTERCHAIN (WITH A HEAVY CHAIN).
55	DISULFID 140 200	
56	DISULFID 246 304	
57	VARIANT 60 60	
58	SITE 156 156	
59	MOD RES 326 326	
60	SEQUENCE 326 AA; 35884 MW; 629390 CN;	
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Query Match 61.4%; Score 2133; DB 3; Length 326;
Best Local Similarity 90.9%; Pred. No. 0.00e+00;

Matches	300;	Conservative	15;	Mismatches	11;	Indels	4;	Gaps
Db	1	astkqpsvfplapcarstseestaalqclvkdyfpepvtvsmnagaltsqyhtfpavilqas	60					
Qy	147	ASTKQPSVFP LAPSKSTSGCTAALGCLVKDYFPEPVTVSMNSGALTSQYHTFPVILQSS	206					
Db	61	glyslsvvtvpasnfqctytcnvdhpkstnkvdktverkcc--ve-ccpcappv-ag	116					
Qy	207	GLYSLSVVTVPSSSLTQTYYICNVNHPKSNTKVDKKAEPKSCDKTHTCPCPAPELLGG	266					
Db	117	psvfifpkipkdtlmiirstpevtcvvdshedpevgfnwyvdgvevhnaktkpreeqfn	176					
Qy	267	PSVFIFFPKPKDTLMIIRSTPEVTCVVVDVSDHEPEVKFNWYVDGVEVHNAKTKREQYN	326					
Db	177	stfrvsvltvvhqdwlnqkeyckvsnkglpapiektsiktqkqprepyvtlppere	236					
Qy	327	STRVSVSVLTVLHQDWLNQKEYCKVSNKALPAPIKTISKAKQPREPYVTLPPSRDE	386					
Db	237	mtknqvalctlvkqgfypsiadiaveangqpennyktppmlsdsgofflyakltcvdkarw	296					
Qy	387	LTKNQVSLTCLVKRGFYPDSIAVESNGQPENNYKTPPVILDSGSGFFLYSKLTVDKSRM	446					
Db	297	qqgnvfscsmhealhnhytqkelslspgk	326					
Qy	447	QQGNVFCSCVMHEALHNHYTKQSLSPGK	476					
RESULT	3							
ID	GC4 HUMAN	STANDARD;	PRT;	327 AA.				
AC	P01861;							
DT	21-JUL-1986 (REL. 01, CREATED)							
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)							
DT	01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)							
DE	IG GAMMA-4 CHAIN C REGION.							
GN	IGH4.							
OS	HOMO SAPIENS (HUMAN)							
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;							
OC	EUTHERIA; PRIMATES.							
RN	[1]							
RX	SEQUENCE FROM N.A.							
RP	MEDLINE; 83157104.							
RA	ELLISON J.W., BUXBAUM J.N., HOOD L.E.;							
RL	DNA 1:11-18(1981).							
RL	[2]							
RX	SEQUENCE OF 1-30 AND 81-326.							
RP	MEDLINE; 70207560.							
RA	PINK J.R.L., BUTTORY S.H., DE VRIES G.M., MILLSTEIN C.;							
RL	BIOCHEM. J. 117:33-47(1970).							
DR	PIR; A02150; G4HU.							
DR	HSP; P01857; IBBU.							
DR	MIM; 147130; 11TH EDITION.							
DR	PROSITE; PS00290; IG MHC.							
KW	IMMUNOGLOBULIN C REGION.							
FT	NON TER 1 1							
FT	DOMAIN 1 98							
FT	DOMAIN 99 110							
FT	DOMAIN 111 220							
FT	DOMAIN 221 327							
FT	DISULFID 14 14							
FT	DISULFID 27 83							
FT	DISULFID 106 106							
FT	DISULFID 109 109							
FT	DISULFID 141 201							
FT	DISULFID 247 305							


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DE IG GAMMA-2 CHAIN C REGION.
OS CAVIA PORCELLUS (GUINEA PIC).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN (1)
RP SEQUENCE OF 1-3.
RA TRISCHMANN T.M.;
RRL SUBMITTED (APR-1975) TO THE PIR DATA BANK.
RN (2)
RP SEQUENCE OF 4-68.
RX MEDLINE; 71058471.
RX BIRSHTEIN B.K., RUSSAIN Q.Z., CEBRA J.J.;
RRL BIOCHEMISTRY 10:18-25(1971).
RN (3)
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE; 71058486.
RA TURNER K.J., CEBRA J.J.;
RRL BIOCHEMISTRY 10:9-17(1971).
RN (4)
RP SEQUENCE OF 134-226.
RX MEDLINE; 75036072.
RA TRACEY D.E., CEBRA J.J.;
RRL BIOCHEMISTRY 13:4796-4803(1974).
RN (5)
RP SEQUENCE OF 227-311.
RX MEDLINE; 75036073.
RA TRISCHMANN T.M., CEBRA J.J.;
RRL BIOCHEMISTRY 13:4804-4811(1974).
RN (6)
RP DISULFIDE BONDS.
RX MEDLINE; 71058474.
RA OLIVEIRA B., LAMM M.E.;
RRL BIOCHEMISTRY 10:26-31(1971).
CC -1- THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN 13 INBRED
CC GUINEA PIGS.
DR PIR; A02151; G2GP.
DR HSP; P01857; IFC1.
DR PROSITE; PS00290; IG MHC.
KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN.
FT NON_TER 1 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 630420 CN;

Query Match 46.5%; Score 1616; DB 3; Length 329;
Best Local Similarity 70.1%; Pred.No. 0.00e+00;
Matches 234; Conservative 39; Mismatches 52; Indels 9; Gaps 6;

Db 1 eartkavfplaaecvtdsgsmntlqclvkgyfpevtykvngaltsgvhtfpavlqs 60
|||:|||||:| |||:||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 146 SASTKGPSVTFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNMGSALTSGVHTFPAVLQS 205

Db 61 -glyaltamvtvpsq--kat--cnvahpasatkvdtkepirtzpbpbctcpcpppen 115
|||||:||||| | |||:||||| ||:| ||| |||:|
Qy 206 SGLYSLSVTVTPSSSLGTTQYICNVNHRKPSNTKVDKKAEP-KSCDKTH-TCPPCPAPEL 263

Db 116 lgvavfifppkpkdklmisltprvtcvvdsqdepevqftwfdvdkpvgnaetkprve 175
|||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY	264	LGCPSVFLFPKPKDTLMI	SRTEPVT	CVVDVSDHEDPEVKNWYDGVGVENAKTKPRE	323	
Db	176	qynttfvresvipchqdwr	gkfkfkyknkalpapi	ektktgkgrmpdytlpps	235	
		: :	: :	: :	: :	
QY	324	QYNSTYRWSVLT	HLQDWLNGKCYKCV	SNKALPALPTEKTISKAGQPREPQVYTLPPS	383	
Db	236	rdelekkevvtclinf	fpadhvewasrvp	vaekeykntpi	edsgsflyekltv	295
		: :	: :	: :	: :	
QY	384	RDLETKNOVSLTCL	VKGFYPSDIA	EVESNGQP--ENNYTTPPVL	SDGSFFLYSKLTV	441
Db	296	kdsawdgvtv	tcsvmheal	hnhvtgkai	rsqg	329
		: :	: :	: :	: :	
QY	442	DKSRNQGNV	FCFSVMHEAL	HNHYTKQSL	SLSPG	475
RESULT	6					
ID	GC3 HUMAN	STANDARD;	PRT;	290 AA.		
AC	P01860;					
DT	21-JUL-1986	(REL. 01, CREATED)				
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)				
DT	01-FEB-1991	(REL. 17, LAST ANNOTATION UPDATE)				
DE	IG	GAMMA-3 CHAIN C REGION (HEAVY CHAIN DISEASE PROTEIN) (HDC).				
DE	IGH3.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC	EUTHERIA; PRIMATES.					
RC	[1]					
RP	SEQUENCE (DISEASE PROTEIN WIS).					
RP	MEDLINE; 81021548.					
RA	FRANGIONE B., ROSENWASSER E., PRELLI F., FRANKLIN E.C.;					
RL	BIOCHEMISTRY 19:4304-4308 (1980).					
[2]						
RP	NORMAL GAMMA-3 CHAINS, REVISIONS TO 12-97 OF PROTEIN WIS.					
RX	MEDLINE; 77118561.					
RX	MICHAELSEN T.E., FRANGIONE B., FRANKLIN E.C.;					
RL	J. BIOL. CHEM. 252:883-889 (1977).					
[3]						
RP	DISEASE PROTEIN ZUC, REVISIONS TO 59-289 OF PROTEIN WIS.					
RP	MEDLINE; 77021516.					
RX	WOLFSTEIN-TODEL C., FRANGIONE B., PRELLI F., FRANKLIN E.C.;					
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 71:907-914 (1976).					
[4]						
RP	SEQUENCE FROM N.A. (DISEASE PROTEIN OMW).					
RX	MEDLINE; 82247835.					
RX	ALEXANDER A., STEINMETZ M., BARRITAU D., FRANGIONE B.,					
RA	FRANKLIN E.C., HOOD L., BUXBAUM J.N.;					
RL	PROC. NATL. ACAD. SCI. U.S.A. 79:3260-3264 (1982).					
CC	-1- THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.					
CC	-1- THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE REF. 2.					
CC	-1- DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION AND ALL OF THE CHI REGION.					
CC	-1- DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL GAMMA-3 HEAVY CHAINS.					
CC	-1- DISEASE PROTEIN OMW MAY REPRESENT AN ALLELIC FORM OR ANOTHER GAMMA CHAIN SUBCLAS.					
CC	-1- THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE SEGMENT (12-28).					
CC	-1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11 NORMALLY PRESENT IN THE HINGE REGION.					
CC	EMBL; J00231; J00231.					
DR	PIR; A02149; G3HUW1.					

DR HSP; P01857; IFC1.
 DR MIM; 147120; 11TH EDITION.
 DR PROSITE; PS00290; IG MHC.
 KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN.

FT DOMAIN 12 73 HINGE.
 FT DOMAIN 74 183 CH2.
 FT DOMAIN 184 289 CH3.
 FT REPEAT 29 43
 FT REPEAT 44 58
 FT REPEAT 59 73
 FT MOD RES 1 1
 FT CARBOHYD 6 6
 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 7 7 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 24 24 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 27 27 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 33 33 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 39 39 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 42 42 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 48 48 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 54 54 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 57 57 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 63 63 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 69 69 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT DISULFID 72 72 INTERCHAIN (WITH HEAVY CHAIN DIMER).
 FT CARBOHYD 140 140
 FT MOD RES 290 290
 FT VARIANT 126 127
 FT VARIANT 134 134
 FT VARIANT 139 139
 FT VARIANT 182 182
 FT VARIANT 227 227
 FT VARIANT 227 227
 FT VARIANT 279 279
 FT VARIANT 279 279
 SQ SEQUENCE 290 AA; 32331 MW; 485009 CN;

REMOVED POST-TRANSLATIONALLY.

QV -> EB (IN ZUC).

P -> L (IN OHM).

F -> Y (IN OHM).

T -> A (IN OHM).

S -> N (IN OHM).

MISSING (IN ZUC).

F -> Y (IN OHM).

Query Match 45.8%; Score 1590; DB 3; Length 290;

Best Local Similarity 90.1%; Pred. No. 0.00e+00;

Matches 210; Conservative 17; Mismatches 6; Indels 0; Gaps 0;

Db 58 pepscdtpppcpapellgpgsvflfppkpkdtlmisrtpevtcvvvdshedpevg 117
 :||||| || |||||

Qy 244 AEPKSCDTHTCPPCAPPELLGGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 303

Db 118 fkyvdgqvhnahtkpreqgnstfrvsvltlqgnwldgkeyckvknalpapiek 177
 :||||| || |||||

Qy 304 FNWYDGVGVNNAHTKPREQYNSTRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEK 363

Db 178 tiaktkgppqvyltppsreemtknqsltlvkgfypsdiaveasgqpenyntt 237
 :||||| || |||||

Qy 364 TISKAGQPREPQVYLTSPRSDELTKNQSLTLVKGFPYSDIAVESNGQPENNYKT 423

Db 238 pmlsdsgfflyskltvdksrwaggnifscvsmhealnhrftqslslepok 290
 :||||| || |||||

Qy 424 PPVLDSDGSFFLYSKLTVDKSRMQGNVFCVSMHEALHNHYTQKSLSLSPGK 476

RESULT 7
 ID GC1 RAT STANDARD; PRT; 326 AA.
 AC P20759;

DT 01-FEB-1991 (REL. 17, CREATED)

DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)

DE IG GAMMA-1 CHAIN C REGION.

OS RATTUS NORVEGICUS (RAT).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.

RM [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 89232738.

RA BRUEGGEMANN M.;

RL GENE 74:473-482 (1988).

DR PIR; PS0017; PS0017.

DR HSP; P01857; IFC1.

DR PROSITE; PS00290; IG MHC.

KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN.

FT NON TER 1 1

FT DOMAIN 1 97 CHI.

FT DOMAIN 98 112 HINGE.

FT DOMAIN 113 219 CH2.

FT DOMAIN 220 326 CH3.

FT DISULFID 27 82

FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 140 200

FT DISULFID 246 304

FT CARBOHYD 176

POTENTIAL.

SQ SEQUENCE 326 AA; 35946 MW; 630958 CN;

Query Match 45.8%; Score 1582; DB 3; Length 326;

Best Local Similarity 63.3%; Pred. No. 0.00e+00;

Matches 209; Conservative 60; Mismatches 57; Indels 4; Gaps 4;

Db 1 aettapsvylapgtalkenavtlgclvkgypvvtvtnsgalagshvhtfpavlg- 59
 :||||| || |||||

Qy 147 ASTKGSVFPLAPSSKSTSGCTAALGCLVKDYFPEPTVWSNNSGALTSGVHTFPAVLQSS 206

Db 60 glyltlsvtvpsetwpcvtcnvaphasstkvdkiiprncg-gd-ckpcictgs-ev 116
 :||||| |||||

Qy 207 GLYSLSVWVTPSSSLGTQTYICNVNHRPSNTKYDKRAEPKSCDKTHTCPCPAPPELLGG 266

Db 117 asvfiipkpkdvlititltpkvtcvvvdisdqddpevhfswfvdvdehtaqtrpseeqfn 176
 :||||| |||||

Qy 267 PSVLEPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTRPEQYN 326

Db 177 strfsvselphldwlngtrfcrckvtsaafpspietkiskpegtrqphvymptkee 236
 :||||| |||||

Qy 327 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREQVYLTSPSRDE 386

Db 237 mtqnevsitcmvkgfypdiyveqmgqgqenykntpmtmdtdqsyflysklnvkkew 296
 :||||| |||||

Qy 387 LTKNQSLFCLVKGFPSDIAVESNGQPENNYKTTPPVLDSDGSSEFFLYSKLTVDKSRW 446

Db 297 cagntfcsvileghlnhhtekslshpgk 326
 :||||| |||||

Qy 447 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 476

RESULT 8
 ID GC3 MOUSE STANDARD; PRT; 329 AA.
 AC P22436;

DT 01-AUG-1991 (REL. 19, CREATED)

DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)

DT 01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)

DE IG GAMMA-3 CHAIN C REGION, SECRETED FORM.

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

Db	180	gtfrvsvltlhiqdmegskfckcnmkdlpslektlekrpgkarktpvylppppreq	239
QY	327	styrsvsvltvlhqdlwlngckeykcnkalpdltektiskakqppepovvltppsrde	386
Db	240	msknksvltcmvtsfypasisevwerneleqdykntlpvlddeseflysklsavdtdsw	299
QY	387	ltnqsvsltlcmkgfypsdiaevewscngcpennyktpvpvldsdgcsfflysklvtvdksrw	446
Db	300	mrgdytcsvvhcaalnhhtknlarspgk	329
QY	447	qogvsvscvnhcaalnhhytorkslslspgk	476

RESULT	12	GCIM MOUSE	STANDARD;	PRT;	393 AA.
ID	AC	P01869;			
DT	DT	21-JUL-1986 (REL. 01, CREATED)			
DT	DT	01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)			
DT	DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)			
DE	DE	IG GAMMA-1 CHAIN C REGION, MEMBRANE-BOUND FORM.			
OS	OS	MUS MUSCULUS (MOUSE).			
OC	OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA.			
RN	RN	[1]			
RX	RX	SEQUENCE FROM N. A.			
RA	RA	MEDLINE; 80045036.			
RA	RA	HONJO T., OBATA M., YAMAWAKI-KATAOKA Y., KATAOKA T., KAWAKAMI TAKAHASHI N., MANO Y.;			
RL	RL	CELL 18:559-568 (1979).			
RN	RN	[2]			
RP	RP	SEQUENCE OF 323-393 FROM N. A.			
RX	RX	MEDLINE; 82197626.			
RA	RA	TYLER B. M., COWMAN A. F., GERONDAKIS S. D., ADAMS J. M., BERNARD			
RL	RL	PROC. NATL. ACAD. SCI. U.S.A. 79:2008-2012 (1982).			
RN	RN	[3]			
RP	RP	SEQUENCE OF 323-366 FROM N. A.			
RX	RX	MEDLINE; 82115295.			
RA	RA	ROGERS J., CHOI E., SOUZA L., CARTER C., WORD C. J., KUEHL M.,			
RL	RL	EISENBERG D., WALL R.;			
RL	RL	CELL 26:19-27 (1981).			
RN	RN	[4]			
RP	RP	SEQUENCE OF 1-44 FROM N. A.			
RX	RX	MEDLINE; 82222190.			
RA	RA	YAMAWAKI-KATAOKA Y., NAKAI S., MIYATA T., HONJO T.;			
RL	RL	PROC. NATL. ACAD. SCI. U.S.A. 79:2623-2627 (1982).			
CC	CC	-/- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO			
CC	CC	SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SE			
CC	CC	GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE ME			
CC	CC	BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, EN			
CC	CC	IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BC			
CC	CC	SEGMENT OF MU CHAINS.			
DR	DR	EMBL; V00793; V00793.			
DR	DR	PIR; B02159; GIMSM.			
DR	DR	HSSP; P01857; IBAF.			
DR	DR	PROSITE; PS00290; IG_MHC.			
KW	KW	IMMUNOGLOBULIN C REGION; ALTERNATIVE SPLICING; TRANSMEMBRANE; GLYCOPROTEIN.			
FT	FT	FT NON TER 1 1			
FT	FT	DOMAIN 1 97			CHI.
FT	FT	DOMAIN 98 110			HINGE.
FT	FT	DOMAIN 111 217			CH2.
FT	FT	DOMAIN 218 324			CH3.
FT	FT	DISULFID 27 82			
FT	FT	DISULFID 102 102			INTERCHAIN (WITH A LIGHT CHAIN).

FT	DLSLFD	104	104	INTERCHAIN (WITH A HEAVY CHAIN) .
FT	DLSLFD	107	107	INTERCHAIN (WITH A HEAVY CHAIN) .
FT	DLSLFD	109	109	INTERCHAIN (WITH A HEAVY CHAIN) .
FT	DLSLFD	138	198	
FT	CARBOHYD	174	174	
FT	DLSLFD	244	302	POTENTIAL.
FT	TRANSEM	340	357	CYTOSOLASMIC (POTENTIAL) .
FT	DOMAIN	358	393	
SQ	SEQUENCE	393 AA; 43386 MW; 88519 CN;		
	Query Match	44.%; Score 1559; DB 3; Length 393;		
	Best Local Similarity	62.0%; Pred. No. 0.00e+00;		
	Matches	204; Conservative 63; Mismatches 56; Indels 6; Gaps		
Db	1 aktppsvyplagsaaqtnemvtlclgkvygpvptvtwnsglsagvhcfavlgqd 60			
	: : : :			
Qy	147 ASTKGSPVFLAPSSKTSGGTAALGCLVKQYFPEPTVYSWNSGALTSGVHFPAPVLQS 206			
	: : : :			
Db	61 -lytlasavtvpssrpaetvtcncnhaasetkdkklivrdcg-ckpci-ctvpev--- 114			
	: : : :			
Qy	207 GLISLSVVTVPSSSLGCTGYICNVNHRPSNTKYDKAKSPKCKTHTCCPCPAPELLGG 266			
	: : : :			
Db	115 ssvfifppkpdvlitltpkvtcvvvdiakddpevgafswfdvdvehtaqtqpzeeqfn 174			
	: : : :			
Qy	267 PSVFLEPPPKADTLMLSRTPETVCVVVDVSHEDPEVKFNWYVDGVENVNAKTREQQYN 326			
	: : : :			
Db	175 stfrsvseipimhqdwlnqkfkcrvnsaafpaplektiektgrkpaqvvtippkkeq 234			
	: : : :			
Qy	327 STRVRVSULTVHQDWNGKEIKCKVSNKAIPALEKTIISKAKGPREQPVITLPDSRDE 294			
	: : : :			
Db	235 makdksvltcmittdffpeditveqwngcpaenykntqlpmntngsyfyysklvqkxw 294			
	: : : :			
Qy	387 LTRNQVSTUCLVGRGFPSDAIVENESNGCPENNYKTPPPVIDSDGSFFLYSKLTVDKSRW 446			
	: : : :			
Db	295 eagntfcsvlhaglhhnbhtekslshspg 323			
	: : : :			
Qy	447 QQGNGFSGVNHVALAHNYTKQSLSPC 475			

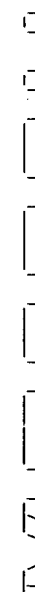
RESULT	13	
ID	GCAA MOUSE	STANDARD; PRT; 330 AA.
AC	P01863;	
DT	21-JUL-1986	(REL. 01, CREATED)
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)
DT	01-FEB-1991	(REL. 17, LAST ANNOTATION UPDATE)
DE	IG GAMMA-2A CHAIN C REGION, A ALLELE.	
OS	MUS MUSCULUS (MOUSE).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA; RODENTIA.	
RN	{1}	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE; 81076554.	
RA	SIKORAV J -L., AUFRAY C., ROUGEON F.;	
RL	NUCLEIC ACIDS RES. 8:3143-3155(1980).	
RN	{2}	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE; 81198976.	
RA	YAMAWAKI-KATAOKA Y., MIYATA T.;	
RL	NUCLEIC ACIDS RES. 9:1365-1381(1981).	
RN	{3}	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE; 81223894.	
RA	OLLO R., AUFRAY C., MORCHAMPS C., ROUGEON F.;	
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:2442-2446(1981).	

RL PROC. NATL. ACAD. SCI. U.S.A. 79:2623-2627 (1982).
 CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
 CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
 CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
 CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
 CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
 CC SEGMENT OF MU CHAINS.
 CC -!- THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE IDENTICAL WITH
 CC THE CORRESPONDING REGION OF THE SECRETED FORM OF THE A ALLELE.
 DR EMBL; J00471; J00471.
 DR PIR: A02154; G2MSAM.
 DR HSP; P01857; IFC1.
 DR PROSITE; PS00290; IG MHC.
 KW IMMUNOGLOBULIN C REGION; ALTERNATIVE SPLICING; TRANSMEMBRANE.
 FT NON_TER 1 1
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT TRANSMEM 346 363
 FT DOMAIN 364 399 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 399 AA; 44020 MW; 926112 CN;

Query Match 44.4%; Score 1542; DB 3; Length 399;
 Best Local Similarity 63.4%; Pred. No. 0.00e+00;
 Matches 210; Conservative 52; Mismatches 65; Indels 4; Gaps 3;
 Db 1 aktapsvylapvcddtgstglcylkygfpevtiltwnsgslssgyhtfpavlqsd 60
 Qy 147 ASTKGSVPFLAPSSKSTSGGTALGCLVKOYFPEPTVWNSGALTSVHTFPAVLQSS 206
 Db 61 -lytlessvvtstwpqsticnvahpasstkvdkieprg-ptlkpccpckcpapnll 118
 Qy 207 GLYSLSVWVTPSSSLGTQTYIGNVHKFSNKKVKAEPKSCDKTHTCPPC--PAPELL 264
 Db 119 ggsqvfiipkikadvlmlslspivtcvvdvseddpdvqlswfvnnvevhtaqtqthred 178
 Qy 265 GGSVFLFPKPKDITLMTISRTPEVTCVVDVSHEDPEVKENMYDGVFNNAKTPREEQ 324
 Db 179 ynsltrvsaipiqhdmsqskfckvnmkdlpapiertiskpkgsrvapqvylpppe 238
 Qy 325 YNSTYRWVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 384
 Db 239 eeatkkvltcmvtdfmpediyvwtngktelnkntepvldsdgsyfmsylrvekk 298
 Qy 385 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPTPPVLDSDGSFELYSLKLTVDKS 444
 Db 289 nwvsnysvscsvhveglnhnhhtkfsertpg 329
 Qy 445 RWQQGNVFSCSVHVEALHNHYTQKSLSLSPG 475

Search completed: Tue Dec 17 15:21:10 1996
 Job time : 33 secs.

(TM)



Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch pp protein - protein database search, using Smith-Waterman algorithm

```
Run on: Tue Dec 17 15:18:11 1996; MasPar time 10.33 Seconds
438.806 Million cell updates/sec
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Tabular output not generated.

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Title: >US-08-487-550-4
Description: (1-476) from US08487550 pep
Perfect Score: 3472
Sequence: 1 MKHLMFFLLLVAAAPRWVLSQ.....

```

Scoring table: PAM 150
Gap 11

Searched: 81589 seqs, 9523651 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq24
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16

Statistics: Mean 35.425; Variance 166.647; scale 0.213

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query			ID	Description	Pred. No.
			Match	Length	DB			
1	3004	86.5	475	16	R3553	Monoclonal antibody D	4.04e-258	
2	2787	80.3	470	4	R2757	Reshaped CAMPATH-1 an	2.68e-238	
3	2785	80.2	481	5	R2442	Sequence of antibody	4.08e-238	
4	2774	79.9	467	4	R22759	Reshaped CD4 antibody	4.12e-237	
5	2772	79.8	467	4	R22758	Reshaped CD4 antibody	2.67e-237	
6	2744	79.0	453	6	R33311	Humanised Ma11 Versi	2.12e-234	
7	2717	78.3	475	3	R20057	Heavy chain of 3D6 an	6.58e-232	
8	2714	78.2	476	6	R31023	Antibody D heavy chal	1.24e-231	
9	2689	77.4	449	7	R43339	Completely humanised	2.36e-229	
10	2689	77.4	461	8	R42162	Anti-HIV-1 recombinan	2.36e-229	
11	2653	76.4	459	8	R42066	Human anti-HBs heavy	4.56e-226	
12	2642	76.1	477	8	R47453	chIT94.12 H3 heavy ch	4.60e-225	

[illegible]

ALIGNMENTS

RESULT	1	
ID	R03553	standard; Protein; 475 AA.
AC	R03553;	
DT	20-AUG-1996	(first entry)
DE	Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.	
KW	Monoclonal antibody chain reaction; primer; amplify; PCR; light chain; MAB;	
DE	Polymerase chain reaction; primer; amplify; PCR; light chain; MAB;	
KW	65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.	
OS	Synthetic.	
FFH	Key	Location/Qualifiers
FT	Peptide	1..19
FT	/note= "Signal peptide"	
FT	Protein	20..475
FT	/note= "Mature heavy chain"	
PN	J08038178-A.	
PD	13-FEB-1996.	
PF	20-FEB-1995; 030742.	
PR	18-FEB-1994; JP-021628.	
PPA	(NIN) NISSHINBO IND INC.	
PPA	(TANA/) TANAKA H.	
DR	WPI; 96-154852/16.	
DR	N-PDSB; T18059.	
PPT	Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -	
PPT	produced by primer amplification, used in the diagnosis of hCMV	
PPT	infection	
PS	Claim 4; Page 16-18; 22pp; Japanese.	
CC	The sequences given in R03553-54 represent the heavy and light chains	
CC	respectively of a monoclonal antibody against a 65 kD antigen of human	

CC cytomegalovirus (hcmv). The DNA's encoding these sequences were
 CC amplified using the sequences given in T18040-58. The monoclonal
 CC antibody may be used in the diagnosis of hcmv.
 SQ Sequence 475 AA;

Query Match 86.5%; Score 3004; DB 16; Length 475;
 Best Local Similarity 89.7%; Pred. No. 4,04e-258;
 Matches 428; Conservative 15; Mismatches 31; Indels 3; Gaps 3;
 Db 1 mkhlfflllvaaprwlsqqlqesgqlvpsqetlaltctvsgdsrsasysgcirg 60
 QY 1 MKHLFFLLVAAPRWLSQQLQESGQLVPSQETLALTCTVSGDSRSASYSGCIRG 59
 Db 61 ppkglewigtlyyagst-yynpslksrvtsjvdaannqfalklsavtaadvayycart 119
 QY 61 PPKGLEWIGTLYYAGST-YYNPSLKSRTSJVDANNQFALKLSAVTAADVAYYCART 119
 Db 60 TPGRGLEIGHYGNAGATTNPNPSIKSRVTISKDTSKNOFFLNINSVTDADTAVYTCARG 119
 QY 60 TPGRGLEIGHYGNAGATTNPNPSIKSRVTISKDTSKNOFFLNINSVTDADTAVYTCARG 119
 Db 120 s-pqyydlitgsfpywgqgtltvssastkgsfvplapskstsggtaalgclvxdyf 178
 QY 120 s-PQYYDLITGSFPHYWGQGTTLTVSSASTKGSFVPLAPSKSTSGGTAALGCLVXDYF 178
 Db 120 PRDCTTTCYCGWVDWGPCDLVTWSSASTKGSFVPLAPSKSTSGGTAALGCLVXDYF 179
 QY 120 PRDCTTTCYCGWVDWGPCDLVTWSSASTKGSFVPLAPSKSTSGGTAALGCLVXDYF 179
 Db 179 peptvsnegaltgqvhtfpavlgsglyalsvvtvpsaslggtqyicnvnkhpsntk 238
 QY 179 PEPTVSNEGALTGQVHTFPAVLGSGLYALSVVTVPSSSLGTTQYICNVNKHPSNTK 239
 Db 239 vdkkvepkscdkthtccpcapeallggpsvflfppkpkdtlmsrtpevtcvvvdvshed 298
 QY 239 VDKKVEPKSCDKHTHTCCPCAPELLGGPSVFLFPPKPKDTLMSRTPVTCVVDVSHED 299
 Db 299 pevknfyvdygvevhnaktkpreeqnystyrsvvltvqhqlngkeyckvsnkalpa 358
 QY 299 PEVKNFYVDYGVVHNAKTKPREEQNSTYRSVVLTVLHQDLNGLNGKEYCKVSNKALPA 359
 Db 359 piektiskakgprepyvtlpprdeltnkvslclvkgfypsdiavewesngqpenn 418
 QY 360 PIEKTISKAKGPREPYVTLPSPRDELTKNQSLLCLVKGFPYSDIAVEWESNGQPENN 419
 Db 419 ykttppvldsdgfflyskltvdkswqgnvfscsvmhhealnhytqkslslepgk 475
 QY 420 YKTTPPVLDSDGFFLYSKLTVDKSRWQGNVFSCSVMHHEALNHHTQKSLSLSPCK 476

RESULT 2
 ID R22757 standard; Protein; 470 AA.
 AC R22757;
 DT 20-OCT-1992 (first entry)
 DE Reshaped CAMPATH-1 antibody heavy chain.
 KW Antigen; CD8; complementarity determining region; graft rejection;
 KW autoimmune diseases; rheumatoid arthritis; allergy.
 OS Rattus rattus.
 FH Key Location/Qualifiers
 FT Region 50..54
 FT /note= "Complementarity determining region 1"
 FT Region 69..87
 FT /note= "Complementarity determining region 2"
 FT Region 101..110
 FT /note= "Complementarity determining region 3"
 FT Peptide 1..19
 FT /note= "signal peptide"
 FT Peptide 20..470
 FT /note= "mature peptide"
 PN W09205274-A.
 PD 02-APR-1992.
 PF 16-SEP-1991; G01578.

PR 17-SEP-1990; GB-020282.
 PA (GORM/) GORMAN S D.
 PI Clark M R, Cobbold S P, Gorman S D, Waldmann H.
 DR WPI; 92-132139/16.
 DR N-PSDB; Q23570.
 PT Humanisation of antibodies binding to human CD4 antigen - by
 PT mutation of framework-encoding regions of DNA encoding variable
 PT domain of rat or mouse antibody chain
 PS Disclosure; Fig 5; 74pp; English.
 CC The sequence is that of the reshaped CAMPATH-1 heavy chain antibody.
 CC Reshaped CD4 antibody can be used to induce tolerance against an
 CC antigen. It can also be used to alleviate autoimmune diseases such
 CC as rheumatoid arthritis, and to prevent graft rejection. Tolerance
 CC to a graft, e.g. an organ graft or a bone marrow transplantation can
 CC also be useful to alleviate allergies. Tolerance to allergens could
 CC also be achieved. See also R22754-R22763.
 SQ Sequence 470 AA;

Query Match 80.3%; Score 2787; DB 4; Length 470;
 Best Local Similarity 86.3%; Pred. No. 2.68e-238;
 Matches 408; Conservative 25; Mismatches 30; Indels 10; Gaps 6;
 Db 6 ililfivatagvhsqqlvpsqetlaltctvsgfttfdym-nwvcpqpgql 64
 QY 6 FFLLVAAPRWLSQQLQESGQLVPSQETLALTCTVSGFTTDFDYM-NWVCPQPGQL 65
 Db 65 ewigfirdkagkyteynpavkgrvtmldsknfslrlesvtaadvayycaregha 124
 QY 65 EWIGFIH-Y-GNGATTNPNPSIKSRVTISKDTSKNOFFLNINSVTDADTAVYTCARGPRD 123
 Db 125 -ap---f-----dywgqgsjltvssastkgsfvplapskstsggtaalgclvxdyf 177
 QY 124 CTTTCYCGWVDWGPCDLVTWSSASTKGSFVPLAPSKSTSGGTAALGCLVXDYFPEV 183
 Db 178 tvwnsgaltsgvhtfpavlgsglyalsvvtvpsaslggtqyicnvnkhpsntkvd 237
 QY 184 TVSNNSGALTSGVHTFPAVLGSGLYALSVVTVPSSSLGTTQYICNVNKHPSNTKYDKK 243
 Db 238 vepkscdkthtccpcapeallggpsvflfppkpkdtlmsrtpevtcvvvdvshedpevk 297
 QY 244 AEPKCDKHTHTCCPCAPELLGGPSVFLFPPKPKDTLMSRTPVTCVVDVSHEDPEVK 303
 Db 298 fnwydygvevhnaktkpreeqnystyrsvvltvqhqlngkeyckvsnkalpaiek 357
 QY 304 FNNYVDYGVVHNAKTKPREEQNSTYRSVVLTVLHQDLNGLNGKEYCKVSNKALPAIEK 363
 Db 358 tiskakgprepyvtlpprdeltnkvslclvkgfypsdiavewesngqpennykt 417
 QY 364 TISKAKGPREPYVTLPSPRDELTKNQSLLCLVKGFPYSDIAVEWESNGQPENNYKT 423
 Db 418 ppvldsdgfflyskltvdkswqgnvfscsvmhhealnhytqkslslepgk 470
 QY 424 PPVLDSDGFFLYSKLTVDKSRWQGNVFSCSVMHHEALNHHTQKSLSLSPCK 476

RESULT 3
 ID R24442 standard; Protein; 481 AA.
 AC R24442;
 DT 02-JAN-1992 (first entry)
 DE Sequence of antibody molecule IgG1.
 KW Antibody; immunoglobulin G1.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc difference 308

FT /label= N
FT /notes "Substn. to create glycan addition site"
FT Misc difference 310
FT /label= S
FT /notes "see above"
FT Misc difference 321
FT /label= N
FT /notes "see above"
FT Misc difference 329
FT /label= N
FT /notes "see above"
FT Misc difference 331
FT /label= S
FT /notes "see above"
FT Misc difference 356
FT /label= N
FT /notes "see above"
FT Misc difference 369
FT /label= N
FT /notes "see above"
PN W09209293-A.
PD 11-JUN-1992.
PF 18-NOV-1991; U08605.
PR 23-NOV-1990; US-618314.
PA (GCHO) GEN HOSPITAL CORP.
PI Seed B, Walz G;
DR WPI: 92-216789/26.
DR N-PSDB; Q25443.
PT Inhibition of cell adhesion mediated through ELAM-1 mol. binding
PT - used in treating chronic inflammation, rheumatoid arthritis,
PT psoriasis, etc.
PS Disclosure; Fig 1; 46pp; English.
CC The IgG1, in its nascent form, bears no sialyl-Lex side chains. The
CC inventors designed a molecule including several such sites for
CC attachment of sialyl-Lex side chains (see R24442, FT). The
CC additional N-linked glycosylation sites are introduced at locations
CC which impair complement fixing and Fc receptor binding ability. They
CC are preferably located in the CH2 region of the Ig molecule.
CC Antibodies bearing multiple sialyl-Lex determinants are useful for
CC disrupting undesirable interactions between cells or proteins.
CC Disrupting this interaction has therapeutic applications, for
CC example, in minimizing inflammation following tissue injury.
SQ Sequence 481 AA;

Query Match 80.2%; Score 2785; DB 5; Length 481;
Best Local Similarity 82.8%; Pred. No. 4,08e-238;
Matches 396; Conservative 30; Mismatches 49; Indels 3; Gaps 3;

Db 5 mdwtwrlffvaatgvsqqlvqsgaevkpgasvkvsckasggtfesyval-swrq 63
Qy 1 MKHLMFFLLV-AAPRWLVLSQVLIQWGGELQPSSETLSRTCVCVSGGSISGYVWIRQ 59
Db 64 apqgglegmggiipifgtanyaqtfqgrvritadeetataymelselreedaavyycard 123
Qy 60 TPGRGLEIGHYXGATTNPNFSLKSRVTISKDTSKNOFFELNLSVTDADTAVYYCARG 119
Db 124 ngaycsgecygswfdpwwgqqlvtvsaatkpsvflapasesketagtgaaalckvdy 183
Qy 120 PRPDCTT-ICYGWVDWVWCPGDLVTVSSASTKGPVFLAPSSKSTSGGTAAALGCIWKDY 178
Db 184 fpepvtvawnegaltsgvhtfpavlgsgqlvlesvvtvpssslgtqtvcvnnhkpsnt 243
Qy 179 FPEPVTVSWNSGALTSCVHTFPVAVLSSGLYSLSVWVTPVSSSLGTQTYICNVNKKPSNT 238

Db 244 kvdkvpekscdtkhtcpopapellgpgsvflfppkpkdtlmisrtpevtcvrvdshe 303
Qy 239 KVDKAEPKSCDKTHTCPPCPAPELIGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 298
Db 304 dpevfknwydvgevhnahtkpreedynstyrsvvltvldqdlngkeyckvsnkalp 363
Qy 299 DPEVKFNWYVDGVEVHNAHTKPREEQYNSTYRVSVLTVLHQDLNGKEYCKVSNKALP 358
Db 364 apiektisakgqprepqvtylpsrdeltknqsvlclvkgfypsdiaweangopen 423
Qy 359 APIETISKAKGPPEQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGOPEN 418
Db 424 nykttppvlidsdgsfflyskltdkserwqgnvfscsvmhealnhnhtkdlalspdk 481
Qy 419 NYKTTTPVLDSDGSFFLYSKLTVDSKRWQQGNVFSVWHEALNHHTYTKSLSLSPDK 476

RESULT 4
ID R22759 standard; Protein; 467 AA.
AC R22759;
DT 20-OCT-1992 (first entry)
DE Reshaped CD4 antibody heavy chain CD4VHNEW-Ser30.
KW Antigen; CDR; complementarity determining region; graft rejection;
KW autoimmune diseases; rheumatoid arthritis; allergy.
OS Rattus rattus.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /notes "signal peptide"
FT Peptide 20..467
FT /notes "mature peptide"
FT Region 50..54
FT /notes "Complementarity determining region 1"
FT Region 69..85
FT /notes "Complementarity determining region 2"
FT Region 118..126
FT /notes "Complementarity determining region 3"
PN W09205274-A.
PD 02-APR-1992.
PF 16-SEP-1991; G01578.
PR 17-SEP-1990; GB-020282.
PA (GORM/) GORMAN S D.
PI Clark M R, Cobbold S P, Gorman S D, Waldmann H.
DR WPI: 92-132139/16.
DR N-PSDB; Q23581.
PT Humanisation of antibodies binding to human CD4 antigen - by
PT mutation of framework-encoding regions of DNA encoding variable
PT domain of rat or mouse antibody chain
PS Disclosure; Fig 7; 74pp; English.
CC The sequence is that of the reshaped CD4 antibody heavy chain
CC CD4VHNEW-Ser30. Reshaped CD4 antibody can be used to induce tolerance
CC against an antigen. It can also be used to alleviate autoimmune diseases
CC such as rheumatoid arthritis, and to prevent graft rejection. Tolerance
CC to a graft, e.g. an organ graft or a bone marrow transplantation can
CC also be useful to alleviate allergies. Tolerance to allergens could
CC also be achieved. See also R22753-R22763.
SQ Sequence 467 AA;

Query Match 79.9%; Score 2774; DB 4; Length 467;
Best Local Similarity 86.6%; Pred. No. 4.12e-237;
Matches 408; Conservative 23; Mismatches 31; Indels 9; Gaps 6;

Db 6 iilflvatqhsqvlqesqgqlvrpsqtlslctvagftfnygm-awrqppqrgl 64
Qy 6 FFLLLVAAPRWLVLSQVLIQWGGELQPSSETLSRTCVCVSGGSISGYVWIRQTPGRGL 65

Query Match 78.24; Score 2714; DB 6; Length 476;
Best Local Similarity 81.8%; Pred. No. 1.24e-231; ~
Matches 390; Conservative 28; Mismatches 57; Indels 2; Gaps 2;

Db	1	mdwtwrlfvvaatqvgqmvgvgaevkpgsavtvcaskaeggtfenvai-awvira	59
Qy	1	MKHLAFELLVAAPRWLSQVKLQWGEGLQPSLTSRLTCVWSGSGISGYIYWTWIRQT	60
Db	60	pggglewmggiipfptqyeqnfqgrvritadkstatetahmeltrsedtavyvcatdr	119
Qy	61	PGGLELHCHYNGATYNNPISLKSRTVTSKDTSKNQFFLNLMSVTDADTAVYVCARG	120
Db	120	yrganfdrarvgwfdpwgggtlvtvssaatkqpsvflapaskatsggtaalqclvkdyf	179
Qy	121	-RDCDTTCYGGWVDVWVGDLVTVSSASTKGPSVFLAPSKSTSGGTAAUGCLVKDYF	179
Db	180	pepvtvsnsgalstqsvhtfpavlaeqglqslselaavtvpssslqctqtiyicnmhkpentk	239
Qy	180	PEPVTVSNISGALTSQVHTFPAVLQSGGLYSSSVTVPSSSLQCTQTYICNNHKPSNKT	239
Db	240	vdtkvpekscdkhtccpccapepallggspevflfppkpktlmisrtepvtcvrvdvshed	299
Qy	240	VDKKAEPKSCDKHTCCPCPAPELLGGSPEVFLFPPPKDITMISRTPEVTCVVDVSHED	299
Db	300	pevkfnvyvdgvevhnaktkpreegynatrvsvslvllhqdwlngkeyckkvenkalpa	359
Qy	300	PEVKFNWYVDCVEVHNAKTKPREEQYNSTRVWSVLTVLHQDWLNGKEYCKKVENKALPA	359
Db	360	piektiskakgpprepvytllpsrdeltnkqvalctlvkgfypsdlavewesngqpenm	419
Qy	360	PIEKTISKAKQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENN	419
Db	420	yktptpvldsgfflysklvtvksrwqgnvfscsvmhealnhhvtqkslspsgk	476
Qy	420	YKTPPVLDSDGFFLYSKLTVDKSRWQGNVFSCSVMEALNHHVTQKLSLSPGK	476
RESULT	9		
ID	R43339	standard; Protein; 449 AA.	
AC	R43339;		
DT	29-NOV-1993	(first entry)	
DE	Completely humanised C4G1 Ig heavy chain.		
KW	Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIb/IIIb;		
KM	monoclonal antibody; platelet agglutination; humanised antibody.		
OS	Synthetic.		
PN	W09313133-A.		
PD	08-JUL-1993.		
PF	15-DEC-1992; J01630.		
PR	20-DEC-1991; US-812111.		
PR	09-JUN-1992; US-895952.		
PR	11-SEP-1992; US-944159.		
PA	(PROT-) PROTEIN DESIGN LABS INC.		
PA	(YAMA) YAMANOUCHI PHARM CO LTD.		
PI	Co MS, Tso JY;		
PT	WPI; 93-227275/28.		
DR	Compan. contg. immunoglobulin specific for the GP-IIb and -IIIa		
PT	protein - for treating disorders related to vascular thrombosis		
PS	Claim 26; Fig 5c; 5dpp; Japanese.		
CC	This is the sequence of the humanised C4G1 immunoglobulin heavy		
CC	chain fragment. See R43338 for the light chain sequence. The		
CC	antibody is specific for the platelet membrane glycoprotein		
CC	GPIIb/IIIa and inhibits platelet agglutination. The Ig is thus		
CC	useful in the treatment of thrombosis.		
SC	Sequence 449 AA;		
Query Match	77.4%;	Score 2689;	DB 7; Length 449;
Best Local Similarity	84.7%;	Pred No. 2.36e-229;	

Matches 387; Conservative 23; Mismatches 39; Indels 8; Gaps 6;

```
Db 1 qvqlvqgaevkpkpgskvkskaasgafntlyl-ewvraqpgglwlgvlypgaggt 59
   ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
Qy 20 QVKLQMGEGGLQPSSETLSRTCVSGSGISGYYWTVIRQTPGRLGLEWIGHI-Y-GNGAT 79
   ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : :
Db 60 ynekfkgrvtlvddestnrmelslrsedtavfyfcar--r-d-gn--yg--wfaewgg 112
   || :||| : : : : ||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 80 YNPSLKSRTVTSKDTSKNQFFLNLSVTDADTAVYCARGRPDCTTICYGWDVWVG 139
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 113 tlvtsaastkpsvflpapskatsqgtaalglvkdypcpvtvsmnsgaltsqvhf 172
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 140 DLVTSSASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTS 199
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 173 pavlasegylsadvvtvpasellgtctyicnvhkpsntkvdtkvkecdkthtccp 232
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 200 PAVLQSSGLYSLSSVTVTPSSSLGTQTVICNVNHRPSNTRKYDKAEPKSCDKTHT 259
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 233 apelligsvflfpkpkdtlmistpvtcvvdvshdpevkfnwydvgevhna 292
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 260 APPELLGGSVFLFPKPKDTLMISRTPEVTCVVDVSHDEPEVKFNWYDVGEVHNA 319
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 293 preegnytrvsvltvlhqdlnqkeyckvsnkalpapietkiskakgpprepqvy 352
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 320 PREEQNSTYTRVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGPREPQV 379
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 353 lpsrdeltknqveltcvkgfypadiaveangpennykttppvldsdgsfflyekl 412
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 380 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF 439
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 413 tvdkerwqgnvfscvsmhealnhnytkelslspgk 449
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 440 TVDKSRWQGNVFCVSMHEALNHNYTKLSLSPCK 476
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
```

RESULT 10

```
ID R42162 standard; Protein; 461 AA.
AC R42162;
DE 27-APR-1994 (first entry)
KW Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;
KW HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
KW acquired immune deficiency syndrome; chimeric antibody;
KW surface glycoprotein gp120; V3 loop.
OS Homo sapiens.
PN W09319785-A.
PD 14-OCT-1993.
PF 23-MAR-1993; U02629.
PR 01-APR-1992; US-861701.
PA (MERI ) MERCK & CO INC.
PA (JOHN/) JOHNSON L S.
PA (PFAR/) PFARR D S.
PI Conley AJ, Emimi EA, Johnson LS, Mark GE, Pfarr DS;
DR WPI; 93-336600/42.
DR N-PSDB; Q49834.
PT New recombinant human antibody - with HIV neutralising activity
PT against at least two isolates, useful for preventing or treating
PT infection in diagnosis, etc.
PS Example 9; Fig 2A; 154pp; English.
CC EBV-transformed cell lines and mouse-human heterohybridomas
CC producing human mAbs specific for the gp120 V3 loop of HIV-1 MN
CC isolate were obtained. Mab 447-52D was found to recognise the
CC tetrapeptide motif GPGR, i.e. the Principal Neutralising
CC Determinant common to the V3 loop of different HIV isolates.
```

CC A recombinant Ab was produced in which the H chain V region was
CC derived from 447-52D and to which a signal sequence and a H chain
CC intronic sequence are appended, fused to a fragment contg. a short
CC intronic segment of the human gamma 1 C region and the human gamma
CC 1 encoding domain in its genomic form.

SQ Sequence 461 AA;

Query Match 77.4%; Score 2689; DB 8; Length 461;
Best Local Similarity 84.0%; Pred. No. 2.36e-229;
Matches 388; Conservative 26; Mismatches 42; Indels 6; Gaps 6;

```
Db 1 evqlvsgglvlpkpgslrltcvaasgftsdwl-nwvraqpgkglwvrikertdgt 59
   QVKLQMGEGGLQPSSETLSRTCVSGSGISGYYWTVIRQTPGRLGLEWIGHI-Y-GNGAT 77
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 60 tyaasvkgftrlddskntlylqmalktedtavyscttdgfmirtgveedyvyynd 119
   || :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 78 TYNPLSKSRVTISKDTSKNQFFLNLSVTDADTAVYCAR-G-PR-PDCTTICYGWD 134
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 120 vwgkttvtvssastkpsvflpapskatsqgtaalglvkdypcpvtvsmnsgalts 179
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 135 WVGPGDLVTSSASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTS 194
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 180 ghvtfpavlasegylsadvvtvpasellgtctyicnvhkpsntkvdtkvkecdktht 239
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 195 GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTVICNVNHRPSNTRKYDKAEPKSCDKTHT 254
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 240 cpcpapeallgpgsvflfpkpkdtlmistpvtcvvdvshdpevkfnwydvgevh 299
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 255 CPCPAPPELLGGSVFLFPKPKDTLMISRTPEVTCVVDVSHDEPEVKFNWYDVGEVH 314
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 300 naktkpreegnytrvsvltvlhqdlnqkeyckvsnkalpapietkiskakgpre 359
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 315 NAKTKPREEQNSTYTRVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGP 374
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 360 pqvyltppsrdeltknqveltcvkgfypadiaveangpennykttppvldsdgsff 419
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 375 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF 434
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 420 lyekltvdkerwqgnvfscvsmhealnhnytkelslspgk 461
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 435 LYSKLTVDKSRWQGNVFCVSMHEALNHNYTKLSLSPCK 476
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
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RESULT 11

```
ID R42066 standard; Protein; 459 AA.
AC R42066;
DE 29-APR-1994 (first entry)
DE Human anti-HBs heavy chain.
KW Antibody; Ab; light; heavy; chain; hepatitis B;
KW HB; surface antigen.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..9
FT /label= sig_peptide
FT Protein 10..459
FT /label= mat_protein
PN W09320205-A.
PD 14-OCT-1993.
PF 30-MAR-1993; J00396.
PR 30-MAR-1992; JP-074678.
PA (SUNR ) SUNTORY LTD.
PI Arima K, Kurihara T, Matsukura S, Nishihara T, Teurouka N;
DR WPI; 93-336913/42.
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Db	235	kscdkthcpcpape	lqggsvflfppkpkdtlmsrtpv	cvvvdshadpevkfnw	294
Qy	247	KSCDKTHCPCPAP	ELGGGSVFLEPPKPKDTLMSRTPV	CVVVDVSHEDPEVKFNW	306
Db	295	yvdgvevhnaakt	kpreeqnyatryvsvlvtlqgdw	lndgkeyckvankalpaiektis	354
Qy	307	YVDGVEVHNAKTP	REEQNYTRYVSVLTVLQGDWLNGKEYCKVANKALPAPEKTIIS		366
Db	355	kakgqprepyvt	lppsreemtqnqvaltclvkgyfpsi	avevesngqpennykttppv	414
Qy	367	KAKGQPREPYVTL	PPSRDELTKNQVSLTCLVKGYFPSIDAVESNGQPENNYKTTTPV		426
Db	415	ldadgefilyeklt	vdksrwaqgnvfacsvmhealhnhvtyqkslslepgk	464	
Qy	427	LDSDGFFLYSKLT	VDKSRWQGNVFSCEVMHEALHNHVTQKLSLSLPGK	476	

RESULT	14	
ID	R40750 standard; Protein; 466 AA.	
AC	R40750;	
DT	01-OCT-1993 (first entry)	
DE	Sequence encoded by the heavy chain expression	
DE	vector pAG4235.	
KW	Chimeric monoclonal antibody; expression plasmid.	
OS	Synthetic.	
PN	W09311252-A.	
PD	10-JUN-1993.	
PF	24-NOV-1992; U10207.	
PR	26-NOV-1991; US-798696.	
PA	(REGC) UNIV CALIFORNIA.	
P1	Hastings A, Morrison SL, Wims L;	
DR	WPI; 93-197069/24.	
DR	N-PSDB; Q43497.	
PT	Expression plasmids and derivs. - used to produce protein	
PT	molecules esp. chimaeric monoclonal antibodies	
PS	Disclosure; Fig 3; 54pp; English.	
CC	The expression plasmid pAG4235 (ATCC No. 75038) is claimed. It is	
CC	used to express chimeric monoclonal antibodies. It contains genes	
CC	with leader sequences and is functional. The variable region and	
CC	constant regions exons were sequenced, however the other sequences	
CC	are from published references and have not been verified for this	
CC	particular plasmid. Regions for which there is no sequence	
CC	information are indicated by N's with the length determined by sizes	
CC	of fragments observed on agarose gels.	
SQ	Sequence 466 AA;	

Query Match	74.9%;	Score	2599;	DB	7;	Length	466;
Best Local Similarity	79.6%;	Pred. No.	3.86e-221;				
Matches	379;	Conservative	33;	Mismatches	54;	Indels	10;
Gaps	7;						
Db	1	mdwllwalfpmaaaqisqigiqilvgsegelkpkpgketvkiackasggyftnngm-nrvkqa	59				
		: : : : : : : : : : : : : : :					
Qy	1	MKUHWFFLLVWAPRWLSQVKLQOGEGLOPSETLSRTCTCVSGSISGYGYYTWIRQT	60				
Db	60	qqgklkwmgwintntgeptyteeekgrfafsleasantayllinnlknedatycag-	118				
		: : : : : : : : : : : : : : :					
Qy	61	PGRGLEWHIYGNGATTNYPNSLKSRVTISKDTSKNQFLNLNVTDADTAVYCARGP	120				
Db	119	--e-gba-wg-fa-yggwtqlvtvsaaastkpssvfplapesketsagtgalcikvkdfp	172				
		: : : : : : : : : : : : : : :					
Qy	121	RPDCTTCYGGWDVWGPDGLVTVSASTKGP SVFP LAPSSKSTSGGTALGCLVKDYFP	180				
Db	173	eptvsnwsгалтсгвhtfpavlgaglyslsvsvtvvpaseeltctylcnvnhkpenktkv	232				

Dec 17 15:05

US-08-487-550-4.rag

19

181 EPVTWNSGALTSVHTFRAVLQSSGLYSLSSWTVFSSSLGTQTYICNVNHPKSNTKV 240
233 dkkvepkscdkthtccppcapellggpavflfppkpkdtlmiartpevtcvvvdvshedp 292
241 DKKAEPKSCDKHTHTCPPCAPELLGPPSVFLFPPKPKDTLMISRPETVCVVVDVSHEDP 300
293 evkfnyvdgvevhnaaktppreeqynstyrwsvltvlhgdwlngkeyckvkenkalpap 352
301 EVKFNWYDGVVHNAKTPREEQYNSTYRWSVLTVLHQDWLNGKEYCKVSNKALPAP 360
353 iektisk--gqpreqyvtlpsrdeltknqvaltcvkgyfypsdiaweengqpenny 410
361 IEKTIKRAKQPREPVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVESNGQPENNY 420
411 ktppvldsgofflyskltvdkrwqgnvfscsvmhhealhhnytcqkclslspgk 466
421 KTTTPVLDSDGFFLYSKLTVDKSRWQGNVFSCSVMHHEALHHNYTKQKSLSLSPGK 476

RESULT 15

ID R30774 standard; protein; 454 AA.
AC R30774;
DT 12-MAY-1993 (first entry)
DE H52H4-160 murine anti-CD18 antibody heavy chain.
KW Humanization; rapid; monoclonal antibody.
OS Mus musculus.
PN W09222653-A.
PD 23-DEC-1992.
PF 15-JUN-1992; 005126.
PR 14-JUN-1991; US-715272.
PA (GETH) GENENTECH INC.
PI Carter PJ, Presta LG.
DR WPI; 93-018139/02.
PT Humanisation of antibodies - by molecular modelling of the variable
PT domains and alteration by gene conversion mutagenesis
PS Disclosure; Fig 6A; 126pp; English.
CC The sequence is that of the heavy chain of murine anti-CD18
CC antibody H52H4-160.
SQ Sequence 454 AA;

Query Match 74.7%; Score 2594; DB 6; Length 454;
Best Local Similarity 80.8%; Pred. No. 1.10e-220;
Matches 370; Conservative 36; Mismatches 47; Indels 5; Gaps 4;

1 qvqlqsggpevlvkgaaevkiscktgytfteytm-hwmkqshgkslewlgfnpknngss 59
20 QVKLQWQEGCLLPSEFLSFTCVWSGSGISGYIYTWIRQTPCRGLEWIGHIYNGCATN 79
60 hmqrfmdkatlavdketstaymelrzeltsesdglyycarwrglmygfdivy--f-dwga 116
80 YNPSLKSRVTISKDTSKNQFFLNINSVTDADTAVYYCARGPRDCT-TICYGQWVDVWGP 138
117 gttvtvasaatkpavfpalapaskatggtaalgclvkdifyfpvptvwnagaltsgvht 176
139 GDLVTVSSASTKGP SVFP LAPSKSTSGCTAALGCLVRDYPPEPVTVSNWSCALTSGVHT 198
177 fpavlqsgglylsavtvpsseigtqtyicnvnhkpentkvdkkvepkcdtkhtcpcpc 236
199 FPAVLQSSGLYSLSSWTVFSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKHTHTCPPC 258
237 papellggpavflfppkpkdtlmiartpevtcvvvdvshedpevkfnwyvdgvevhnaakt 296
259 PAPELLGPPSVFLFPPKPKDTLMISRPETVCVVVDVSHEDPEVKENWYDGCVEVHNAKT 318

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20

297 kpreeqynsttrvavltvlhgdwlngkeyckvkenkalpapiektiekakgqpreqvy 356
319 KPREEQYNSTYRWSVLTVLHQDWLNGKEYCKVSNKALPAP IEKTIKRAKQPREPVY 378
357 tlppearemtknqvaltcvkgyfypsdiaweengqpennyktppvldsdgofflysk 416
379 TLPPSRDELTKNQVSLTCLVKGYFSPDSIAVESNGQPENNYKTTPPVLDSDGFFLYSK 438
417 ltvdksrwqgnvfscsvmhhealhhnytcqkclslspgk 454
439 LTVDKSRWQGNVFSCSVMHHEALHHNYTKQKSLSLSPGK 476

Search completed: Tue Dec 17 15:19:00 1996
Job time : 49 secs.

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protein - protein database search, using Smith-Waterman algorithm

```
Run on: Tue Dec 17 15:24:09 1996; MasPar time 9.18 Seconds
        661.706 Million cell updates/sec
```

Tabular output not generated.

```

Title: >US-08-487-550-6
Description: (1-239) from US08487550 pep
Perfect Score: 1666
Sequence: 1 MSLPAQLGLGLLLLCVPGSSG.....

```

Scoring table: PAM 150
Gap 11

Searched: 82130 seqs. 25426960 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

```
Database:
plr47
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unann10
14:unrev
```

Statistics: Mean 44.330; Variance 149.331; scale 0.297

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			ID	Description	Pred. No.
		Match	Length	DB			
1	1132	67.9	215	11	A23746	Ig kappa chain V-III	7.14e-120
2	1119	67.2	219	12	S52028	Ig kappa light chain	2.94e-118
3	1099	66.0	219	12	S16112	Ig kappa chain V reg	8.96e-116
4	1090	65.4	219	12	S39855	Ig kappa chain - mou	1.17e-114
5	1082	64.9	217	12	S42772	Ig kappa chain - mou	1.15e-113
6	1058	63.5	240	12	S05094	Ig kappa chain precu	1.09e-110
7	1057	63.4	225	12	JL0029	Ig light chain precu	1.45e-110
8	1000	60.0	220	12	A31790	Ig kappa chain V reg	1.66e-103
9	964	57.9	225	12	S37494	Ig kappa chain - mou	4.65e-99
10	930	55.8	230	12	S33161	Ig kappa chain - she	7.27e-95
11	930	55.8	234	12	S01320	Ig kappa chain precu	7.27e-95
12	911	54.7	197	12	S29593	Ig kappa chain (MM65	1.59e-92

13	907	54.4	210	12	A56169	Ig kappa chain V reg	4.96e-92
14	898	53.9	178	12	S14237	Ig kappa chain precu	6.36e-91
15	843	50.6	234	12	P70219	Ig kappa chain V-C r	3.64e-84
16	842	50.5	235	14	S25058	Ig kappa chain - mou	4.83e-84
17	802	48.1	229	12	O20969	Ig kappa chain precu	3.85e-79
18	790	47.4	135	11	S57059	JC-kappa protein - h	1.13e-77
19	763	45.8	133	5	S42611	HUNK protein precu	2.24e-74
20	756	45.4	133	2	K2HURP	Ig kappa chain precu	1.60e-73
21	753	45.2	136	11	S40357	Ig kappa light chain	3.72e-73
22	749	45.0	142	11	S22902	Ig kappa chain V reg	1.14e-72
23	748	44.9	133	5	S23230	Ig kappa chain precu	1.52e-72
24	744	44.7	133	11	S40324	Ig kappa light chain	4.66e-72
25	737	44.2	132	11	S26882	Ig kappa chain V reg	3.32e-71
26	735	44.1	133	5	S24352	Ig kappa chain precu	5.81e-71
27	732	43.9	135	11	S40342	Ig kappa chain - hum	1.35e-70
28	721	43.3	106	2	K3HU	Ig kappa chain C reg	2.94e-69
29	718	43.1	132	11	S40327	Ig kappa chain - hum	6.81e-69
30	716	43.0	105	11	S02577	Ig kappa chain C reg	1.19e-68
31	716	43.0	132	14	PH0106	anti-digoxin transfe	1.19e-68
32	709	42.6	238	11	A96333	lambda-like immunogl	8.45e-68
33	708	42.5	128	11	S40373	Ig kappa chain - hum	1.12e-67
34	699	42.0	131	11	S40355	Ig kappa chain - hum	1.39e-66
35	698	41.9	131	5	B34904	Ig kappa chain precu	1.83e-66
36	697	41.8	126	11	S40312	Ig kappa chain - hum	2.42e-66
37	694	41.7	131	11	S40372	Ig kappa light chain	5.61e-66
38	692	41.5	131	5	B34904	Ig kappa chain precu	9.80e-66
39	692	41.5	131	5	S30577	Ig kappa chain precu	9.80e-66
40	688	41.3	131	5	D34904	Ig kappa chain precu	3.00e-65
41	688	41.3	131	5	B32513	Ig kappa chain precu	3.00e-65
42	686	41.2	131	5	B34903	Ig kappa chain precu	5.24e-65
43	682	40.9	99	5	B37927	Ig kappa chain C reg	1.60e-64
44	682	40.9	144	5	P10106	Ig kappa chain precu	1.60e-64
45	680	40.8	125	11	S40355	Ig kappa chain - hum	2.80e-64

ALIGNMENTS

```

RESULT      1
ENTRY       A23746      #type complete
TITLE       Ig kappa chain V-III (KAU cold agglutinin) - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change
            23-Mar-1993
ACCESSIONS  A23746
REFERENCE    A23746
#authors     Leoni, J.; Chiso, J.; Goni, F.; Frangione, B.
#journal     J. Biol. Chem. (1991) 266:2836-2842
#title       The primary structure of the Fab fragment of protein KAU, a
            monoclonal immunoglobulin M cold agglutinin.
#cross-references MUID:91131575

```

Query Match 67.9%; Score 1132; DB 11; Length 215;
Best Local Similarity 79.4%; Pred. No. 7.14e-120;
Matches 173: Conservative 22; Mismatches 19; Indels 4; Gaps 2;

1 eivltspatls|sperat|sgasgvs-an---vlawvdkpcaaprlliydagra 56

Qv 21 EVVMTOSPISLPITPGEPAISICSSSOSIKHNSGDTFELSWYOOKPGOPPRILIYKVSNRD 80

Db	57	tgipdrfagsgagt	dftltierlepedfavyvqqvgspltfgggtkveikrtvaapsv	116
QY	81	SGVPDRFSGSGAGT	DTLTKISAVEAEDVGWVFQCGTRTPPTFGGCTKVEIKRTVAAPSV	140
Db	117	fifpsdeqlksgt	aavvglllmfyreakvqkwkvdhalqgnsqsevtqdsksdtsyl	176
QY	141	FIFPDSQLKSGTASV	WCLLNIFYPREAKVQWVDNALSGNSQESVTFQDSKSDTSYL	200
Db	177	astltsladyekhk	vyagevthqglsepvtksfnrge	214
QY	201	SSTLTLSKADYEHK	KVYACEVTHQGLSPVTKSNRGE	238

```

RESULT      2
ENTRY
TITLE      Ig kappa light chain - mouse
ORGANISM   Mus musculus #common name house mouse
DATE       07-May-1995 #sequence_revision 21-Jul-1995 #text_change
           21-Jul-1995
ACCESSIONS S52028
REFERENCE   S52028
AUTHOR     van Engelen, F.; Schouten, A.; Moltthoff, J.W.; Roosien,
           Dirkse, W.G.; Schots, A.; Bakker, J.; Gommers, F.J.;
           Jongasma, M.A.; Bosch, D.; Stiekema, W.J.
SUBMISSION submitted to the EMBL data library, August 1994
DESCRIPTION Coordinate expression of antibody subunit genes yields
           levels of functional antibodies in roots of transgenic
           tobacco.
ACCESSION  S52028
STATUS     preliminary
MOLECULE   #molecule_type mRNA
RESIDUES   1-219 #label VAN
CROSS-REF #cross-references EMBL:I35138
LENGTH    219 #molecular-weight 24049 #checksum 5937
SUMMARY

```

Query Match	67.2%	Score 1119;	DB 12;	Length 219;
Best Local Similarity	69.4%;	Pred. No. 2.94e-118;		
Matches 152;	Conservative 35;	Mismatches 32;	Indels 0;	Gaps 0;
Ddb	1 dvmvtgspislpvelgdqasiesrsgsiwhngntylwlylkdqqgqpklllykvsnrff 60 : :: :: : :: : :: : :: : :: : :: :			
Qy	21 EWVMTGSPISLPITPGEPASISCRSSQSILKSHNGDTFLSWYQQKPQPPLRLLYKYSNRD 80 : :: : :: : :: : :: : :: : :: : :: :			
Ddb	61 agvdpvfsgsgtgdtflklisrveaedgvyyfcfgshvptfpggtlnleikradaaptv 120 : :: : :: : :: : :: : :: : :: : :: :			
Qy	81 SGVPDRFSGSAGTGDTFLKISAVEADGVYFCQGQTTPPTFGGKTVEIKRTVAAPSV 140 : :: : :: : :: : :: : :: : :: : :: :			
Ddb	121 eifppaseqltggasvvcflnmfypdklnfwkiidgaerqmgvlmswtddgsksdstsym 180 : :: : :: : :: : :: : :: : :: : :: :			
Qy	141 FIFPPDEQLKSCTASVVCLLNMFYPREAKVQWVDNALASGNQSIEQDSKDSTSYSL 200 : :: : :: : :: : :: : :: : :: : :: :			
Ddb	181 astlttkdyevrhnaytceathktstetpvkfmrnc 219 : :: : :: : :: : :: : :: : :: : :: :			
Qy	201 SSTLTLSRADYEKHKVACEVTHGLSPPVTKSFNRGEC 239 : :: : :: : :: : :: : :: : :: : :: :			

RESULT	3
ENTRY	s16112 #type complete
TITLE	Ig kappa chain V region (G2a) - mouse
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
ACCESSIONS	s16112
REFERENCE	s16112

```
#authors Vaesen, M.; Frosch, M.; Weisgerber, C.; Eckart, K.; Kratzin,
#journal H.; Bitter-Suermann, D.; Hillechmann, N.
#title Biol. Chem. Hoppe-Seyler (1991) 372:451-453
#cross-references MUD:92000313
#accession S16112
#status preliminary
#molecule_type protein
#residues 1-219
#label BIT
#length 219
#molecular_weight 24216
#checksum 7375
```

Query Match	55.0%	Score 1099;	DB 12;	Length 219;
Best local Similarity	68.9%	Pred. No. 8,96e-116;		
Matches	151;	Conservative 34;	Mismatches 34;	Indels 0; Caps 0;
Db	1	dvmvttqtlslpvlgdqasiecrssglshngntylywylcdqsgsqkpllyrvsnrf	60	
		: : : : : : : : : : :		
Qy	21	EWVMTQSPQLSPITGPAPASISCRSSQSLKHSNGDTFLSWYQKQCPQPRLLIYKVSNRD	80	
Db	61	sgvpdrfsgsgctdflklisrvaeadlgvyfcfgagthvpytfgggtlrleikradaapty	120	
		: : : : : : : : : : :		
Qy	81	SGVPDRFSGSGAGDTFLKISAVEADGVGYFCGGQTRTPPTFGGCTKVEIKRTVAAPSV	140	
Db	121	siifpssedqltgasvvcflmfpdklnvkwldgserqngvlnswtdqdkdkdyem	180	
		: : : : : : : : : : : :		
Qy	141	RIFFPDEQLKSGTASVVCLLNFPYREAKVQWYDNALSGNSGSVTEQDSKDSYSL	200	
Db	181	astltltkdyerhnsytcceathktstspivksfmrnc	219	
		: : : : : : : : : : : :		
Qy	201	SSTLTLSKADYEKHVYACEVTHQGLSSPVTKFSNRCZ	239	

```

RESULT      4
ENTRY
TITLE      S38865      #type fragment
ORGANISM    Ig kappa chain - mouse (fragment)
            #formal_name Mus musculus #common_name house mouse
DATE        06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
            06-Jan-1995
ACCESSIONS  S38865
REFERENCE   S38864
            Kipp, B.; Becker, W.; Schlaak, M.
            #authors
            #submission submitted to the EMBL Data Library, November 1993
            #description Combination of a defined specificity and desired isotype by
                        cloning of an anti ovalbumine recombinant mouse IgG1/IgE
                        Antibody.
            #accession S38865
            #status preliminary
            #molecule_type mRNA
            ##residues 1-219 ##label KIP
            ##cross-references EMBL:Z27396
            #length 219 #checksum 6119
SUMMARY

```

```
Query Match      65.4%; Score 1090; DB 12; Length 219;  
Best Local Similarity 68.9%; Pred. No. 1.17e-114;  
Matches 151; Conservative 34; Mismatches 34; Indels 0; Gaps 0  
  
Db      1 elvmtgslleavlgdgcasiscssqslvhtngntylhwyldkpglcpkllyivsnrf 60  
          |:|::|||::|:|||||::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Qy     21 EWMVTGSPULPTPGEPASISCRSSQSILKHNGDTFLSMYQKQPQQPRLLIYKVSRND 80  
  
Db     61 gsvpdrrfsgsgsgtdflklisrveaedlgyvfcsqrthvpwtfgggtklekkradaaptv 120  
          |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
```


Qy 65 PGQPPRLIYKVNRSQGVDRFSGSGAGTDTLKISAVEAEDVGVCQGTTRPTPTFG 124
 Db 116 ggtntveikredapsvllfkpseeqlrtgtvavvclvndfykpdinvkvkdvgtqnsnf 175
 Qy 125 GGTKEIKRTVAAPSVFIPFPDSQGLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNS 184
 Db 176 qnftdqdkstysltstlsseseyqghnayacevshkltplalvksfnknc 230
 Qy 185 QESVTEQDSKSTYSLSTLTLSKADYKHVKYACEVTHQGLSPVTKSFNRGEC 239

RESULT 11
 ENTRY S01320 #type complete
 TITLE Ig kappa chain precursor - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Mar-1993
 ACCESSIONS S01320
 REFERENCE S01320
 #authors de Waele, P.; Feys, V.; van de Voorde, A.; Molenans, F.; Fiers, W.
 #journal Eur. J. Biochem. (1988) 176:287-295
 #title Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed against the tumour marker human placental alkaline phosphatase.
 #cross-references MUID:88329081
 #accession S01320
 #molecule_type mRNA
 #residues 1-234 ##label DE1
 #cross-references EMBL:X13187
 #note this sequence was determined from the differentiated gene

FEATURE
 1-20 #domain signal sequence #label SIG
 21-234 #product Ig kappa chain #label MAT
 SUMMARY #length 234 #molecular_weight 25920 #checksum 6431
 Query Match 55.8%; Score 930; DB 12; Length 234;
 Best Local Similarity 54.4%; Pred. No. 7.27e-95;
 Matches 130; Conservative 56; Mismatches 48; Indels 5; Gaps 2;

Db 1 msvptqvlglillwldardcldmtgcpasievsgesvtitcraseni-yan---law 55
 Qy 1 MSIPAQLGLLLCVPGSGEWMVQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSW 60
 Db 56 yqqkqgqpqllyvatklvdyvrsfsgsggtqyelkinelgsedfgsyycqfwdtp 115
 Qy 61 YQKQPGQPPRLIYKVNRSQGVDRFSGSGAGTDTLKISAVEAEDVGVCQGTTRP 120
 Db 116 ftfgsklenkradaaptvsiifpsseqltggasvvcflnmfypkdnvkwkldgser 175
 Qy 121 PTFGGKTKVEIKRTVAAPSVFIPFPDSQGLKSGTASVVCLLNNFYPREAKVQKVDNALQ 180
 Db 176 qnqvlnswtdqskdstysmatstltckdeyhrnsvtceatkstspkvksfnrnc 234
 Qy 181 SGNSQESVTEQDSKSTYSLSTLTLSKADYKHVKYACEVTHQGLSPVTKSFNRGEC 239

RESULT 12
 ENTRY S29593
 TITLE Ig kappa chain (W65) - mouse (fragment)
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change


ACCESSIONS S29593
 REFERENCE S29593
 #authors Seymour, R.
 #submission submitted to the EMBL Data Library, February 1991
 #accession S29593
 #status preliminary
 #molecule_type mRNA
 #residues 1-197 ##label SEY
 #cross-references EMBL:X57856
 SUMMARY #length 197 #checksum 9664

Query Match 54.7%; Score 911; DB 12; Length 197;
 Best Local Similarity 66.0%; Pred. No. 1.59e-92;
 Matches 130; Conservative 34; Mismatches 33; Indels 0; Gaps 0;
 Db 1 eflqlilvlpigalqdivmtcaapsipvtggesasiacrseksallhenadtylywflqrp 60
 Qy 6 QLLGLLLLCVPGSGEWMVQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQKQ 65
 Db 61 gqppqlllyrmenlasgvpdrfsgsgsgtsftlrisveaedvgvfcqhleyppfyfg 120
 Qy 66 QQPPRLIYKVNRSQGVDRFSGSGAGTDTLKISAVEAEDVGVCQGTTRPTPTFG 125
 Db 121 gtlkleikradaaptvsiifpsseqltggasvvcflnmfypkdnvkwkldgserqngv 180
 Qy 126 GTKVEIKRTVAAPSVFIPFPDSQGLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQ 185
 Db 181 nswtdqskdstysms 197
 Qy 186 ESVTEQDSKSTYSLSS 202

RESULT 13
 ENTRY A56169 #type fragment
 TITLE Ig kappa chain V region (clone 23.2) - mouse (fragment)
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
 ACCESSIONS A56169
 REFERENCE A56169
 #authors Monfardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; Godillot, A.P.; Kaushansky, K.; Brown, C.B.; Voet, D.; McCallus, D.E.; Weiner, D.B.; Williams, W.V.
 #journal J. Biol. Chem. (1995) 270:6628-6638
 #title Recombinant antibodies in bioactive peptide design.
 #accession A56169
 #status preliminary; not compared with conceptual translation
 #molecule_type mRNA
 #residues 1-210 ##label MON
 SUMMARY #length 210 #checksum 4986

Query Match 54.4%; Score 907; DB 12; Length 210;
 Best Local Similarity 58.6%; Pred. No. 4.96e-92;
 Matches 123; Conservative 44; Mismatches 42; Indels 1; Gaps 1;
 Db 1 divltgspasltvelgqraticrasksvs-essgymhwgqgkpgppkviylaenle 59
 Qy 21 EWMVQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQKQPGQPPRLIYKVNRS 80
 Db 60 gvypprfsgsgtdftlnhpveedaatyycqhsrelpwtfgggtreikradaaptv 119
 Qy 81 SCVPDRFSGSGAGTDTLKISAVEAEDVGVCQGTTRPTPTFGGKTKVEIKRTVAAPSV 140

(ML)



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protein - protein database search, using Smith-Waterman algorithm

```
Run on: Tue Dec 17 15:25:19 1996; MasPar time 5.87 Seconds
707.578 Million cell updates/sec
```

Tabular output not generated.

Title: >US-08-487-550-6

Description: (1-239) from US08487550.pep

Perfect Score: 1666

Sequence: 1 MSLPAQLGLGLLLCVPSSG.....EVTHQGLSSPVTKSFNRGEC 239

Scoring table: PAM 150

Gap 11

Searched: 49340 seqs, 17385503 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot32

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9

Statistics: Mean 44.652: Variance 76.053: scale 0.587

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Query	Length	DB	ID	Description	Pred. No.
1	756	45.4	133	5	KV2F	HUMAN	IG KAPPA CHAIN PRECUR	1.62e-147	
2	721	43.3	106	4	KAC	HUMAN	IG KAPPA CHAIN C REGI	4.13e-139	
3	656	39.4	113	5	KV2G	MOUSE	IG KAPPA CHAIN V-II R	1.44e-123	
4	656	39.4	117	5	KV2E	HUMAN	IG KAPPA CHAIN PRECUR	1.44e-123	
5	624	37.5	113	5	KV2D	HUMAN	IG KAPPA CHAIN V-II R	5.91e-116	
6	621	37.3	112	5	KV2C	HUMAN	IG KAPPA CHAIN V-II R	3.05e-115	
7	602	36.1	133	5	KV4B	HUMAN	IG KAPPA CHAIN PRECUR	9.75e-111	
8	594	35.7	113	5	KV2B	HUMAN	IG KAPPA CHAIN V-II R	7.64e-109	
9	594	35.7	132	5	KV3F	MOUSE	IG KAPPA CHAIN PRECUR	7.64e-109	
10	589	35.4	115	5	KV2A	HUMAN	IG KAPPA CHAIN V-II R	1.16e-107	
11	584	35.1	134	5	KV4C	HUMAN	IG KAPPA CHAIN PRECUR	1.77e-106	
12	578	34.7	129	5	KV3L	HUMAN	IG KAPPA CHAIN PRECUR	4.62e-105	
13	564	33.9	129	5	KV3M	HUMAN	IG KAPPA CHAIN PRECUR	9.26e-102	

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14	563	33.8	129	5	KV3H_HUMAN	IG KAPPA CHAIN PRECUR	1.59e-101
15	562	33.7	131	5	KV3I_MOUSE	IG KAPPA CHAIN V-II R	2.74e-101
16	544	32.7	113	5	KV2F_MOUSE	IG KAPPA CHAIN V-II R	4.70e-97
17	542	32.5	113	5	KV2E_MOUSE	IG KAPPA CHAIN V-II R	1.39e-96
18	538	32.3	112	5	KV3G_MOUSE	IG KAPPA CHAIN V-III	1.21e-95
19	538	32.3	114	5	KV4A_HUMAN	IG KAPPA CHAIN V-IV R	1.21e-95
20	529	31.8	112	5	KV2D_MOUSE	IG KAPPA CHAIN V-II R	1.56e-93
21	527	31.6	121	5	KV4O_HUMAN	IG KAPPA CHAIN PRECUR	4.58e-93
22	523	31.4	111	5	KV3H_MOUSE	IG KAPPA CHAIN V-III	3.66e-92
23	523	31.4	128	5	KV3K_HUMAN	IG KAPPA CHAIN PRECUR	3.96e-92
24	513	30.8	111	5	KV3O_MOUSE	IG KAPPA CHAIN V-III	8.46e-90
25	512	30.7	111	5	KV3M_MOUSE	IG KAPPA CHAIN V-III	1.48e-89
26	510	30.6	111	5	KV3N_MOUSE	IG KAPPA CHAIN V-III	4.34e-89
27	510	30.6	111	5	KV3C_MOUSE	IG KAPPA CHAIN V-III	4.34e-89
28	510	30.6	112	5	KV3B_MOUSE	IG KAPPA CHAIN V-III	4.34e-89
29	506	30.4	113	5	KV2C_MOUSE	IG KAPPA CHAIN V-II R	3.73e-88
30	506	30.4	120	5	KV2B_MOUSE	IG KAPPA CHAIN PRECUR	3.73e-88
31	505	30.3	109	5	KV3D_HUMAN	IG KAPPA CHAIN V-III	6.38e-88
32	505	30.3	110	5	KV3P_MOUSE	IG KAPPA CHAIN V-III	6.38e-88
33	504	30.3	111	5	KV3A_MOUSE	IG KAPPA CHAIN V-III	1.09e-87
34	503	30.2	106	4	KACB_RAT	IG KAPPA CHAIN C REGI	1.87e-87
35	503	30.2	111	5	KV3J_MOUSE	IG KAPPA CHAIN V-III	1.87e-87
36	501	30.1	109	5	KV3B_HUMAN	IG KAPPA CHAIN V-III	5.47e-87
37	502	30.1	111	5	KV3L_MOUSE	IG KAPPA CHAIN V-III	3.20e-87
38	501	30.1	115	5	KV3I_HUMAN	IG KAPPA CHAIN PRECUR	5.47e-87
39	500	30.0	111	5	KV3R_MOUSE	IG KAPPA CHAIN V-III	9.36e-87
40	499	30.0	111	5	KV3T_MOUSE	IG KAPPA CHAIN V-III	1.60e-86
41	499	30.0	111	5	KV3D_MOUSE	IG KAPPA CHAIN V-III	1.60e-86
42	498	29.9	106	4	KACA_RAT	IG KAPPA CHAIN C REGI	2.74e-86
43	498	29.9	109	5	KV3F_HUMAN	IG KAPPA CHAIN V-III	2.74e-86
44	498	29.9	111	5	KV3Q_MOUSE	IG KAPPA CHAIN V-III	2.74e-86
45	496	29.8	111	5	KV3K_MOUSE	IG KAPPA CHAIN V-II	8.01e-86

ALIGNMENTS

RESULT	1
ID	KV2F HUMAN STANDARD; PRT; 133 AA.
-AC	P06310;
DT	01-JAN-1988 (REL. 06, CREATED)
DDT	01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
TDT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE	IG KAPPA CHAIN PRECURSOR V-II REGION (RPMI 6410).
OS	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 86041852.
RR	KLOBECK H.G., MEINDL A., COMBIATO G., SOLOMON A., ZACHAU H.G.; NUCLEIC ACIDS RES. 13:6499-6513(1985).
RRL	EMBL; 200020; 200020.
DR	PIR; A01890; KZHURP.
DR	HSP; P01607; 4FAR.
KW	IMMUNOGLOBULIN V REGION; SIGNAL.
FT	SIGNAL 1 20
CH	CHAIN 21 133 IG KAPPA CHAIN V-II REGION (RPMI 6410).
D	DOMAIN 21 43 FRAMEWORK 1.
F	DOMAIN 44 59 COMPLEMENTARITY--DETERMINING 1.
D	DOMAIN 60 74 FRAMEWORK 2.
F	DOMAIN 75 81 COMPLEMENTARITY--DETERMINING 2.
D	DOMAIN 82 113 FRAMEWORK 3.
F	DOMAIN 114 122 COMPLEMENTARITY--DETERMINING 3.
D	DOMAIN 123 132 FRAMEWORK 4.

RESULT	2	STANDARD;	PRT;	106 AA.
ID	KAC HUMAN			
AC	P01834;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)			
DE	IG KAPPA CHAIN C REGION.			
GN	IGKC.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
[1]	SEQUENCE (MYELOMA PROTEIN EU).			
RX	MEDLINE; 71064023.			
RA	GOTTLIEB P.D., CUNNINGHAM B.A., RUTISHAUSER U., EDELMAN G.M.;			
RL	BIOCHEMISTRY 9:3155-3161(1970).			
[2]				
RP	EU, DISULFIDE BONDS.			
RP	MEDLINE; 71064027.			
RA	GALL W.E., EDELMAN G.M.;			
RL	BIOCHEMISTRY 9:3188-3196(1970).			
[3]				
RP	SEQUENCE (BENCE-JONES PROTEIN TI).			
RX	MEDLINE; 72188439.			
RA	SUTER L., BARNIKOL H.U., WATANABE S., HILSCHMANN N.;			
RL	HOPPE-SEYLER S Z. PHYSIOL. CHEM. 353:189-208(1972).			
[4]				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 81042304.			
RA	HIETER P.A., MAX E.E., SEIDMAN J.G., MAIZEL J.V. JR., LEDER P.;			
RL	CELL 22:197-207(1980).			
[5]				
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).			
RA	HILSCHMANN N., BARNIKOL H.U., HESS M., LANGER B., PONSTINGL H.,			
RA	STEINMETZ-KAYNE M., SUTER L., WATANABE S.;			
RL	(IN) GAMMA GLOBULINS: STRUCTURE AND FUNCTION, FRANEK F., SHUGAR D.,			
RL	EDS., PP.57-74, ACADEMIC PRESS, NEW YORK, (1969).			
[6]				
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).			
RX	MEDLINE; 68242259.			
RA	HILSCHMANN N.;			
RL	HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 348:1718-1722(1967).			
[7]				

RP	SEQUENCE (BENCE-JONES PROTEIN AG).
RX	MEDLINE; 69234734.
RA	TITANI K., SHINODA T., PUTNAM F.W.;
RL	J. BIOL. CHEM. 244:3550-3560(1969).
[8]	
RN	SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX	MEDLINE; 70201507.
RA	KOHLER H., SHIMIZU A., PAUL C., PUTNAM F.W.;
RL	SCIENCE 169:56-59(1970).
CC	-!- THE EU SEQUENCE HAS THE INV (3) ALLOTYPEIC MARKER, 45-ALA & 83-VAL.
CC	-!- THE EU SEQUENCE HAS THE INV (1,2) ALLOTYPIC MARKER, 45-ALA AND
CC	83-LEU.
DR	PIR; A021116; K3HU.
DR	HSP; P01842; IDFB.
DR	MM; 147200; 11TH EDITION.
DR	PROSITE; PS00290; IG MHC.
KW	IMMUNOGLOBULIN C REGION.
FT	NON TER 1 1
FT	DISULFID 26 86
FT	SULFID 106 106
FT	VARIANT 83 83
FT	CONFLICT 14 14
FT	CONFLICT 57 57
SQ	SEQUENCE 106 AA; 11609 MW; 64333 CN;
	INTERCHAIN (WITH A HEAVY CHAIN).
	V -> L (IN INV(1,2) MARKER).
	D -> N (IN REF. 7 AND 8).
	E -> Q (IN REF. 5 AND 6).
	Query Match 43.3%; Score 721; DB 4; Length 106;
	Best Local Similarity 100.0%; Pred.No. 4.13e-139;
	Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps
Db	1 tvaapsvifppdsdeqlsgtsavcvcclnnfyprkakvqkvkdnlqsgnsqvteqds 60
Qy	134 TVAAPSVIFPPDSDEQLSGTSAVVCCLNNFYPRKAYQKVQVDNALQSGNSQSVEEQDS 193
Db	61 kdetsylstltiskadyekhkvyacevthglspsvtksfnrgec 106
Qy	194 KDTSYLSLSTLTISKADYEKHKYACEVTHGGLSSPVTKSFNRGEC 239
RESULT	3
ID	KVZG_MOUSE STANDARD; PRT; 113 AA.
AC	P01631;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE	IG KAPPA CHAIN V-II REGION (26-10).
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA.
RN	[1]
RN	SEQUENCE.
RC	STRAIN=A/J;
RC	MEDLINE; 83178921.
RA	NOVOTNY J., MARGOLIES M.N.;
RL	BIOCHEMISTRY 22:1153-1158(1983).
CC	-!- THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA PROTEIN THAT
CC	BINDS DIOXIN.
DR	PIR; A01914; KWMS26.
DR	HSP; P01607; IIGI.
KW	IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY; HYBRIDOMA.
FT	DOMAIN 1 23 FRAMEWORK 1.
FT	DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN 40 54 FRAMEWORK 2.
FT	DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN 62 93 FRAMEWORK 3.

[illegible][illegible]

Query Match	39.4%;	Score 656;	DB 5;	Length 117;
Best Local Similarity	80.3%;	Pred. No. 1.44e-123;		
Matches	94;	Conservative	9;	Mismatches 14;
			Indels	0;
			Gaps	0;
Db	1	gsgdvmntgplslvptgcpaeiacrsgallhshgnyldwylktpqsgpqllylg	60	
QY	17	GSGGEWNTOSPLPIPTGEPASISCRSSOSLKHSGDTELSWYQKRPQPPRLLIYKV	76	
Db	61	snraagvdrfsgsgsgdftklisrveadvvyvymagltqtpctfgqtkvkeir	117	
QY	77	SNRDSGVPDRFSGSAGDTFTKISAVEAEADVGVYFCGGATTPPTFTGGGKVEIKR	133	

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RESULT 5
ID KV2D HUMAN STANDARD; PRT; 113 AA.
AC P01617;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN V-II REGION (TEW).
DE
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
[1]
RN SEQUENCE (BENCE-JONES PROTEIN TEW).
RP MEDLINE; 74148480.
RR PUTNAM F.W., WHITLEY E.J. JR., PAUL C., DAVIDSON J.N.;
RXL BIOCHEMISTRY 12:3763-3780 (1973).
RRL [2]
RN SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RP MEDLINE; 73166638.
RR TERRY W.D., PAGE D.L., KIMURA S., ISOBE T., OSSERMAN E.F.,
RXL GLENNER G.G.;
RRL J. CLIN. INVEST. 52:1276-1281 (1973).
CCC -1- THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL WITH THE BENCE
JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
CCC -1- THIS PROTEIN WAS ISOLATED FROM THE URINE OF A PATIENT WITH
PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.
CCC -1- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
RR PIR; A01888; K2HUTW.
DR HSP; P01679; LCBV.
RXL IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; AMYLOID.
RR DOMAIN 1 23 FRAMEWORK 1.
24 39 COMPLEMENTARITY-DETERMINING 1.
20 54 FRAMEWORK 2.
55 61 COMPLEMENTARITY-DETERMINING 2.
62 93 FRAMEWORK 3.
94 102 COMPLEMENTARITY-DETERMINING 3.
103 112 FRAMEWORK 4.
DISULFID 23 93 BY SIMILARITY.
NON_TER 113 113
SQ SEQUENCE 113 AA; 12316 MW; 69216 CN;

Query Match 37.5%; Score 624; DB 5; Length 113;
Best Local Similarity 75.2%; Pred.No. 5.91e-116;
Matches 85; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

Ddb 1 divmtcspplpvtgpgpasiscrsqslhsdgdfylnwlykqpgspzliiyalenra 60
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 21 EVVMVTSQPSLPIPTGEPASISCRSSQSISKUNGDTFLSWYQKPGQPPELLIYKVSNRD 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Ddb 61 sgvdrrfsgsgsqdftlkisrveaedgvvyvcmzalqapifgggtlriekr 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 81 SGVDRFSGSGCACTDFTLKISAVEAEDGVVFCQGTTRPTTFGGGTKEIKR 133
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
ID KV2C HUMAN STANDARD; PRT; 112 AA.
AC P01616;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN V-II REGION (MIL).
DE
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.

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[1]
RN SEQUENCE..
RA DREYER W.J., GRAY W.R., HOOD L.E.;
RL COLD SPRING HARB. SYMP. QUANT. BIOL. 32:353-367(1967).
CC -I- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- THIS IS A BENGE-JONES PROTEIN.
DR PIR; A01887; K2HUM1.
DR HSP; P01679; ICBV.
KW IMMUNOGLOBULIN V REGION; BENGE-JONES PROTEIN.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; 77514 CN;

Query Match 37.3%; Score 621; DB 5; Length 112;
Best Local Similarity 69.9%; Pred. No. 3.05e-115;
Matches 79; Conservative 23; Mismatches 10; Indels 1; Gaps 1;

Db 1 divltqslslptpgpasiscrsqnlzabqbyldwylzkgzspzlllylgenra 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 EVMWTSPLSLPTPGPASISCRSSQSLKHSNGDTFLSWYQKPGQPRLIIYKVSND 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 60 sqvnpfsgsgtbfktlksrvzabvgvycmqalqptlfgggttnveikr 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 81 SGVPDRFSGSGAGDTFLKLSAVEADVGVYFCQGQTRTPPTFGGKVEIKR 133

RESULT 7
ID KV4B HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DE 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-IV REGION (JI).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86041853.
RA KLOBECK H.G., BORKAMM G.W., COMBRIATO G., MOCIKAT R., POHLENZ H.D.,
RA ZACHAU H.G.;
RL NUCLEIC ACIDS RES. 13:6515-6529(1985).
DR PIR; A01904; K4HUTJ.
DR HSP; P01607; IMCP.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-III REGION (JI).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 61 75 FRAMEWORK 2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 83 114 FRAMEWORK 3.
FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 123 132 FRAMEWORK 4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON TER 133 133
SQ SEQUENCE 133 AA; 14632 MW; 101063 CN;
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Query Match 36.1%; Score 602; DB 5; Length 133;
Best Local Similarity 64.2%; Pred. No. 9.75e-111;
Matches 86; Conservative 24; Mismatches 22; Indels 2; Gaps 2;

Db 1 mvlqtqvfiisllwiegaydvmtqpsdlsavelgeratlnckesqsvlyesnnknyla 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 MSIPAQLGLGLLLVTPGSSGEVMTQSPSLPTPGPASISCRSSQSLKHSNGDTFLS 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 wyqdkgqgpkliiywaetresgvpdrrfsgsgtdftitisslqaedvavvyccq-ydt 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 WYQKPGQPRLIIYKVSNDGVPDRFSGSGAGDTFLKLSAVEADVGVYFCQGQTRT 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 120 lptfgggtkveikr 133
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 120 PPTFGGKVEIKR 133

RESULT 8
ID KV2B HUMAN STANDARD; PRT; 113 AA.
AC P01615;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-II REGION (FR).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 76253627.
RA RISEN W.F., JAYON J.-C.;
RL BIOCHEMISTRY 15:3829-3833(1976).
CC -I- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR; A01886; K2HUFR.
DR HSP; P01607; IJEL.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 40 54 FRAMEWORK 2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 62 93 FRAMEWORK 3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 103 112 FRAMEWORK 4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 77707 CN;

Query Match 35.7%; Score 594; DB 5; Length 113;
Best Local Similarity 71.7%; Pred. No. 7.64e-109;
Matches 81; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

Db 1 dvmtqslfipvtlgepasicrsqslvyrbqbtlylbwylqkpgspelliylasyrd 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 21 EVMWTSPLSLPTPGPASISCRSSQSLKHSNGDTFLSWYQKPGQPRLIIYKVSND 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 sqvdpdrfsgsgtdftlksrvzabvgvycmqatzpzytfgggtklzkr 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 81 SGVPDRFSGSGAGDTFLKLSAVEADVGVYFCQGQTRTPPTFGGKVEIKR 133

RESULT 9
ID KV3F_MOUSE STANDARD; PRT; 132 AA.
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FT	DISULFID	43	114	BY SIMILARITY.
FT	NON TER	134	134	
SQ	SEQUENCE	134 AA;	14966 MW; 102930 CN;	
Query Match 35.1%; Score 584; DB 5; Length 134;				
Best Local Similarity 61.2%; Pred. No. 1.77e-106;				
Matches 82; Conservative 27; Mismatches 24; Indels 1; Gaps 1;				
Db	1	mvlqtqvfslilwlsqayqdvmtqapdplavslgeratincskssgilyasdnkyla	60	
Qy	1	MSLPAQLGLLLCPGSSGEVVMVTSQSLPISLITPGEFASISCRSSKLHNGDT-FLS	59	
Db	61	wyqkpqppklllywastregvdpdfsgsgtgtdftltiselaqadvayvycqaynl	120	
Qy	60	WYQKRPQPPRLLIYKVSNRDGVDPDFSGSGAGTDFTLKISAVEADVGVCQGT	119	
Db	121	pwtfqggtkveikr	134	
Qy	120	PPTFGGKTVEIKR	133	

RESULT	12	STANDARD;	PRT;	129 AA.
ID	KV3L HUMAN			
AC	P18135;			
DT	01-NOV-1990 (REL. 16, CREATED)			
DT	01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)			
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)			
DE	IG KAPPA CHAIN PRECURSOR V-III REGION (HAH).			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
BN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 88171307.			
RA	KIPPS T.J., TOMHAVE E., CHEN P.P., CARSON D.A.;			
RL	J. EXP. MED. 167:840-852(1988).			
CC	-I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M			
CC	AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC			
CC	LEUKEMIA.			
DR	PIR; P10022; K3HUHA.			
DR	HSSP; P01607; 1DFB.			
KW	IMMUNOGLOBULIN V REGION; SIGNAL.			
FT	SIGNAL 1 20			
FT	CHAIN 21 129			
FT	DOMAIN 21 43			
FT	DOMAIN 44 55			
FT	DOMAIN 56 70			
FT	DOMAIN 71 77			
FT	DOMAIN 78 109			
FT	DOMAIN 110 118			
FT	DOMAIN 119 129			
FT	DISULFID 43 109			
FT	NON TER 129 129			
FT	SEQUENCE 129 AA; 14070 MW; 95429 CN;			
DR	HSSP; P01607; 1AAG.			

[illegible]

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	
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MPsrch pp protein - protein database search, using Smith-Waterman algorithm

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Run on: Tue Dec 17 15:23:18 1996; MasPar time 6.07 Seconds
        374.956 Million cell updates/sec
```

Tabular output not generated.

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Title:
Description:
Perfect Score:
Sequence:

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Scoring table:

Scoring table: PAM 150

Searched: 81589 seqs, 9523651 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq24

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16

Statistics: Mean 32.388: Variance 166.059: scale 0.195

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query		DB	ID	Description	Pred. No.
			Match	Length				
1	1401	84.1	238	16	R3354	Monoclonal antibody D	7.72e-104	
2	1339	80.4	242	15	R6323	Chimeric 6G4.2.5 light	1.08e-98	
3	1327	79.7	241	5	R2809	Vector pMDR1007.	1.07e-97	
4	1254	75.3	239	5	R24811	Sequence encoded by t	1.21e-91	
5	1247	74.8	234	10	R2951	Human anti-1G6 MAb li	1.41e-89	
6	1217	73.0	349	2	R12128	Human anti-1G6 MAb li	1.41e-88	
7	1217	73.0	414	2	R13111	1B1 IgG aberrant light	1.41e-88	
8	1217	73.0	414	2	R13018	1B1 IgG aberrant light	1.41e-88	
9	1208	72.5	234	3	R20058	Light chain of 3D6 an	7.84e-88	
10	1204	72.3	236	15	R77614	Humanised 5G1.1 VL +	1.68e-87	
11	1202	72.1	236	8	R42065	Human anti-Hbs light	2.46e-87	
12	1190	71.4	218	6	R33312	Humanised Mab11 Versi	2.42e-86	

13	1190	71.4	234	7	R38162	Sequence of the kappa	2.42e-86
14	1174	70.5	233	6	R30777	pH52-9.0 humanised mu	5.11e-85
15	1161	69.7	233	4	R22754	Reshaped CAMPATH-1 an	6.08e-84
16	1154	69.3	236	4	R22565	V11ys-HuKappa region	2.31e-83
17	1151	69.1	214	6	R30776	H5216-158 murine anti	4.09e-83
18	1151	69.1	234	3	R13050	CD4-specific CDR-graf	4.09e-83
19	1148	68.9	214	7	R43338	Completely humanised	7.23e-83
20	1146	68.8	241	15	R77613	Humanised 5G1.1 VL +	1.06e-82
21	1142	68.5	240	15	R77612	Humanised 5G1.1 VL +	2.27e-82
22	1140	68.4	237	4	R24047	Light chain of 4D5 Fa	3.32e-82
23	1138	68.3	236	1	P93910	Y22 light chain of an	4.86e-82
24	1132	67.9	234	8	R47452	chT84.12 L6 light ch	1.52e-81
25	1128	67.7	233	4	R22755	Reshaped CD4 antibody	3.26e-81
26	1127	67.6	235	16	R94558	Humanised antibody MN	3.94e-81
27	1125	67.5	237	15	R86319	Anti-IL-8 Mab 5.12.14	5.77e-81
28	1123	67.4	232	15	R80616	Anti-human IL-4 human	8.44e-81
29	1108	66.5	219	15	R77608	Chameric light chain	1.47e-79
30	1055	63.3	239	13	R76087	Mab 55.1 light chain.	3.49e-75
31	1053	63.2	218	14	R75461	Mouse antibody H3-3 1	5.10e-75
32	1050	63.0	239	12	R65702	Anti-tobacco mosaic v	9.02e-75
33	1020	61.2	220	10	R53802	FAB light chain for 1	2.69e-72
34	989	59.4	219	13	R76086	Mab 55.1 light chain.	9.65e-70
35	961	57.7	219	8	R44495	Sequence of the immun	1.95e-67
36	950	57.0	218	14	R75457	Mouse antibody FB3-2	1.57e-66
37	950	57.0	218	14	R75457	Mouse antibody FB3-2	1.57e-66
38	913	54.8	223	4	P40031	Kappa anti-carcinoemb	1.73e-63
39	911	54.7	215	12	R74781	Light chain of 59.1 a	2.53e-63
40	910	54.6	212	10	R52659	Porphyrin antibody 1i	3.06e-63
41	905	54.3	172	3	R15199	R6-5-D6 anti-ICAM-1	7.87e-63
42	903	54.2	235	8	R47451	T84.12 L4-12.1 light	1.15e-62
43	903	54.2	235	8	R47449	T84.12 light chain.	1.15e-62
44	891	53.5	173	3	R15039	Murine anti-ICAM mono	1.11e-61
45	867	52.0	215	8	R43674	Mouse anti-bovine mro	1.04e-59

ALIGNMENTS

RESULT	1	
ID	R93554 standard; Protein; 238 AA.	
AC	R93554;	
DT	20-AUG-1996 (first entry)	
DE	Monoclonal antibody DNA light chain against 65 kD hCMV antigen.	
KW	Polymerase chain reaction; primer; amplify; PCR; light chain; MAB;	
KW	65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.	
OS	Synthetic.	
Key	Location/Qualifiers	
FT	Peptide 1..20	
FT	/note="Signal peptide"	
FT	Protein 21..238	
FT	/note="Mature light chain"	
PN	J08038178-A.	
PD	13-FEB-1996.	
PF	20-FEB-1995; 030742.	
PR	18-FEB-1994; JP-021628.	
PA	(N1S) NISSHINO IND INC.	
PA	(TANA/) TANAKA H.	
DR	WPI; 96-154852/16.	
DR	N-PSDB; T18060.	
PT	Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -	
PT	produced by primer amplification, used in the diagnosis of hCMV	
PT	infection	
PS	Claim 5; Page 19; 22pp; Japanese.	
CC	The sequences given in R93553-54 represent the heavy and light chains	
CC	respectively of a monoclonal antibody against a 65 kD antigen of human	

J09209305-A.
 11-JUN-1992.
 27-NOV-1991; U08843.
 27-NOV-1990; US-618547.
 (BIOL J BIOGEN INC.
 Burkly LC, Chisholm PL, Rosa JJ, Rosa MD, Thomas DW;
 WPI; 92-398399/48.
 N-PSDB; Q30920.
 New anti-CD4 antibody homologues - which bind CD4, do not block
 binding of HIV gp120 to CD4 but block HIV-induced syncytia
 formation between CD4+ cells
 Disclosure; Page 166-7; 205pp; English.
 The sequence given is encoded by the insert of the vector pMDR1007.
 pMDR1006 (see Q30919) and pSAB132 (see Q30906) were used in the
 construction of this vector. Three fragments were ligated together
 to generate pMDR1006; a 572 bp fragment of pMDR985 (see Q30913), a
 3442bp AatII/EcoRV fragment of pMDR986 (see Q30918) and a 326 bp
 EcoRV/BglII fragment of pMDR1003 (see Q30900). The ligation mixture
 was used to transform E. coli JAZ21(Iq) to ampicillin resistance.
 pMDR1006 was cleaved with NotI and the 1693 bp fragment isolated was
 ligated into NotI linearised pSAB132 which had been dephosphorylated
 by calf alkaline phosphatase. This generates the plasmid pMDR1007.
 The dephosphorylated mixture was fractionated through low temperature
 melting agarose and used to transform E. coli JAZ21(Iq) to ampicillin
 resistance. The pMDR1007 insert comprises DNA encoding, in a 5' to 3'
 order, the immunoglobulin kappa chain signal peptide, amino acid (AA)
 1-AA112 of the humanised 5A8 light chain variable region (LV) followed
 by genomic DNA encoding AA108-AA214 of the human kappa light chain,
 ie. the light chain constant region (LC). This polypeptide is an
 antibody homolog which was shown to bind to CD4 but did not block the
 binding of gp120 to CD4. CD4 is a cell surface glycoprotein of CD4+
 lymphocytes (helper/inducer cells). The homolog blocked HIV-induced
 syncytia formation. This homolog can be used in the detection,
 prophylaxis and treatment of diseases caused by infective agents whose
 primary targets are CD4+ cells.
 Sequence 241 AA;

Query Match 79.7%; Score 1327; DB 5; Length 241;
Best Local Similarity 80.0%; Pred. No. 1.07e-97;
Matches 192; Conservative 23; Mismatches 23; Indels 2; Gaps 2;

[illegible]

RESULT 4

RZ48II standard; Protein; 739 AA.

AC	RZ4811;
DT	28-DEC-1992 (first entry)

DE Sequence encoded by the chimeric kappa chain cDNA (lgkv)
DE in pTB1427

Chimeric monoclonal antibody; anti-fibrin antibody; primer;	
antithrombotic agent; myocardial infarction therapy.	
Synthetic.	
Key	Location/Qualifiers
Peptide	1..20
/label= leader	
Region	21..133
/label= V-kappa	
Region	134..239
/label= C-kappa	
Misc difference 130	
/note= "Alternatively = Glu"	
EP-491351-A.	
24-JUN-1992.	
17-DEC-1991; 121591.	
18-DEC-1990; JP-413829.	
11-NOV-1991; JP-294464.	
(TAKE) TAKEDA CHEM IND LTD.	
Iwasa S, Taka H, Watanabe T, Tada H;	
WPI; 92-209528/26.	
N-PSDB; Q25691.	
Chimeric monoclonal antibodies - contain anti-human fibrin	
antibody light and heavy chain variable and constant for treating	
thrombotic conditions e.g. myocardial infarction	
Example; Figure 9; 87pp; English.	
Poly(A)+ RNA was prepd. from the anti-fibrin chimeric Ab-producing	
transformant FIB1-H01/X63 and used as a template to clone human	
C-kappa cDNA, using the oligo-dT (Pharmacia) primer as a primer for	
first strand cDNA synthesis and the 3'E-kappa and 5'C-kappa primers	
for the PCR. An amplified DNA fragment of about 0.33kb was isolated	
and used to create a C-kappa cDNA contg. vector, pTB1394. Using the	
same technique, with the 3'E-kappa primer as a primer for first	
strand synthesis and the 5'L-kappa and 3'C-kappa primers for the	
PCR, an anti-fibrin V-kappa (V-kappa-v) cDNA was amplified.	
Furthermore, using the 3'E-kappa primer for first stand synthesis	
and the 5'mv-kappa and the 3'mv-kappa primers for the PCR, an	
anti-fibrin V-kappa cDNA (V-kappa-FIB) was amplified. In addition,	
a leader sequence cDNA (L-kappa) was amplified using the 3'C-kappa	
as a primer for first strand synthesis and the 5'S-kappa and 3'L-	
kappa primers for the PCR. The amplified gene fragments (L-kappa:	
V-kappa-v; V-kappa-FIB) were isolated and used to construct	
respectively plasmids pTB1391, pTB1392, and pTB1393. L-kappa, V-	
kappa and C-kappa were joined together to give a plasmid, pTB1427,	
contg. the whole length of the chimeric kappa chain cDNA.	
Sequence 239 AA;	

Query Match 75.3%; Score 1254; DB 5; Length 239;
Best Local Similarity 77.0%;
Pred. No. 1.21e-91;
Matches 184; Conservative 29; Mismatches 25; Indels 1; Caps 1;

[illegible]

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US-08-487-550-6.rag

7

Qy 181 SGNQSVTEQDSKDSYSLSTLTKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 5

ID R52951 standard; Protein; 234 AA.
AC R52951;
DT 27-OCT-1994 (first entry)
DE Human anti-IgE MAb light chain.
KW Human IgE; CH4 region; triggers mediator release;
KW Mast cells; Monoclonal antibody; allergy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 21..128
FT /label= light chain variable region
PN EP-592230-A.
PD 13-APR-1994.
PF 07-OCT-1993; 308006.
PR 07-OCT-1992; JP-293800.
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
PI Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N;
PI Yoshida T;
DR WPI; 94-120330/15.
DR N-PSDB; Q71872.
PT Human monoclonal anti-IgE peptide antibody - inhibits histamine
PT releasing from mast cells by allergen stimulation, useful for
PT preventing allergies
PS Claim 3; Page 12; 21pp; English.
CC R52951 shows the light chain of a human type anti-IgE peptide
CC monoclonal antibody which inhibits the signal transmission for
CC the release of chemical mediator from mast cells and basophils
CC stimulated with allergen. The antibody can be used for the
CC prophylaxis and the therapy of allergy.
SQ Sequence 234 AA;

Query Match 74.8%; Score 1247; DB 10; Length 234;

Best Local Similarity 76.2%; Pred. No. 4,61e-91;

Matches 182; Conservative 30; Mismatches 22; Indels 5; Gaps 3;

Db 1 meapqllflllllwlptdgtelvmgtgatlavspggraalectrasqgv--sn-n--law 55

Qy 1 MSIPAGLLGLLCLVCPSSGEVWMTQSPUSLPTTPGEPASISCRSSQSLKHSNGDTFLSW 60

Db 56 yqqkpaqprlllygastratgiparfsgsggtfdltlisselgsedfaiyyccqyswp 115

Qy 61 YQOKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEADVGVYFCQGRTP 120

Db 116 rtfqggtkvdllkgtaavpffpsdeqlkgatavvcllmfypreakvqkvdnalq 175

Qy 121 PTFGGGTVEIKRTVAAPSVFIFPPSDEQKLSCTASVWCLLNINYPREAKVQMKVDNALQ 180

Db 176 sgnqsqvteqdekdstalstltskadylekkyacevthgglaspvtskfnrgec 234

Qy 181 SGNQSVTEQDSKDSYSLSTLTKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 6

ID R12128 standard; Protein; 349 AA.
AC R12128;
DT 01-AUG-1991 (first entry)
DE 1B1 IgE aberrant light chain with duplicated variable region.
KW immunoglobulin G; light chain; variable region; duplication;
KW passive immunity; group B streptococci.
OS Homo sapiens.
FH Key Location/Qualifiers

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US-08-487-550-6.rag

8

FT Peptide 1..17
FT /label= leader peptide
FT Region 18..130
FT /label= variable region
FT /note= "L'V 1" 131..243
FT Region 131..243
FT /label= variable region
FT /note= "L'V 2" 244..345
FT Region 244..345
FT /label= constant region
PN W09106305-A.
PD 16-MAY-1991.
PF 06-NOV-1990; U06426.
PR 07-NOV-1989; US-432700.
PA (BRIM) BRISTOL-MYERS SQUIB.
PI Shuford WW, Harris LJ, Raff HV;
DR WPI; 91-163947/22.
DR N-PSDB; Q11878.
PT Oligomeric immunoglobulin(ε) with high avidity for antigen(ε) -
PT formed by duplicating esp. variable region of light chain of IgG
PT class
PS Example 5; Fig 16; 104pp; English.
CC This sequence is deduced from the cDNA clone 4B9-Vk15 and includes
CC the amino acid sequence beyond the first stop codon. The clone is
CC incomplete, starting from the G of the ATG initiator codon, but the
CC initial Met is given. Antibody molecules of the invention can
CC include one or two aberrant light chains containing a duplicated
CC variable region, to produce heavier antibodies. These heavier
CC antibodies were found to have higher avidity than antibodies with
CC just a single copy of the L'V region. The antibodies can be used to
CC treat disease, e.g. infection by Streptococcus agalactiae. They are
CC able to pass across the placenta.
CC See also Q11879 and Q11880.
SQ Sequence 349 AA;

Query Match 73.0%; Score 1217; DB 2; Length 349;

Best Local Similarity 79.0%; Pred. No. 1.41e-88;

Matches 177; Conservative 27; Mismatches 13; Indels 7; Gaps 4;

Db 131 ttgeivltsgpatlslspgrratlsctraesgv----q-sylawycqkpgaprpilydas 185

Qy 18 SSGEWMVMTQSPUSLPTTPGEPASISCRSSQSLKHSNGDTFLSWYQOKPGQPPRLLIYKVS 77

Db 186 nratgiparfsgsggtfdltlisselgsedfaiyyccqkvdnalq 245

Qy 78 NRDSGVPDRFSGSGAGTDFTLKISAVEADVGVYFCQ-CTRTP-PTFGGTVEIKRTV 135

Db 246 aapsvfifpsdeqlkgatavvcllmfypreakvqkvdnalqsgnqsqvteqdek 305

Qy 136 RAPSVPFIFPPSDEQKLSCTASVWCLLNINYPREAKVQMKVDNALQSGNSQESVTEQDSKD 195

Db 306 styelestltltskadylekkyacevthgglaspvtskfnrgec 349

Qy 196 STYLSLSTLTKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 7

ID R13111 standard; Protein; 414 AA.
AC R13111;
DT 10-MAR-1993 (revised)
DT 01-AUG-1991 (first entry)
DE 1B1 IgE aberrant light chain with duplicated variable region.
KW immunoglobulin G; light chain; variable region; duplication;
KW passive immunity; group B streptococci.

OS Homo sapiens. Location/Qualifiers
 FH Key
 FT Peptide 1..17
 FT /label= leader peptide
 FT Region 18..130
 FT /label= variable region
 FT /notes= "L'V 1"
 FT Region 131...243
 FT /label= variable region
 FT /notes= "L'V 2"
 FT Region 244...345
 FT /label= constant region
 PN W09106305-A.
 PD 16-MAY-1991.
 PF 06-NOV-1990; U06426.
 PR 07-NOV-1989; US-432700.
 PA (BRIM) BRISTOL-MYERS SQUIB.
 PI Shuford WM, Harris LJ, Raff HV;
 DR WPI; 91-163947/22.
 DR N-PSDB; Q11878.
 PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
 PT formed by duplicating esp. variable region of light chain of IgG
 PT class
 PS Example 5; Fig 16; 104pp; English.
 CC This sequence is deduced from the cDNA clone 4B9-Vk15 and includes
 CC the amino acid sequence beyond the first stop codon ("x" in the
 CC sequence represents a nonsense codon). The clone is incomplete,
 CC starting from the G of the ATG initiator codon, but the initial Met
 CC is given. Antibody molecules of the invention can include one or two
 CC aberrant light chains containing a duplicated variable region, to
 CC produce heavier antibodies. These heavier antibodies were found to
 CC have higher avidity than antibodies with just a single copy of the
 CC L'V region. The antibodies can be used to treat disease, e.g.
 CC infection by Streptococcus agalactiae. They are able to pass across
 CC the placenta.
 CC See also Q11879 and Q11880.
 SQ Sequence 414 AA;

Query Match 73.0%; Score 1217; DB 2; Length 414;
 Best Local Similarity 79.0%; Pred. No. 1.41e-88;
 Matches 177; Conservative 27; Mismatches 13; Indels 7; Gaps 4;
 Db 131 ttgeivltgspatlslspgeratlsacraagsv----g-sylawqqkpgaprpiliydas 185
 Qy 18 SSGEVWMTQSPLSLPTPCEPASISCRSSQSLKSHNGDTFLSWYQKPGQPPRLIIYKVS 77
 Db 186 nratgiparfegsgtdftltisslepedfavvyqchrdnwpqgafgggtkveikrtv 245
 Qy 78 NRDSGVDPDRFSGSGAGTDTFLIKISAVEAEDVGVFYFCGQ-GTRTP-PTFGGKTKVEIKRTV 135
 Db 246 aapsvfifppadeqlkqgtasvvccllmfypreakvqkvkvdnalsqnsqesvteqdsd 305
 Qy 136 AAPSVFIFPPDSDEQLKSGTASVWCLINNFYPREAKVQKVDNALQSGNSQESVTEQDSK 195
 Db 306 styslsstltlskadyekhkvyacevthglspsvtfksfnrgcc 349
 Qy 196 STYLSLSSTLTLSKADYKHKVYACEVTHGLSLSPVTKSFNRGEC 239
 RESULT 8
 ID R13018 standard; Protein; 414 AA.
 AC R13018;
 DT 01-AUG-1991 (first entry)
 DE 181 IgC aberrant light chain with duplicated variable region.

KW immunoglobulin G; light chain; variable region; duplication;
 OS Homo sapiens. Location/Qualifiers
 FH Key
 FT Peptide 1..17
 FT /label= leader peptide
 FT Region 18..130
 FT /label= variable region
 FT /notes= "L'V 1"
 FT Region 131..243
 FT /label= variable region
 FT /notes= "L'V 2"
 FT Region 244..345
 FT /label= constant region
 PN W09106305-A.
 PD 16-MAY-1991.
 PF 06-NOV-1990; U06426.
 PR 07-NOV-1989; US-432700.
 PA (BRIM) BRISTOL-MYERS SQUIB.
 PI Shuford WM, Harris LJ, Raff HV;
 DR WPI; 91-163947/22.
 DR N-PSDB; Q11878.
 PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
 PT formed by duplicating esp. variable region of light chain of IgG
 PT class
 PS Example 5; Fig 16; 104pp; English.
 CC This sequence is deduced from the cDNA clone 4B9-Vk15 and includes
 CC the amino acid sequence beyond the first stop codon ("x" in the
 CC sequence represents a nonsense codon). The clone is incomplete,
 CC starting from the G of the ATG initiator codon, but the initial Met
 CC is given. Antibody molecules of the invention can include one or two
 CC aberrant light chains containing a duplicated variable region, to
 CC produce heavier antibodies. These heavier antibodies were found to
 CC have higher avidity than antibodies with just a single copy of the
 CC L'V region. The antibodies can be used to treat disease, e.g.
 CC infection by Streptococcus agalactiae. They are able to pass across
 CC the placenta.
 CC See also Q11879 and Q11880.
 SQ Sequence 414 AA;

Query Match 73.0%; Score 1217; DB 2; Length 414;
 Best Local Similarity 79.0%; Pred. No. 1.41e-88;
 Matches 177; Conservative 27; Mismatches 13; Indels 7; Gaps 4;
 Db 131 ttgeivltgspatlslspgeratlsacraagsv----g-sylawqqkpgaprpiliydas 185
 Qy 18 SSGEVWMTQSPLSLPTPCEPASISCRSSQSLKSHNGDTFLSWYQKPGQPPRLIIYKVS 77
 Db 186 nratgiparfegsgtdftltisslepedfavvyqchrdnwpqgafgggtkveikrtv 245
 Qy 78 NRDSGVDPDRFSGSGAGTDTFLIKISAVEAEDVGVFYFCGQ-GTRTP-PTFGGKTKVEIKRTV 135
 Db 246 aapsvfifppadeqlkqgtasvvccllmfypreakvqkvkvdnalsqnsqesvteqdsd 305
 Qy 136 AAPSVFIFPPDSDEQLKSGTASVWCLINNFYPREAKVQKVDNALQSGNSQESVTEQDSK 195
 Db 306 styslsstltlskadyekhkvyacevthglspsvtfksfnrgcc 349
 Qy 196 STYLSLSSTLTLSKADYKHKVYACEVTHGLSLSPVTKSFNRGEC 239
 RESULT 9
 ID R20058 standard; Protein; 234 AA.
 AC R20058;

DT 25-MAR-1992 (first entry)
DE Light chain of 3D6 anti-HIV antibody.
KW Plaamid pUC3D6LC; human immunodeficiency virus; AIDS;
KW complementarity determining region.
OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..22

FT /label= signal

FT Protein 23..234

FT Region 23..45

FT /label= Framework_1

FT Region 46..56

FT /label= CDR_1

FT Region 57..71

FT /label= Framework_2

FT Region 72..78

FT /label= CDR_2

FT Region 79..110

FT /label= Framework_3

FT Region 111..117

FT /label= CDR_3

FT Region 118..127

FT /label= Framework_4

FT Region 128..234

FT /label= Constant_region

PN W09118983-A.

PD 12-DEC-1991.

PF 28-MAY-1991; 100067.

PR 29-MAY-1990; AT-001178.

PA (JUNG/) JUNGRAUER A.

PI Felgenhauer M, Himmel G, Kohl J, Steindl F;

DR WPI; 92-007468/01.

DR N-PSDB; Q20067.

PT Recombinant protein which binds to complex viral antigen and

PT HIV-1 - contains variable region of antibody derived from 3D6

PT cell line, used for detecting HIV-1 antigen

PS Claim 3; Page 28; 52pp; German.

CC The variable region of the light chain is used in a recombinant

CC protein with the variable region from the heavy chain of 3D6,

CC the two V regions being joined by a linker. The recombinant

CC protein binds to HIV gp160.

CC See also Q20066 and Q20068.

SQ Sequence 234 AA;

Query Match 72.5%; Score 1208; DB 3; Length 234;

Best Local Similarity 74.5%; Pred. No. 7,84e-88;

Matches 178; Conservative 29; Mismatches 25; Indels 7; Gaps 4;

Db 3 mrvpaqlqllllwlpgakcdlqmtqspstlaasvqdrvtitccasqi--ar---wlaw 57

Qy 1 MSIPAQLLGLLLLCVPGSSGEVWWTQSPISLPIPTGEPASISCRSSQSIKHSNGDTFLSW 60

Db 58 yqkpkpvpklllykassleagvpsrfsgsgteftltlsslgpddfatyvcqq-vnsy 116

Qy 61 YQKPKQPRLLIYKVSNRDVGVPDRFSGSGAGTDFTLKISAVEADVGVYFCGGQTRTP 120

Db 117 -sfqgpkvdkrtvaapsvfifpsdeqlkgetasvvccllmmfypreakvqkvhdnqlq 175

Qy 121 PTFGGGKTVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLLNNFYPREAKVQKVDNALQ 180

Db 176 agnsqesvteqdskdstyslestltlekadyekhhkvacevthgqlspvtskfnrgce 234

Qy 181 SGNSESQSVTEQDQSDSTYSLSSTLTLSKADYKHKVYACEVTHGQLSPVTSKFNRGEC 239

RESULT 10

ID R77614 standard; Protein; 236 AA.

AC R77614;

DT 15-MAR-1996 (first entry)

DE Humanised 5G1.1 VL + 012.

KW Complement C5; haemolysis; kidney; glomerulonephritis;

KW monoclonal antibody; antiinflammatory; antibody engineering;

KW humanised antibody; complementarity determining region; CDR;

ds.

OS Synthetic.

FH Key Location/Qualifiers

FT Peptide 1..23

FT /label= sig_peptide

FT Peptide 23..236

FT /label= mat_peptide

FT Region 47..57

FT /label= CDR-L1

FT Region 73..79

FT /label= CDR-L2

FT Region 112..120

FT /label= CDR-L3

PN W09529697-A1.

PD 09-NOV-1995.

PF 01-MAY-1995; U05688.

PR 02-MAY-1994; US-236208.

PA (ALEX-) ALEXION PHARM INC.

PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;

PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;

PI Wang Y, Wilkins JA;

DR WPI; 95-392923/50.

DR N-PSDB; T08486.

PT Treating glomerulonephritis with antibody against complement C5

PT component - to inhibit complement induced cell lysis

PS Claim 40; Page 132-34; 181pp; English.

CC A humanised CDR-grafted light chain, designated 5G1.1 VL + 012

CC (R77614), includes CDRs derived from mouse anti-C5 monoclonal

CC antibody 5G1.1. DNA (T08486) coding for the light chain can be

CC subcloned together with DNA (T08484) coding for a humanised Fd

CC (R77611) into vector APEX-3P (T08476) for expression of humanised

CC antibody in human 293 EBNA cells. Such recombinant antibodies retain

CC the ability of mAb 5G1.1 to block human complement C5a generation and

CC thus to reduce glomerular inflammation and kidney dysfunction

CC associated with glomerulonephritis.

SQ Sequence 236 AA;

Query Match 72.3%; Score 1204; DB 15; Length 236;

Best Local Similarity 74.5%; Pred. No. 1.68e-87;

Matches 178; Conservative 26; Mismatches 30; Indels 5; Gaps 4;

Db 3 mrvpaqlqllllwlrgarcdlqmtqspstlaasvqdrvtitccaseni--g-a-lnw 57

Qy 1 MSIPAQLLGLLLLCVPGSSGEVWWTQSPISLPIPTGEPASISCRSSQSIKHSNGDTFLSW 60

Db 58 yqkpkpvpklllygatnldqvpvrsfsgsgteftltlsslgpddfatyvcqvlnp 117

Qy 61 YQKPKQPRLLIYKVSNRDVGVPDRFSGSGAGTDFTLKISAVEADVGVYFCGGQTRTP 120

Db 118 lfqgqtkveikrtvaapsvfifpsdeqlkgetasvvccllmmfypreakvqkvhdnqlq 177

Qy 121 PTFGGGKTVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLLNNFYPREAKVQKVDNALQ 180

Db 178 agnsqesvteqdskdstyslestltlekadyekhhkvacevthgqlspvtskfnrgce 236

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Qy 181 SGNQSEVTEQDSKDSYLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 11

ID R42065 standard; Protein; 236 AA.
AC R42065;
DT 29-APR-1994 (first entry)
DE Human anti-HBs light chain.
KW Antibody; Ab; light; heavy; chain; hepatitis B;
KW HB; surface antigen.
OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..22

FT /label= sig_peptide

FT Protein 23..236

FT /label= mat_protein

PN W09320205-A.

PD 14-OCT-1993.

PF 30-MAR-1993; J00396.

PR 30-MAR-1992; JP-074678.

PA (SUNR) SUNTORY LTD.

PI Arima K, Kurihara T, Matsukura S, Nishihara T, Tsuruoka N;

DR WPI; 93-336913/42.

DR N-PSDB; Q49943.

PT Human anti-hepatitis B surface antigen antibody gene - can be

PT used to produce L and H chains of the antibody in large quantity

PS Disclosure; Fig 4-5; 46pp; Japanese.

CC Polynucleotides encoding the L and H chains of human anti-HBs

CC Ab are given in Q49943-Q49944. The Ab can be easily produced in

CC large quantities for therapeutic use.

SQ Sequence 236 AA;

Query Match 72.1%; Score 1202; DB 8; Length 236;

Best Local Similarity 73.6%; Pred. No. 2.46e-87;

Matches 176; Conservative 29; Mismatches 29; Indels 5; Gaps 2;

Db 3 mrpaelqlgllllwfgardcldmtqspamaaavdvrtitcrasqgi----gn-vlww 57

Qy 1 MSPLAQLGILLLLCVPGSGEWMVTPSLIPITPGEPASISCRSSQSLKHSNGDTLSW 60

Db 58 fqqkpkvprklyaaeslqgvpsrfsqsgstefltlslrqpdefatyylhnnyp 117

Qy 61 YQQKPGQPRLLIYKVSNDGVPDRFSGSGAGTDTLKISAVEAEDVGVEGCGGTRTP 120

Db 118 lsfqggtkveikrtvaapsvfifpsdeqlkegtasvcllnmfypreakvqkvdhnlq 177

Qy 121 PTFGGTKVEIKRTVAAPSVFIFPPSDEQIKSGTASVCLLNMFYPREAKVQKVQVDMALQ 180

Db 178 sgnqesvteqdsksdetysestltlsekadyekhyacevthqglssptksfnrgec 236

Qy 181 SGNQSEVTEQDSKDSYLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 12

ID R33312 standard; Protein; 218 AA.

AC R33312;

DT 05-JUL-1993 (first entry)

DE Humanised MaEl1 Version 1 (intact IgG) light chain.

KW Antibody; high affinity; FcE_H; low affinity; FcE_L;

KW IgE receptor; histamine; mast cell; basophil; Kabat;

KW CDR; murine; MAEl1; Fab; humaellv1.

OS Synthetic.

PN W09304173-A.

PD 04-MAR-1993.

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14

PF 14-AUG-1992; U06860.
PR 14-AUG-1991; US-744768.
PR 07-MAY-1992; US-879495.
PA (GETH) GENENTECH INC.
PI Jardieu PM, Presta LG;
DR WPI; 93-094004/11.
PT Polypeptide(s) binding to specific Fc epsilon receptors - act as
PT IgE antagonists; useful for treating and preventing IgE-mediated
PT disorders e.g. allergies
PS Example 4; Fig 3; 113pp; English.
CC Residues were selected from MaEl1 and inserted or substituted into
CC a human Fab antibody background (Vh region Kabat subgroup III and Vh
CC region kappa subgroup I). A first version, humaellv1 or version 1 is
CC given below. The affinity of version 1 was assayed and found to be
CC ca. 100 times lower than that of the donor antibody MaEl1.
CC Therefore, further modifications in the sequence of version 1
CC were made.
SQ Sequence 218 AA;

Query Match 71.4%; Score 1190; DB 6; Length 218;
Best Local Similarity 76.7%; Pred. No. 2.42e-86;
Matches 168; Conservative 26; Mismatches 24; Indels 1; Gaps 1;

Db 1 diqltqspesisaavdvrtitcrasqsvdy-dqdsymvwyqgkpkapkllyaaayle 59

Qy 21 EWMVTQSPILPITPGEPASISCRSSQSLKHSNGDTLSWYQKPGQPRLLIYKVSNRD 80

Db 60 egypsrfsqsgstefltlslrqpdefatyycqshedyfqqgtkveikrtvaapsv 119

Qy 81 SGVPDRFSGSGAGTDTLKISAVEAEDVGVEGCGGTRTPPTFGGTKVEIKRTVAAPSV 140

Db 120 fifpsdeqlkegtasvcllnmfypreakvqkvdhnlqsgnsgesvteqdsksdetyl 179

Qy 141 FIFPPSDEQIKSGTASVCLLNMFYPREAKVQKVQVDMALQSGNSQESVTEQDSKDSYSL 200

Db 180 estltlsekadyekhyacevthqglssptksfnrgec 218

Qy 201 SSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 13

ID R38162 standard; Protein; 234 AA.

AC R38162;

DT 01-OCT-1993 (first entry)

DE Sequence of the kappa light chain variable region (VK) of human

DE immunoglobulin G3 (IgG3) produced by transformed human B-cell line

DE 88BV59, ATCC CRL 10624.

KW B-cell; immunoglobulin g; cancer; tumour.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 1..214

FT /tag= a

FT /label= 1st AA denoted AA#1

FT Region 24..49

FT /tag= b

FT /label= CDR 1

FT Region 50..88

FT /tag= c

FT /label= CDR 2

FT Region 89..108

FT /tag= d

FT /label= CDR 3

FT Region 109..214

FT /tag= e

```

FT      /label= CON
PN      EP-546634-A.
PD      16-JUN-1993.
PF      09-DEC-1992; 203827.
PR      13-DEC-1991; US-807300.
PP      (ALKU ) AKZO NV.
PA      Crichton VZ, Kobern BJ;
PI      WPI: 93-190019/24.
PT      N-PSDB; Q43773.
PT      Transformed human B-cell line for monoclonal antibody prodn. for
PT      cancer diagnosis - prepd from peripheral blood B-cells of cancer
PT      patients actively immunised with autologous tumour antigen, for
PT      treating cancers
PS      Claim 9; Fig 3; 18pp; English.
PS      The 88BV59 kappa light chain sequence is indicated by the posns.
CCC     of the CDRs and the constant region exon. 88BV59 utilises Vx1 and
CCC     Jx5. The first NH2 terminal 22 residues were confirmed by AA
CCC     sequencing.
CC      Sequence 234 AA;
SQ

```

Query Match	71.4%;	Score 1190;	DB 7;	Length 234;
Best Local Similarity	74.3%;	Pred. No. 2.42e-86;		
Matches	176;	Conservative	30; Mismatches	25; Indels 6; Gaps 3;
Db	3	paqlglilllwpgarcdilqtgpfleasvgdvrtitcrsaqj--s---sylawyqq 57		
		: : : : : : : : : : : : : : : :		
QY	4	PAQLGLLLLCVPGSGGEWMTOSP.LSLTPGEPASISCRSSQSLKHSNGDTFLSMYYQQ 63		
Db	58	kpgakpaklllyaaaslqsgvpsfsgsggtftltislalqpdefatycyqqdngyprit 117		
		: : : : : : : : : : : : : : : : :		
QY	64	KTGPQRLLLYKYNSRDSGVDPDRFSFGSAGTDFTKLSAVEADVGYYVCQGTRTP-T 122		
Db	118	fqgqtrleirtrvaapsvfiipdsedqlksqtaavccllmfyreakvwkvvdhalqsq 177		
		: : : : : : : : : : : : : : : : :		
QY	123	FCGGTKVEIKRTVAAPSVFIIPPSSDQLKSQTASVWCCLLNNEYPREAKVQWKVDNALQS 182		
Db	178	nqaesvtqdskdstyslestltistadyekhkyyacevthqslspvtsfnreqc 234		
		: : : : : : : : : : : : : : : : :		
QY	183	NQSESVTEQSDSKOSTYSLSSTLTLSKADYEKKHYACEVTHQGLSPVTXSFNREQC 239		

RESULT	14	
ID	R30777	standard; protein; 233 AA.
AC	R30777;	
DT	12-MAY-1993	(first entry)
DE	ph52-9.0 humanised murine anti-CD18 antibody light chain.	
KE	Humanisation; rapid; monoclonal antibody.	
OS	Mus musculus.	
PN	W09222653-A.	
PD	23-DEC-1992.	
PF	15-JUN-1992;	U05126.
PR	14-JUN-1991;	US-715272.
PA	(GETH) GENENTECH INC.	
PI	Carter PJ, Presta LG.	
DR	WPI; 93-018139/02.	
PT	Humanisation of antibodies - by molecular modelling of the variable domains and alteration by gene conversion mutagenesis	
PS	Dislosure; Fig 68; 126pp; English.	
CC	The sequence is that of the humanised light chain sequence of	
CC	murine anti-CD18 antibody pH52-9.0.	
CC	Sequence	233 AA;

Query Match 70.5%; Score 1174; DB 6; Length 233;
Best Local Similarity 74.9%; Pred. No. 5.11e-85;

Matches	173;	Conservative	26;	Mismatches	26;	Indels	6;	Gaps	4;
Db	8	lflvatatgvdhsgdmgtspseelaaevndrvlttcrasqdi---	n-n-ylmwyacqakga	62					
Qy	10	LLLLCVP--GSGSEVMTQSP.LSLIPTPGEPASTISCRSSGSLKHSNGD	TFLSWYQKQCP	68					
Db	63	pklllyltstlhgvpvrfsgsgsgtdvltklslapedefatvycqgntlpptf	qgatk	122					
Qy	69	PRLLYIKVSRNDSGVPDFSGSGAGDFTLIKISAVEAEDVGVEFGCGTR	TPTPTFGGGTK	128					
Db	123	veikrtvaapsvfi fopdeqlksgtasvwlhnmfypreakvqvkvdhalsgnsqesv	182						
Qy	129	VEIKRTVAAPSVFIFPPSDEQLKSGTASVSWVLNNFYPREAKVQVKVDNALSGNSQESV	188						
Db	183	tecdakdetsylstlslstladyekhkvyacevthqaglsyptkfmrqec	233						
Qy	189	TEQDSKSTYSLSSTLTLSRADYEKHVYACEVTHQGLSPVPTKSFNRGEC	239						

RESULT 15
ID R22754 standard; Protein; 233 AA.
AC R22754;
DT 20-OCT-1992 (first entry)
DE Reshaped CAMPATH-1 antibody light chain.
DE Antigen; CDR; complementarity determining region; graft rejection;
KW autoimmune diseases; rheumatoid arthritis; allergy.

RESULT 15
ID R22754 standard; Protein; 233 AA.

AC	R22754;	
DE	20-OCT-1992 (dt entry)	
DE	Reshaped CAMPATH-1 antibody light chain.	
DE	Antigen; CDR; complementarity determining region; graft rejection;	
KW	autoimmune diseases; rheumatoid arthritis; allergy.	
OS	Rattus rattus.	
FH	Key	Location/Qualifiers
FT	Region	43..53
FT	/note= "Complementarity determining region 1"	
FT	Region	69..75
FT	/note= "Complementarity determining region 2"	
FT	Region	109..117
FT	/note= "Complementarity determining region 3"	
FT	Peptide	1..19
FT	/note= "signal peptide"	
FT	Peptide	20..214
FT	/note= "mature peptide"	
PN	W09205274-A.	
PD	02-APR-1992.	
PF	16-SEP-1991; G01578.	
PR	17-SEP-1990; GB-020282.	
PR	(GORM/) GORMAN S D.	
PI	Clark M R, Cobbold S P, Gorman S D, Waldmann H.	
DR	WPI; 92-132139/16.	
DR	N-PSDB; Q23567.	
PT	Humanisation of antibodies binding to human CD4 antigen - by	
PT	mutation of framework-encoding regions of DNA encoding variable	
PT	domain of rat or mouse antibody chain	
PT	Disclosure; Fig 2; 74pp; English.	
PS	The sequence is that of the reshaped CAMPATH-1 light chain antibody.	
CC	Reshaped CD4 antibody can be used to induce tolerance against an	
CC	antigen. It can also be used to alleviate autoimmune diseases such	
CC	as rheumatoid arthritis, and to prevent graft rejection. Tolerance	
CC	to a graft, e.g. an organ graft or a bone marrow transplantation can	
CC	also be useful to alleviate allergies. Tolerance to allergens could	
CC	also be achieved. See also R22754-R22763.	
SQ	Sequence	233 AA;
SQ		Sequence

Query Match 69.7%; Score 1161; DB 4; Length 233;
Best Local Similarity 73.2%; Pred. No. 6.08e-84;
Matches 169; Conservative 32; Mismatches 24; Indels 6; Gaps 2;

Db 8 lflvatatgvhsdiqmtqspsslsasvgdrvtitckasni-----dkylnwyqkpgka 62

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[illegible]

Search completed: Tue Dec 17 15:23:52 1996
Job time : 34 secs.

Result	Query			Description	Pred. No.
	No.	Score	Match Length		
1	2339	67.5	330	2 GHU	Ig gamma-1 chain C r 1.18e-243
2	2335	67.4	329	5 S36861	Ig gamma-1 chain C r 3.38e-243
3	2133	61.5	326	2 GHU	Ig gamma-2 chain C r 4.04e-220
4	2133	61.5	327	2 GHU	Ig gamma-4 chain C r 4.04e-220
5	2043	58.9	470	5 S22080	Ig heavy chain precu 7.47e-210
6	2017	58.2	472	12 S31459	Ig gamma-1 chain - s 6.88e-207
7	1999	57.7	469	12 S37483	Ig gamma-2a chain - 7.75e-205
8	1878	54.2	446	12 S42057	Ig gamma-2a chain (m 4.68e-191
9	1871	54.0	474	12 S25057	Ig gamma-2b chain - 2.93e-190
10	1814	52.3	475	12 S01321	Ig gamma-2b chain pr 8.93e-184
11	1747	50.4	377	5 A23511	Ig gamma-3 chain C r 3.68e-176
12	1747	50.4	377	5 A50764	Ig gamma-3 chain C r 3.68e-176

ALIGNMENTS

RESULT	1
ENTRY	GHUU
TITLE	Ig gamma-1 chain C region - human
ORGANISM	#formal name Homo sapiens #common name man
DATE	31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 08-Dec-1994
ACCESSIONS	A93433; B90563; A90564; B91668; A91723; A02146
REFERENCE	A93433
#authors	Ellison, J.W.; Berson, B.J.; Hood, L.E.
#journal	Nucleic Acids Res. (1982) 10:4071-4079
#title	The nucleotide sequence of a human immunoglobulin C-gamma gene.

#cross-references WUID:82274238
#accession A93433
#molecule_type DNA
#residues 1-330 #label ELL
#note this sequence has the Glm(17) allotypic marker, 97-Lys,
and the Glm(1) markers, 239-Asp and 241-Leu
Lys-330 is removed after translation
#note A90563
#authors Cunningham, B.A.; Rutishauser, U.; Galli, W.E.; Gottlieb,
P.D.; Waxdal, M.J.; Edelman, G.M.
#journal Biochemistry (1970) 9:3161-3170
#title The covalent structure of a human gammaG-immunoglobulin. VII.
Amino acid sequence of heavy-chain cyanogen bromide
fragments H-1-H-4.
#cross-references WUID:71064024

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#contents      myeloma protein Eu
#accession    B90563
#molecule_type protein
#residues     1-96, 'R', 98-135 ##label CUN
#note         this sequence has the G1m(3) marker, 97-Arg
REFERENCE
#authors      Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg,
                W.H.; Edelman, G.M.
#journal      Biochemistry (1970) 9:3171-3181
#title        The covalent structure of a human gammaG- immunoglobulin.
                VIII. Amino acid sequence of heavy-chain cyanogen bromide
                fragments H-5-H-7.
#cross-references MUID:71064025
#contents      Eu
#accession    A90564
#molecule_type protein
#residues     136-154, 'Q'
#note         this sequence has the G1m(non-1) markers, 239-Glu and
                241-Met
REFERENCE
#authors      Ponetling, H.; Hilschmann, N.
#journal      Hoppe-Seyler's Z. Physiol. Chem. (1976) 357:1571-1604
#title        Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins
                (Myelomprotein Nie), III. Die chymotryptischen Peptide der
                H-Kette, Anordnung der tryptischen Peptide und Diskussion
                der vollstaendigen Primaerstruktur.
#cross-references MUID:77070269
#contents      myeloma protein Nie
#accession    B91668
#molecule_type protein
#residues     1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D',
                240, 'L', 242-268, 'E', 270-271, 'D', 273-330 ##label PON
                this sequence has the G1m(17) and G1m(1) markers
#note         A91723
REFERENCE
#authors      Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
#journal      Hoppe-Seyler's Z. Physiol. Chem. (1983) 364:713-747
#title        Die Primaerstruktur des kristallisierbaren monoklonalen
                Immunglobulins IgG1 KOL, I.
#cross-references MUID:83289131
#contents      myeloma protein KOL; disulfide bonds
#accession    A91723
#molecule_type protein
#residues     1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'W', 242-266, 'D',
                268-271, 'D', 273-330 ##label SCH
                this sequence has the G1m(3) and G1m(non-1) markers
#note         A90565
REFERENCE
#authors      Gall, W.E.; Edelman, G.M.
#journal      Biochemistry (1970) 9:3188-3196
#title        The covalent structure of a human gammaG- immunoglobulin. X.
                Intrachain disulfide bonds.
#cross-references MUID:71064027
#contents      annotation; disulfide bonds
REFERENCE
#authors      Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
#journal      Hoppe-Seyler's Z. Physiol. Chem. (1976) 357:1515-1540
#title        Rule of antibody structure. The primary structure of
                monoclonal IgG1 immunoglobulin (myeloma protein Nie), I:
                purification and characterization of the protein, the L-
                and H-chains the cyanogenbromide cleavage products, and the L-
                disulfide bridges.
#cross-references MUID:77070267
#contents      annotation; disulfide bonds

```

GENETICS	
#gene	GDB:IGHG1
#map_position	14q32.33
#introns	99/1; 114/1; 224/1
CLASSIFICATION	#superfamily immunoglobulin C region; immunoglobulin homology
KEYWORDS	glycoprotein
FEATURE	
20-85	#domain immunoglobulin homology #label IGG1\
137-206	#domain immunoglobulin homology #label IGG2\
243-310	#domain immunoglobulin homology #label IGG3\
27-83,144-204,	- #disulfide_bonds #status experimental\
250-308	#disulfide_bonds interchain (to light chain) #status
103	experimental\
109,112	#disulfide_bonds interchain (to heavy chain) #status
180	experimental\
	#binding site carbohydrate (Asn) (covalent) #status
SUMMARY	#length 330 #molecular-weight 36106 #checksum 8773
Query Match	67.5%; Score 2339; DB 2; Length 330;
Best Local Similarity	99.7%; Pred. No. 1.18e-243;
Matches 329; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Db	1 aetkgsvfplapskategtaalclvkdypcpvtvsnsgaltsgvhtfpavlgas 60
Qy	149 ASTKGSVFPLAPSSTSGTAAALCLVVDYFPEPTVVSNNSCALTSGVHTFPVVLQSS 208
Db	61 glvlasvvtvpasellgtqyicvnvhtpsntkvdtkvepscdktcpcpapellag 120
Qy	209 GLVLSVSVTPSSSLGTQYICVNVHKEPSNTKYDKAEKPSCDKTHTCPAPPELLGG 268
Db	121 psvflfpkpkdltmstpevtcvrvdshdepvtfmvvdydevhnahtkpreecyn 180
Qy	269 PSVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVGVHNAKTKPREQYN 328
Db	181 etrvvsvltvlhqdlnqkeyckvksnkalspapieltlsakagqprepyvtlpperde 240
Qy	329 STRVSVVLTVLHQLWLNQKEYCKVKSNAKLPAPIEKTIKAKAQPREQYVTLPSRDE 388
Db	241 ltknqvslctclvkgfypsdiavewengcpennykttptpvdsgsflyekltvdksrw 300
Qy	389 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 448
Db	301 qqgnvfscsvmhealnhhtctslslspgk 330
Qy	449 QQGNVFSCSVMHEALNHHTYTKSLSPGK 478
RESULT	2
ENTRY	S36861 #type fragment
TITLE	Ig gamma-1 chain C region
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 02-Aug-1994
ACCESSIONS	S36861; S33887
REFERENCE	S33904
#authors	Harris, L.J.
#submission	submitted to the EMBL Data Library, October 1992
#accession	S36861
#molecule_type	DNA
#residues	1-329 ##label HAR
#cross-references	EMBL:217370
REFERENCE	S33887

```
#authors      Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.;
#journal      Honjo, T.
#title        Cell (1982) 29:671-679
#             Structure of human immunoglobulin gamma genes: implications
#             for evolution of a gene family.
#accession    S33887
#molecule_type DNA
#residues     87-112:234-329 ##label TAK
#cross-references EMBL:217370

GENETICS
#introns      98/1; 113/1; 223/1
#superfamily  #superfamily immunoglobulin C region; immunoglobulin homology
#length 329 #checksum 6336

Query Match      67.4%; Score 2335; DB 5; Length 329;
Best local Similarity 99.7%; Pred. No. 3.38e-243;
Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1  atgpgavflapssaketsgtaaalgcldvdyfpepvtvsmgaltqgvtfpavlgsg 60
|||||
Qy 150 STKCPVFLAPSSKSTGCTAALGCLVQDYFPEPVTVSMNSGALTGCVITFPVAVLSSG 209
|||||
Db 61 lysaevvtvpssalgtqyicnvnhkpkvdkvpektscdkthccpccpaeligqp 120
|||||
Qy 210 LYSLSVWTVPSLSGLGTQYICNVNHKPSNTKVKDKAEKPSCKDTHTCPPCPAPELIGGP 269
|||||
Db 121 evflfpkpkdktlmisrtpetvctvvdshedpevkfnwydvgrvnhaktpreeqyna 180
|||||
Qy 270 SVFLFPKPKDktlmisrtpetvctvvdshedpevkfnwydvgrvnhaktpreeqyns 329
|||||
Db 181 tyrvsvltvhqdwlngkyekyckvknkalpapietkiskakgqprepyvlpsrdel 240
|||||
Qy 330 TYRWSVLTVLHQDLWLNKYEKCKVSNKALPAPTEKTSKAGQPREPYVTLPPSRDEL 389
|||||
Db 241 tknqvslclvkgfypsdiavewesngqpennyyktpvldsdgsefflyskltvdksrwq 300
|||||
Qy 390 TRNQVSLCLVKGfypsdiavewesngqpennyyktpvldsdgsefflyskltvdksrwq 449
|||||
Db 301 qgnvfscvmbcalhnytkqlsispqk 329
|||||
Qy 450 QGNVFCVMBEALHNYTKQLSLSPGK 478

RESULT 3
ENTRY   GZHU      #type complete
TITLE   Ig gamma-2 chain C region - human
ORGANISM 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change
DATE    08-Dec-1994
ACCESSIONS A93906; A92809; A90752; A93132; A02148
REFERENCE  A93906
#authors   Ellison, J.; Hood, L.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1982) 79:1984-1988
#title     Linkage and sequence homology of two human immunoglobulin
#           gamma heavy chain constant region genes.
#cross-references MUID:82197621
#accession A93906
#molecule_type DNA
#residues 1-326 ##label ELL
#note      Lys-326 is probably removed posttranslationally
REFERENCE  A92809
#authors   Wang, A.C.; Tung, E.; Fudenberg, H.H.
#journal   J. Immunol. (1980) 125:1048-1054
#title     The primary structure of a human IgG2 heavy chain: genetic,
```

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evolutionary, and functional implications.
#cross-references MUID:81007873
#contents     myeloma protein T11
#accession    A92809
#molecule_type protein
#residues     1-19,'Q','21-57','2','59','A','61-193','D','195-325 ##label WAN
#note         Trp-156 is at or near the complement-binding site
REFERENCE     A90752
#authors      Connell, G.E.; Parr, D.M.; Hofmann, T.
#journal       Can. J. Biochem. (1979) 57:758-767
#title        The amino acid sequences of the three heavy chain constant
#             region domains of a human IgG2 myeloma protein.
#cross-references MUID:80001357
#contents     myeloma protein Zie
#accession    A90752
#molecule_type protein
#residues     1-24,'E','26-57','EV','60-85;132-171,'ZZZ','175','B','177-193,
#             'D','195-196,'Q','198-234,'Z','236-263,'BCEPZ','269-325
#             ##label CON
#note         this sequence has since been revised
REFERENCE     A93132
#authors      Hofmann, T.; Parr, D.M.
#journal       Mol. Immunol. (1979) 16:923-925
#title        A note on the amino acid sequence of residues 381-391 of
#             human immunoglobulin gamma chains.
#cross-references MUID:80114419
#contents     Zie
#accession    A93132
#molecule_type protein
#residues     238-275 ##label HOF
REFERENCE     A94591
#authors      Hofmann, T.; Parr, D.M.
#submission   submitted to the Atlas, March 1980
#contents     annotation; Zie, revisions to residues 25, 59, 60, and
#             264-268
#note         the revised sequence differs from that shown in having 60-Ala
#             and in the amidation states of residues 58, 194, and 197;
#             the amidation states of residues 172-174, 176, and 235 were
#             not determined
REFERENCE     A90253
#authors      Milstein, C.; Frangione, B.
#journal       Biochem. J. (1971) 121:217-225
#title        Disulphide bridges of the heavy chain of human immunoglobulin
#             G2.
#cross-references MUID:72033500
#contents     annotation; myeloma protein Sa, disulfide bonds
REFERENCE     A93157
#authors      Frangione, B.; Milstein, C.; Pink, J.R.L.
#journal       Nature (1969) 221:145-148
#title        Structural studies of immunoglobulin G.
#cross-references MUID:69064124
#contents     annotation; Sa, disulfide bonds
GENETICS
#gene        GDB:IGHG2
#map position 14q32.33
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
FEATURE
20-85        #domain immunoglobulin homology #label IGG1\
133-202      #domain immunoglobulin homology #label IGG2\
239-306      #domain immunoglobulin homology #label IGG3\
14           #disulfide_bonds_interchain (to light chain) #status
#             experimental\
27-83,140-200,
246-304      #disulfide_bonds #status experimental\
```

102,103,106,109 #disulfide_bonds_interchain (to heavy chain) #status									
experimental									
SUMMARY #length 326 #molecule-weight 35884 #checksum 7982									
Query Match 61.5%; Score 2133; DB 2; Length 326;									
Best Local Similarity 90.9%; Pred. No. 4.04e-220;									
Matches 300; Conservative 15; Mismatches 11; Indels 4; Gaps 3;									
Db	1	aetkgsvfplapcsrteesteaaalclvkdyfpepvtvsmnsgaltsgvhtfpavlgss	60						
QY	149	ASTKGSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNsgALTsgVHTFPavLGSS	208						
Db	61	glylesvvtvpssnfgtqytcnvdhkpstkvdtkverckc---ve-cppcpappv-ag	116						
QY	209	GLYSLSSVVTVPSSSLGTQTICNVNHKPSNTYKDKAEFKSCDKTHTCTCPAPELLGG	268						
Db	117	psvifppkpkdtlmisrtpevtcvvvvshdpevfqfnwywdgvevhnaktkpreeqfn	176						
QY	269	PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYN	328						
Db	177	stfrvsvltvnhqdwlngkeyckvsnkglpapietktisktkgqprepqvylppsrce	236						
QY	329	STRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIETKTISKAKGQPREPQVYTLPPSRDE	388						
Db	237	mtknqsvltclvkgfypsdiavewesngppennyktptpmlsdgsfflysklitvdksrw	296						
QY	389	LTKNQSVLTCLVKGFPSDIAVESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW	448						
Db	297	qggnvfscsvmhealnhytqklsalspgk	326						
QY	449	QGGNVFSCSVMHEALNHYTQKLSLSPGK	478						
RESULT	4								
ENTRY	G4HU #type complete								
TITLE	Ig gamma-4 chain C region - human								
ORGANISM	#formal_name Homo sapiens #common_name man								
DATE	02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 23-Mar-1995								
ACCESSIONS	A90933; A90249; A02150								
REFERENCE	A90933								
#authors	Ellison, J.; Ruxbaum, J.; Hood, L.								
#journal	DNA (1981) 1:11-18								
#title	Nucleotide sequence of a human immunoglobulin C-gamma4 gene.								
#cross-references	MUID:8315704								
#accession	A90933								
#molecule_type	DNA								
#residues	1-327 #label ELL								
#note	the sequence was determined from the germline gene								
REFERENCE	A90249								
#authors	Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.								
#journal	Biochem. J. (1970) 117:33-47								
#title	Human immunoglobulin subclases. Partial amino acid sequencing of the constant region of A gamma4 chain.								
#cross-references	MUID:70207560								
#accession	A90249								
#molecule_type	protein								
#residues	1-30;81-326 #label PIN								
GENETICS									
#gene	GDB:IGHG4								
#map_position	14q32.33								
#introns	99/1; 111/1; 221/1								
CLASSIFICATION	#superfamily immunoglobulin C region; immunoglobulin homolog								
FEATURE									

20-85	#domain immunoglobulin homology #label IGG1\
99-110	#region hinge\
134-203	#domain immunoglobulin homology #label IGG2\
240-307	#domain immunoglobulin homology #label IGG3\
14	#disulfide bonds interchain (to light chain) #status experimental\
27-83, 141-201,	
247-305	#disulfide bonds #status predicted\
106,109	#disulfide_bonds experimental
SUMMARY	#length 327 #molecular-weight 35940 #checksum 907
Query Match	61.5%; Score 2133; DB 2; Length 327;
Best Local Similarity	90.6%; Pred. No. 4,04e-220;
Matches 299;	Conservative 17; Mismatches 11; Indels 3; Gaps 3;
Db 1	askgsvfplapozsrstseetaalgclykdyfpeptvwmnsgaltegwhfapvlgs 60
Qy 149	ASTKGSVPFLAPSKRSTSGCTAALGCLVKDYFPEPTVWNSGALTSGVHFPFPAVLQSS 208
Db 61	glyslasvvtvpsslgtktytcndvdkpsntkvdkrveak-yg-p-pcspcpapeflgg 117
Qy 209	GLYSLSSVVTVPSSSLGCTGYICNVNHNKSNTRKDKAEKSCDKTHTCTPCPELGLG 268
Db 118	psvflppkpdltlmartpevtcvvvdvsqedbevgfnwydvgevhnaktkpreegn 177
Qy 269	PSVFLPPRPKNDTLMISRPEVTCVVDVDSHEDPEVKFNWYDVGVEVHNAKTKPREEQYN 328
Db 178	styrsvsvltvlhqdlnoqkyckvknkglpssiektlsakagkppepytllpqee 237
Qy 329	STYRVSVSLTVLHQDLNGEKYCKVSNKALPAPIETKTSKAGQPREPOVYTLPPSRDE 388
Db 238	mtknqsvslclvkgfydsiadewesngpennyktptpvladsqsflyslrltvdksrw 297
Qy 389	LTKNQSVSLTCLVKGFPSPDIAVESNGQPENNYKTPPVLVSDSGSFFLYSKLTVDKSRW 448
Db 298	qegnfvscsvmhealnhytqtslselgk 327
Qy 449	QQGNFVSCSVMHEALNHNHYTQKLSLSLSPCK 478
RESULT 5	
ENTRY	S22080 #type complete
TITLE	Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
ALTERNATE_NAMES	Ig gamma-1 chain C region (clone 8.10)
ORGANISM	#formal_name Bos primigenius taurus #common_name cattle
DATE	06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-May-1995
ACCESSIONS	S22080; S06610; A31303
REFERENCE	S22080
#authors	Sanders, P.C.
#submission	submitted to the EMBL Data Library, November 1991
#accession	S22080
#status	preliminary
#molecule_type	mRNA
#residues	1-470 ##label SAN
#cross-references	EMBL:X62916
REFERENCE	S06610
#authors	Symons, D.B.A.; Clarkson, C.A.; Beale, D.
#journal	Mol. Immunol. (1989) 26:841-850
#title	Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 2 genes.
#cross-references	MJID:90097956
#accession	S06610

##molecule_type DNA
##residues 142-670 ##label SYM
##cross-references EMBL:X16701
##note the sequence was determined from the germline gene

GENETICS

fgene Ig OH gamma-1
#introns 98/1; 111/1; 221/1
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
KEYWORDS antibody; complement; immunoglobulin; membrane protein
FEATURE
318 #binding site carbohydrate (Asn) (covalent) #status
predicted

SUMMARY #length 470 #molecular-weight 50625 #checksum 2181

Query Match 58.9%; Score 2043; DB 5; Length 470;
Best Local Similarity 61.2%; Pred. No. 7,47e-210;
Matches 290; Conservative 83; Mismatches 89; Indels 12; Gaps 8;

Db 7 llfvlapigvlsqvlreagpslvkpsqtlcltctvsqfslsyaltrwraqpkalew 66

Qy 7 llfvlavatrvcqevqlvesgclvqpgslrvscavsgctfSDHYMYFRQAPCKPEW 66

Db 67 vggj----teggttynpalksrleikensqsvlsavasvpedtatyycars--ty-- 119

Qy 67 VGFIRKPNMGGTTEYAASVKORFTISRDDSKSIAYLQMSLKIEDTAVYYCTTSYISHCR 126

Db 120 gevqdgaiadawggllvtvsaattapkvpplascgdkssastvtlqclvsympervt 179

Qy 127 GGVCGVGFEEFGGALVTVSSASTKGPVFPPLAPSSKSTSGTAAALGCLVKDYFPEPT 186

Db 180 vtmsnqalksgvhtfpavilqesqlyslasmtvvpqstg-qtfcnvahpaestkvdkav 238

Qy 187 VSMNSGALTSGVHTFPVAVLQSSGLYLSVVVTPSSSLGTQYICNVNHNKPSNTKVDKKA 246

Db 239 dp-tc-kpepcdcppelpggpsvfifppkpkdtltiagtpevtcvvvdghdpevkf 296

Qy 247 EPKSCDKHTHTCCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 306

Db 297 sfwfvddvevmtattkpreeqfnstyrvsalrighqdwgkfkckvhneglpapivrt 356

Qy 307 NWIVDGVGVHNAKTKPREEQYNSTRVVSVLTVLHQDWLNGKEYCKVSNKALPAPTEXT 366

Db 357 lartkpareqvylappqeelsketvaltcmtvstfyfpydiavewqngqpseedykt 416

Qy 367 ISKAKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPEN-N-YKT 424

Db 417 tppqldasdyfysklrvdrnswqegdytcvnmhealnhnyhtqsktsagk 470

Qy 425 TTPVLDSDGSFFLYSKLTVDKSRHQQGVFSCSVWHEALHNHYTQKSLSLSPGK 478

RESULT 6 S31459 #type fragment
ENTRY Ig gamma-1 chain - sheep (fragment)
TITLE #formal name Ovis orientalis aries, Ovis ammon aries
ORGANISM #common name domestic sheep

DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995

ACCESSIONS

REFERENCE S31459

#authors Patri, S.; Nau, F.

#submission submitted to the EMBL Data Library, December 1992

#accession S31459

##status preliminary

##molecule_type mRNA
##residues 1-472 ##label PAT
##cross-references EMBL:X69797
SUMMARY #length 472 #checksum 9485

Query Match 58.2%; Score 2017; DB 12; Length 472;
Best Local Similarity 58.6%; Pred. No. 6.88e-207;
Matches 279; Conservative 91; Mismatches 94; Indels 12; Gaps 10;

Db 5 llfvlapigvlsqvlreagpslvkpsqtlcltctvsqfslsyaltrwraqpkalew 64

Qy 7 llfvlavatrvcqevqlvesgclvqpgslrvscavsgctfSDHYMYFRQAPCKPEW 66

Db 65 lq---gsydedidynpvlsrleiktdskqvslclstvttdtavycarvdyds-s 120

Qy 67 VGFIRKPNMGGTTEYAASVKORFTISRDDSKSIAYLQMSLKIEDTAVYYCT-TSYISHC 125

Db 121 hafa-yasy-dfwgpgllisvlsasttpkvpplteccgdtessivtlgclvsymperv 178

Qy 126 RGVCGVGFEEFGGALVTVSSASTKGPVFPPLAPSSKSTSGTAAALGCLVKDYFPEPV 185

Db 179 tvtnsgaltesgvhtfpailqesqlyslasvvtvpaestagctfclcnvahpasestkvdkr 238

Qy 186 TVSNNSGALTSGVHTFPVAVLQSSGLYLSVVVTPSSSLGTQYICNVNHNKPSNTKVDK 245

Db 239 vep-gcpdpckhcr-cppelpggpsvfifppkpkdtltiagtpevtcvvvdgddpev 296

Qy 246 AEPKSC-DKTHTCPCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEV 304

Db 297 qsfwfdvnevtartkpreeqfnstfrvvaalpihqdwgkfkckvhneglpapiv 356

Qy 305 KFNWYDGVGVHNAKTKPREEQYNSTRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIE 364

Db 357 rtierktgareqvylappqeelsketvaltcvtclvtgfyfpydiavewqngqpseedyk 416

Qy 365 NTISKAKGQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPEN-N-Y 422

Db 417 qttqldasdyfysklrvdrnswqegdytcvnmhealnhnyhtqsktsakppk 472

Qy 423 KTFPPVLDSDGSFFLYSKLTVDKSRHQQGVFSCSVWHEALHNHYTQKSLSLSPGK 478

RESULT 7

ENTRY S37483 #type complete

TITLE Ig gamma-2a chain - mouse

ORGANISM #formal name Mus musculus #common name house mouse

DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

ACCESSIONS

REFERENCE S37483

#authors Duncanson, F.F.D.

#submission submitted to the EMBL Data Library, February 1993

#accession S37483

##status preliminary

##molecule_type mRNA

##residues 1-469 ##label DUC

##cross-references EMBL:X70423

SUMMARY #length 469 #molecular-weight 51549 #checksum 7833

Query Match 57.7%; Score 1999; DB 12; Length 469;

Best Local Similarity 57.7%; Pred. No. 7.75e-205;

Matches 277; Conservative 88; Mismatches 102; Indels 13; Gaps 8;

Db 1 mgwewiflfllegtagvchqclqlsqgpevlvkgasvkieckasgyfttdyyinwvqkp 60

SUMMARY #length 474 #molecular-weight 52069 #checksum 4891

Query Match 54.0%; Score 1871; DB 14; Length 474;
Best Local Similarity 55.1%; Pred. No. 2,93e-190;
Matches 267; Conservative 90; Mismatches 110; Indels 18; Gaps 7;

Db 1 mewsliflllgtagvheevqlqgagelpnpgasvmsckasgtyftitymhwkqp 60
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 1 MWSLILFLVAVATRVQCEVQLVESGGGLVQPGSLRVSCAVSGFTFSDHYMWFQAP 60
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 61 gqglwewiyi-n-pnkdtktfnefkgtatltcdksentaymleelstedeavyyard 118
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 61 GKPEWVGFI RNKENGCTTEAASVVKDRFTISRDDSKSIAYLQWSSLIKIEDTAVYYCTTS 120
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 119 y-----d-yd-wfaywqgqtlvtvaaktppsvyplapcgcdgtgsvtgcclvkg 169
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 121 YISHCRGGVCGYGVFEFWQCGALTVSSASTKGPSVFP LAPSSKSTSGCTAALGCLVKDY 180
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 170 fpeavtvtwmsglssvhtleqalqsglytmsavtvpstpsqdtvtcavahpasst 229
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 181 FPEVTVSNWNSGALTSVHTFPALVSSGLYSLSSVTVPSSSLGCTQTYICNVNHPKSN 240
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 230 tvdkklepsgipstlnpcpcckechkcpapnleggpavfifppnikdvmlsltpkvtc 289
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 241 KVOKAEPKSCDKT-HYCPCC-----PAPELLGGPSVFLFPPPKDRLIMSRPEVTCV 293
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 290 vdvseddpdpqlwfvnnvhttaqtqthredynstirvvetlpqhqdmsgkfkck 349
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 294 VDVSHEDPEVKENWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHODWLNGKEYCK 353
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 350 vnnkdilpapiertiskigivrapqvylppaqlerkdvelclvngfnpgdisvewt 409
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 354 VSNKALPAP IEKTSIRAKQPREQVYVTPPSRDELTKQVSLTCLVKGYFSPDAVEME 413
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 410 enghteenykdapvidsgyfiycklnmktskwktksfecnvrhglknylkkttis 469
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 414 SNGQPENNYKTTTPVLDSDGFFLYSKLTVDKSRMQQGNVFCSCVMHEALHNHYTQKSL 473
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 470 rsgpk 474
| | | | |
Qy 474 LSPGK 478

RESULT 10
ENTRY S01321 #type complete
TITLE Ig gamma-2b chain precursor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Mar-1993
ACCESSIONS S01321
REFERENCE S01320
#authors de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
#journal Eur. J. Biochem. (1988) 176:287-295
#title Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed against the tumour marker human placental alkaline phosphatase.
#cross-references MUID:88329081
#accession S01321
#molecule type mRNA
#residues 1-475 ##label DE1
#cross-references EMBL:X13188
#note this sequence was determined from the differentiated gene

FEATURE

1-19 #domain signal sequence #label SIG
20-475 #product Ig gamma-2b chain #label MAT
SUMMARY #length 475 #molecular-weight 51567 #checksum 4120
Query Match 52.3%; Score 1814; DB 12; Length 475;
Best Local Similarity 54.0%; Pred. No. 8,93e-184;
Matches 262; Conservative 97; Mismatches 109; Indels 17; Gaps 9;
Db 1 mewsliflllgtagvheevqlqgagelpnpgasvmsckasgtyftitymhwkqp 60
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 1 MWSLILFLVAVATRVQCEVQLVESGGGLVQPGSLRVSCAVSGFTFSDHYMWFQAP 60
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 61 gqglwewiyi-y-pgsgnseyfnefkgtatltcdksentaylhllelstedeaavycagp 118
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 61 GKPEWVGFI RNKENGCTTEAASVVKDRFTISRDDSKSIAYLQWSSLIKIEDTAVYYCTTS 120
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 119 --rqv-gllpfg-y---wqgqtlvtasaaktppsvyplapcgcdgtgsvtgcclvkg 171
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 121 YISHCRGGVCGYGVFEFWQCGALTVSSASTKGPSVFP LAPSSKSTSGCTAALGCLVKDY 180
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 172 fpeavtvtwmsglssvhtfpallgs-glytmsavtvpstpsqdtvtcavahpasst 230
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 181 FPEVTVSNWNSGALTSVHTFPALVSSGLYSLSSVTVPSSSLGCTQTYICNVNHPKSN 240
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 231 tvdkklepsgipstlnpcpcckechkcpapnleggpavfifppnikdvmlsltpkvtc 290
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 241 KVOKAEPKSCDKT-HYCPCC-----PAPELLGGPSVFLFPPPKDRLIMSRPEVTCV 293
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 291 vdvseddpdpqlwfvnnvhttaqtqthredynstirvvetlpqhqdmsgkfkck 350
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 294 VDVSHEDPEVKENWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHODWLNGKEYCK 353
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 351 vnnkdilpapiertiskigivrapqvylppaqlerkdvelclvngfnpgdisvewt 410
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 354 VSNKALPAP IEKTSIRAKQPREQVYVTPPSRDELTKQVSLTCLVKGYFSPDAVEME 413
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 411 enghteenykdapvidsgyfiycklnmktskwktksfecnvrhglknylkkttis 470
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 414 SNGQPENNYKTTTPVLDSDGFFLYSKLTVDKSRMQQGNVFCSCVMHEALHNHYTQKSL 473
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 471 rsgpk 475
| | | | |
Qy 474 LSPGK 478

RESULT 11
ENTRY A23511 #type complete
TITLE Ig gamma-3 chain C region (allotype G3m(b)) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 30-Sep-1993
ACCESSIONS A23511
REFERENCE A23511
#authors Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
#journal Nucleic Acids Res. (1986) 14:1779-1789
#title Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: comparison with the other human C-gamma genes.
#cross-references MUID:86148507
#accession A23511
#molecule type DNA
#residues 1-377 ##label HUC


```
|||||
Qy 427 PVLDSGFFLYSLVTKSRWQGNFSCVMHEALHNHYTKSLSPGK 478
|||||

RESULT 14
ENTRY PT0207 #type complete
TITLE Ig gamma chain C region - chimpanzee
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 12-Apr-1995
ACCESSIONS PT0207
REFERENCE PT0207
#authors Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
#journal Mol. Immunol. (1991) 28:319-322
#title Nucleotide sequence of chimpanzee Fc and hinge regions.
#cross-references M01D:91287716
#accession PT0207
#molecule_type mRNA
#residues 1-234 ##label EHR
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
SUMMARY #length 234 #molecular-weight 26330 #checksum 6128

Query Match 48.4%; Score 1677; DB 5; Length 234;
Best Local Similarity 98.3%; Pred. No. 3.26e-168;
Matches 230; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1 antkvdkvpeksdcthtcpaapellggsvfifppkpkdtlmisrtpevtcvvvdv 60
|||||
Qy 238 SNTKVDKKAEPKSDKTHTCPAPPELLGGSVFLFPPKPKDTLMISRTPEVTCVVVDV 297
|||||

Db 61 shedpevfnyvdgvevhnaktpreeqnystyrsvvsvltvldqwlngkeyckvsnk 120
|||||
Qy 298 SHEDPEVFNVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNK 357
|||||

Db 121 alpakietskagqprepyqlppsrdeitknqvslcivkgyfpadiavewessgq 180
|||||
Qy 358 ALPAPKTEXTISKAGQPREPYQLPPSRDELTKNQVSLTCLVKGFYPSDIAVEENSGQ 417
|||||

Db 181 pennykttppvldsdgfflyskltdkervqgnvfscsvmhealhnhytqks 234
|||||
Qy 418 PENNYKTTPPVLDSDGFFLYSKLTVDKSRWQGNFSCVMHEALHNHYTKS 471
|||||

RESULT 15
ENTRY GHRB #type complete
TITLE Ig gamma chain C region - rabbit
ORGANISM #formal_name Oryctolagus cuniculus #common_name domestic rabbit
DATE #sequence_revision 15-Nov-1984 #text_change 04-Nov-1994
ACCESSIONS A91749; A90290; A93928; A90245; A94416; A02161
REFERENCE A91749
#authors Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
#journal Immunogenetics (1983) 18:387-397
#title Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-1 haplotype.
#cross-references M01D:84030930
#accession A91749
#molecule_type mRNA
#residues 1-323 ##label BER
#note this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr

REFERENCE A90290
#authors Pratt, D.M.; Mole, L.E.
#journal Biochem. J. (1975) 151:337-349
```

```
#title Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.
#cross-references M01D:76135469
#accession A90290
#molecule_type protein
#residues 1-47,'E',49-71,'PV',72-128 ##label PRA
REFERENCE A93928
#authors Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
#journal Proc. Natl. Acad. Sci. U.S.A. (1982) 79:6018-6022
#title Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain and identification of two genomic C-gamma genes.
#cross-references M01D:83299917
#accession A93928
#molecule_type mRNA
#residues 88-103,'M',105-143,'E',145-184,'A',186,'E',188-266 ##label MAR
#note this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker, 185-Ala

REFERENCE A90245
#authors Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
#journal Biochem. J. (1970) 116:249-259
#title Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G.
#cross-references M01D:70110015
#accession A90245
#molecule_type protein
#residues 132-143,'E',145-161 ##label FRU
REFERENCE A94416
#authors Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
#book In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell, Stockholm, 1967
#accession A94416
#molecule_type protein
#residues 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',234-245,'D',247-255,'G',257-259,'D',261-265,'D',267-279,'W',281-283,'S',285-322 ##label HIL
#note this has the e15 allotypic marker, 185-Ala
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
FEATURE
20-82 #domain immunoglobulin homology #label ICG1\
130-199 #domain immunoglobulin homology #label ICG2\
236-303 #domain immunoglobulin homology #label ICG3
SUMMARY #length 323 #molecular-weight 35404 #checksum 1467

Query Match 48.2%; Score 1669; DB 2; Length 323;
Best Local Similarity 70.0%; Pred. No. 2.64e-167;
Matches 229; Conservative 46; Mismatches 45; Indels 7; Gaps 3;

Db 4 kapsvfplapccgdtosstvtlgclvkgyldpvyvtwnsgltngvrtfpsvgsqgly 63
|||||
Qy 152 KGPSVFPLAPSSKSTGGTALGLVQKDYFPEPVTVSWNSGALTSGVHTFPAIVQSSGLY 211
|||||

Db 64 elssvsvtsas---qprtcnvahpatntkvdktvapstskp-tcpp---pellggpsv 116
|||||
Qy 212 SLSSWTVPSLSLTQTYICNVNKKPSNTKDKAEKPKSCDKTHCTCPAPPELLGSPV 271
|||||

Db 117 fifpkipkdtlmisrtpevtcvvdsqddpevftwyinneqvrtarplreqfnsti 176
|||||
Qy 272 FIFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATPKREEYNSTY 331
|||||

Db 177 rvwtlptlthqdwlrgekfkckvhnkalpapietkiskarggplepkvymgppreles 236
```

91

Search completed: Tue Dec 17 15:30:15 1996
Job time : 52 secs.

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 15:30:33 1996; MasPar time 11.42 Seconds
727.395 Million cell updates/sec

Tabular output not generated.

Title: >US-08-487-550-8

Description: (1-478) from US08487550 pep

Perfect Score: 3466
Sequence: 1 MGWSLILFLVAVATRVQCE.....MHEALHNHYTQKSLSLSPGK 478

Scoring table: PAM 150

PAM 150

Gap 11

Searched: 49340 segs. 17385503 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot32

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9

Statistics: Mean 48.438; Variance 80.927; scale 0.599

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Query †	DB	ID	Description	Pred. No.
1	2339	67.5	330	3	GC1	HUMAN	IG GAMMA-1 CHAIN C RE	0.00e+00
2	2133	61.5	326	3	GC2	HUMAN	IG GAMMA-2 CHAIN C RE	0.00e+00
3	2133	61.5	327	3	GC4	HUMAN	IG GAMMA-4 CHAIN C RE	0.00e+00
4	1669	48.2	323	3	GC	RABIT	IG GAMMA CHAIN C REGI	0.00e+00
5	1616	46.6	329	3	GC2	CANVO	IG GAMMA-2 CHAIN C RE	0.00e+00
6	1590	45.9	290	3	GC3	HUMAN	IG GAMMA-3 CHAIN C RE	0.00e+00
7	1584	45.7	329	3	GC3	MOUSE	IG GAMMA-3 CHAIN C RE	0.00e+00
8	1582	45.6	326	3	GC1	RAT	IG GAMMA-1 CHAIN C RE	0.00e+00
9	1570	45.3	398	3	GC3M	MOUSE	IG GAMMA-3 CHAIN C RE	0.00e+00
10	1566	45.2	324	3	GC1	MOUSE	IG GAMMA-1 CHAIN C RE	0.00e+00
11	1559	45.0	329	3	GC2	RAT	IG GAMMA-2C CHAIN C R	0.00e+00
12	1559	45.0	393	3	GC1M	MOUSE	IG GAMMA-1 CHAIN C RE	0.00e+00
13	1549	44.7	330	3	GC4A	MOUSE	IG GAMMA-2A CHAIN C R	0.00e+00

	14	1546	44.6	333	3	GBR_RAT	IG GAMMA-2B CHAIN C	R	0.00e+00
	15	1542	44.5	339	3	GCAM_MOUSE	IG GAMMA-2A CHAIN C	R	0.00e+00
	16	1518	43.8	335	3	GCAB_MOUSE	IG GAMMA-2A CHAIN C	R	0.00e+00
	17	1501	43.3	322	3	GCAR_RAT	IG GAMMA-2A CHAIN C	R	0.00e+00
	18	1478	42.6	336	3	GCB_MOUSE	IG GAMMA-2B CHAIN C	R	0.00e+00
	19	1471	42.4	405	3	GCBB_MOUSE	IG GAMMA-2B CHAIN C	R	0.00e+00
	20	595	17.2	144	4	HV26_MOUSE	IG HEAVY CHAIN PRECUR	R	1.04e-108
	21	566	16.3	117	4	HV3C_HUMAN	IG HEAVY CHAIN PRECUR	R	8.88e-102
	22	565	16.3	142	4	HV01_RAT	IG HEAVY CHAIN PRECUR	R	1.54e-101
	23	554	16.0	116	4	HV05_CARAU	IG HEAVY CHAIN PRECUR	R	6.43e-99
	24	553	16.0	123	4	HV18_MOUSE	IG HEAVY CHAIN V REGI	R	1.11e-98
	25	552	15.9	123	4	HV19_MOUSE	IG HEAVY CHAIN V REGI	R	1.92e-98
	26	547	15.8	117	4	HV17_MOUSE	IG HEAVY CHAIN V REGI	R	2.97e-97
	27	544	15.7	122	4	HV21_MOUSE	IG HEAVY CHAIN V REGI	R	1.54e-96
	28	540	15.6	117	4	HV54_MOUSE	IG HEAVY CHAIN PRECUR	R	1.37e-95
	29	542	15.6	123	4	HV23_MOUSE	IG HEAVY CHAIN V REGI	R	4.59e-96
	30	539	15.6	123	4	HV22_MOUSE	IG HEAVY CHAIN V REGI	R	2.37e-95
	31	539	15.6	126	4	HV3K_HUMAN	IG HEAVY CHAIN V-III	R	2.37e-95
	32	539	15.6	353	1	ALC1_HUMAN	IG ALPHA-1 CHAIN C RE	R	2.37e-95
	33	535	15.4	122	4	HV20_MOUSE	IG HEAVY CHAIN V REGI	R	2.11e-94
	34	532	15.3	117	4	HV25_MOUSE	IG HEAVY CHAIN PRECUR	R	1.09e-93
	35	530	15.3	136	4	HV16_MOUSE	IG HEAVY CHAIN PRECUR	R	3.24e-93
	36	532	15.3	353	1	ALC11_CORGO	IG ALPHA-1 CHAIN C RE	R	1.09e-92
	37	526	15.2	122	4	HV3A_HUMAN	IG HEAVY CHAIN V-III	R	2.87e-92
	38	527	15.2	344	1	ALC_MOUSE	IG ALPHA CHAIN C REGI	R	1.66e-92
	39	528	15.2	455	5	MUC_MOUSE	IG MU CHAIN C REGION	R	9.64e-93
	40	524	15.1	123	4	HV25_MOUSE	IG HEAVY CHAIN V REGI	R	8.54e-92
	41	523	15.1	123	4	HV24_MOUSE	IG HEAVY CHAIN V REGI	R	1.47e-91
	42	520	15.0	116	4	HV36_MOUSE	IG HEAVY CHAIN PRECUR	R	7.56e-91
	43	519	15.0	122	4	HV3G_HUMAN	IG HEAVY CHAIN V-III	R	1.30e-90
	44	515	14.9	476	5	MUCM_MOUSE	IG MU CHAIN C REGION	R	1.15e-89
	45	510	14.7	117	4	HV53_MOUSE	IG HEAVY CHAIN V REGI	R	1.75e-88

ALIGNMENTS

RESULT	1
ID	GC1 HUMAN STANDARD; PRT; 330 AA.
AC	P01857;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE	IG GAMMA-1 CHAIN C REGION.
GN	IGHG1.
OS	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; PRIMATES.
[1]	
RN	SEQUENCE FROM N.A.
RP	MEDLINE; 82274238.
RX	
RA	ELLISON J.W., BERSON B.J., HOOD L.E.;
RL	NUCLEIC ACIDS RES. 10:4071-4079(1982).
[2]	
RN	SEQUENCE OF I-135 (MYELOMA PROTEIN EU).
RP	MEDLINE; 71064024.
RX	CUNNINGHAM B.A., RUTISHAUSER U., CALL W.E., GOTTlieb P.D.,
RA	MAXDAL M.J., EDELMAN G.M.;
RL	BIOCHEMISTRY 9:3161-3170(1970).
[3]	
RN	SEQUENCE OF 13c-329 (EU).
RP	MEDLINE; 71064025.
RX	
RA	RUTISHAUSER U., CUNNINGHAM B.A., BENNETT C., KONIGSBERG W.H.,
RA	EDELMAN G.M.;
RL	BIOCHEMISTRY 9:3171-3181(1970).

RN [4] SEQUENCE (MYELOMA PROTEIN NIE).
 RX MEDLINE; 77070269.
 RA PONTING L. H., HILSCHMANN N. J.
 RL HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 357:1571-1604 (1976).
 RN [5]
 RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
 RX MEDLINE; 83289131.
 RA SCHMIDT W. E., JUNG H.-D., PALM W., HILSCHMANN N. J.
 RL HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 364:713-747 (1983).
 RN [6]
 RP DISULFIDE BONDS.
 RX MEDLINE; 71064027.
 RA CALL W. E., EDELMAN G. M. J.
 RL BIOCHEMISTRY 9:3188-3196 (1970).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE; 77070267.
 RA DREKER L., SCHWARZ J., REICHEL W., HILSCHMANN N. J.
 RL HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 357:1515-1540 (1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE; 81208100.
 RA DEISENHOFER J. J.
 RL BIOCHEMISTRY 20:2361-2370 (1981).
 CC -!- NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS,
 CC 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM
 CC (NON-1) MARKERS.
 CC -!- NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.
 CC -!- EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155, 166, 177,
 CC 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.
 CC -!- KOL ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 198,267&272.
 DR EMBL; J00228; J00228.
 DR PIR; A02146; GHU.
 DR PDB; 1FC1; 15-JUL-92.
 DR PDB; 1FC2; 15-JUL-92.
 DR MIM; 147100; 11TH EDITION.
 DR PROSITE; PS00290; IG MHC.
 KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN; 3D-STRUCTURE.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISULFID 27 83
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT VARIANT 97 97 K -> R (IN GIM(3) MARKER).
 FT VARIANT 239 239 D -> E (IN GIM(NON-1) MARKER).
 FT VARIANT 241 241 L -> M (IN GIM(NON-1) MARKER).
 FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
 FT STRAND 123 126
 FT HELIX 130 134
 FT TURN 136 137
 FT STRAND 141 148
 FT STRAND 158 162
 FT TURN 163 164
 FT STRAND 165 166
 FT STRAND 175 178
 FT STRAND 183 190

FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 206
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 240
 FT TURN 241 242
 FT STRAND 245 256
 FT STRAND 260 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 312
 FT TURN 313 314
 FT TURN 316 317
 FT STRAND 320 324
 SQ SEQUENCE 330 AA; 36106 MM; 642285 CN;
 Query Match 67.5%; Score 2339; DB 3; Length 330;
 Best Local Similarity 99.7%; Pred. No. 0.00e+00;
 Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 astkqpsvflapssktsqgtaalgcLvkdYfpepytvswngaltsqvhfipavlgss 60
 Qy 149 ASIRKGSVFELAPSSKSTSGGTAALGCLVRLDIFPEPYTVSWNSGALTSQVHTFPVAVLGSS 208
 Db 61 glyeasvvtvpsslgtctyicnvnhkpsntkvdkkvepkcdkthtccpcapellgg 120
 Qy 209 GLYSLSVTVVPSSSLGTCTYICNVNHRPSNTKYDKAEFKSCDKTHTCPCPAPPELLGG 268
 Db 121 psvflfpkpkdtlmirtpevtcvvvdsvedpevkfnwvdgvevhnaktkpreecyn 180
 Qy 269 PSVFLFPKPKDITMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 328
 Db 181 atyrwsvltvlhqdwlngkeyckvsnkalpapietkikakggprepytllpperde 240
 Qy 329 STYRVSVTLVHLDWLNCKEYCKYVSNKALPAPIEKTISKAKGPREPVYTLPPSRDE 388
 Db 241 ltknqvsltlvkgfypsdiavewesngqpennkttppvldsdgsfflyskltvdkerw 300
 Qy 389 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 448
 Db 301 qqgnvfscsvmhcalhnyhtqklsLspgk 330
 Qy 449 QQGNVFSCSVMEALHNHYTQKLSLSPGK 478
 RESULT 2
 ID GC2 HUMAN STANDARD; PRT; 326 AA.
 AC P01859;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE IG GAMMA-2 CHAIN C REGION.
 GN IGHG2.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 82197621.
RA ELLISON J.W., HOOD L.E.;
RL PROC. NATL. ACAD. SCI. U.S.A. 79:1984-1988(1982).
RN [2]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE; 81007873.
RA WANG A.-C., TUNG E., FUDENBERG H.H.;
RL J. IMMUNOL. 125:1048-1054(1980).
RN [3]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE; 80001357.
RA CONNELL G.E., PARR D.M., HOFMANN T.;
RL CAN. J. BIOCHEM. 57:758-767(1979).
RN [4]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE; 80114419.
RA HOFMANN T., PARR D.M.;
RL MOL. IMMUNOL. 16:923-925(1979).
RN [5]
RP ZIE, REVISIONS TO 25; 59; 60 AND 264-268.
RA HOFMANN T., PARR D.M.;
RL SUBMITTED (MAR-1980) TO THE PIR DATA BANK.
RN [6]
RP SEQUENCE OF 1-121 (DOT).
RA STOPPINI M., BELLOTTI V., NEGRI A., MERLINI G., GARVER F., FERRI G.;
RL EUR. J. BIOCHEM. 0:0-0(1995).
RN [7]
RP MYELOMA PROTEIN SA, DISULFIDE BONDS.
RX MEDLINE; 72033500.
RA MILSTEIN C., FRANGIONE B.;
RL BIOCHEM. J. 121:217-225(1971).
RN [8]
RP SA, DISULFIDE BONDS.
RX MEDLINE; 69064124.
RA FRANGIONE B., MILSTEIN C., PINK J.R.L.;
RL NATURE 221:145-148(1969).
DR EMBL; V00554; V00554.
DR PIR; A02148; G2HU.
DR HSP; P01857; IBBJ.
DR MIM; 147110; 11TH EDITION.
DR PROSITE; PS00290; IG_MHC.
KW IMMUNOGLOBULIN C REGION.
FT NON TER 1 1
FT DOMAIN 1 98
FT DOMAIN 99 110
FT DOMAIN 111 219
FT DOMAIN 220 326
FT DISULFID 14 14
FT DISULFID 27 83
FT DISULFID 102 102
FT DISULFID 103 103
FT DISULFID 106 106
FT DISULFID 109 109
FT DISULFID 140 200
FT DISULFID 246 304
FT VARIANT 60 60
FT SITE 156 156
FT MOD RES 326 326
SQ SEQUENCE 326 AA; 35884 MW; 629390 CN;
S -> A (IN MYELOMA PROTEINS TIL & ZIE).
AT OR NEAR THE COMPLEMENT-BINDING SITE.
REMOVED POST-TRANSLATIONALLY (PROBABLE).
Query Match 61.5%; Score 2133; DB 3; Length 326;
Best Local Similarity 90.9%; Pred. No. 0.00e+00;
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Matches 300; Conservative 15; Mismatches 11; Indels 4; Gaps 3;
Db 1 aatkgpavfplacsrsteestaalgclvkdypcpvtvawnsagaltgvtftfavlqss 60
Qy 149 ASTGFSVFP LAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 208
Db 61 gylasavvtvpsefngtqtvtcnvdhkpentkvdktkverkkc--ve-cppcpappv-ag 116
Qy 209 GLYSLSSVWTVPESSSLGTQTYICNVNHRGNTKDKKAEKSCDKTHTCPPCPAPELGG 268
Db 117 pavfipppkpkdtlmisrtpetvctvvvdvshedpevqfnwyvdgvevhnaktkpreedfn 176
Qy 269 PSEVLEPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEDYN 328
Db 177 atfrvsvltvvhqdwlngkckvknkglpapiektskktgqprepqvvtlpsree 236
Qy 329 STYRWVSVLTVLHQDWLNGCKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 388
Db 237 mtknqvslctlvkgyfypsdiavewnsngqpennykttppmldsdgsfflyskltvdkerw 296
Qy 389 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 448
Db 297 qqgnvfscavmhealhhvhtqkelaalepdk 326
Qy 449 QQGNVFSCVMEALHHVHTQKLSLSLSPGK 478
RESULT 3
ID GC4 HUMAN STANDARD; PRT; 327 AA.
AC P01861.
DT 21-JUL-1986 (REL. 01, CREAT SEQUENCE)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE IG GAMMA-4 CHAIN C REGION.
GN IGHG4.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83157104.
RA ELLISON J.W., BUXBAUM J.N., HOOD L.E.;
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE; 70207560.
RA PINK J.R.L., BUTTERY S.H., DE VRIES G.M., MILSTEIN C.;
RL BIOCHEM. J. 117:33-47(1970).
DR PIR; A02150; G4HU.
DR HSP; P01857; IBBJ.
DR MIM; 147130; 11TH EDITION.
DR PROSITE; PS00290; IG_MHC.
KW IMMUNOGLOBULIN C REGION.
FT NON TER 1 1
FT DOMAIN 1 98
FT DOMAIN 99 110
FT DOMAIN 111 220
FT DOMAIN 221 327
FT DISULFID 14 14
FT DISULFID 27 83
FT DISULFID 106 106
FT DISULFID 109 109
FT DISULFID 141 201
FT DISULFID 247 305
INTERCHAIN (WITH A LIGHT CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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DE IG GAMMA-2 CHAIN C REGION.
OS CAVIA PORCELLUS (GUINEA PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE OF 1-3.
RA TRISCHMANN T.M.;
RL SUBMITTED (APR-1975) TO THE PIR DATA BANK.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE; 71058471.
RA BIRSHTEIN B.K., HUSSAIN Q.Z., CEBRA J.J.;
RL BIOCHEMISTRY 10:18-25 (1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE; 71058486.
RA TURNER K.J., CEBRA J.J.;
RL BIOCHEMISTRY 10:9-17 (1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE; 75036072.
RA TRACEY D.E., CEBRA J.J.;
RL BIOCHEMISTRY 13:4796-4803 (1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE; 75036073.
RA TRISCHMANN T.M., CEBRA J.J.;
RL BIOCHEMISTRY 13:4804-4811 (1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE; 71058474.
RA OLIVEIRA B., LAMM M.E.;
RL BIOCHEMISTRY 10:26-31 (1971).
CC -!- THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN 13 INBRED
CC GUINEA PIGS.
DR PIR; A02151; G2GP.
DR HSP; P01857; 1FC1.
DR PROSITE; PS00290; IG.MHC.
RW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN.
FT NON TER 1 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 63074 MW; 630420 CN;

Query Match 46.6%; Score 1616; DB 3; Length 329;
Best Local Similarity 70.1%; Pred. No. 0.00e+00;
Matches 234; Conservative 39; Mismatches 52; Indels 9; Gaps 6;

'Db 1 eartapsvfplaaacvdtsgmmtlclgvkyfpepvtvknsgaltsqvtfpavlqs 60
|||:|||||:| |||:|||||:| |||:|||||:| |||:|||||:| |||:|||||:|
Qy 148 SASTKGPSVFPLAPSSKSTSGGTAALCLLKVDFEPEVTVVNSGALTSGVHTFPAVLQ 207
|||:|||||:| |||:|||||:| |||:|||||:| |||:|||||:| |||:|||||:|
Db 61 -glyltslntvtpssq--kat--cnvahpasatkvdktveprtzbpbctcpkcppe 115
|||:|||||:| |||:|||||:| |||:|||||:| |||:|||||:| |||:|||||:|
Qy 208 SGLYSLSSVTVTPSSSLGTQTYICNVNHPKPNTRKVDKAEK-PSKDKTH-TCP 265
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 116 lggpsvfiifpkipktdlmlslprvtcvvvdsqdepevqftwfdvdkpvgnaetkprve 175
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

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Qy 266 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENYVDGVGVNNAKTPREE 325
Db 176 qynttfresvliqhdqlrgkfkckynkalpapielktstkgapmpdvytlpps 235
|||:|||||:| |||:|||||:| |||:|||||:| |||:|||||:| |||:|||||:|
Qy 326 QYNSTRVSVLTVLHQDLNGKEYCKKYSKALPAPIEKTISKAKGQPREQVYTTLP 385
Db 236 rdelstksvstclliinfpadinhwasnrvtvsekeykntppledadgsflyekltv 295
|||:|||||:| |||:|||||:| |||:|||||:| |||:|||||:| |||:|||||:|
Qy 386 RDELTRNQSVLTCLVKGFTPSDIAVWESNGQP--ENNYKTTTPPVLDSDGSEFFLYSKLTV 443
Db 296 dksawdgtvytcsvmhealnhvhtqkaisrapg 329
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Qy 444 DKSRWQGNQGVFSVMHEALNHVHTQKSLSPG 477

RESULT 6
ID GC3 HUMAN STANDARD; PRT; 290 AA.
AC P01860;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE IG GAMMA-3 CHAIN C REGION (HEAVY CHAIN DISEASE PROTEIN) (HDC).
GN IGHG3.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE (DISEASE PROTEIN WIS).
RX MEDLINE; 81021548.
RA FRANGIONE B., ROSENWASSER E., PRELLI F., FRANKLIN E.C.;
RL BIOCHEMISTRY 19:4304-4308 (1980).
RN [2]
RP NORMAL GAMMA-3 CHAINS, REVISIONS TO 12-97 OF PROTEIN WIS.
RX MEDLINE; 71118561.
RA MICHAELSEN T.E., FRANGIONE B., FRANKLIN E.C.;
RL J. BIOL. CHEM. 252:883-889 (1977).
RN [3]
RP DISEASE PROTEIN ZUC, REVISIONS TO 59-289 OF PROTEIN WIS.
RX MEDLINE; 77021516.
RA WOLFENSTEIN-TODEL C., FRANGIONE B., PRELLI F., FRANKLIN E.C.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 71:907-914 (1976).
RN [4]
RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX MEDLINE; 82247835.
RA ALEXANDER A., STEINMETZ M., BARRITAU D., FRANGIONE B.,
RA FRANKLIN E.C., HOOD L., BUxbaum J.N.;
RL PROC. NATL. ACAD. SCI. U.S.A. 79:3260-3264 (1982).
CC -!- THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
CC -!- THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE REF. 2.
CC -!- DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION AND ALL OF THE
CC CHI REGION.
CC -!- DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CHI
CC REGION, AND PART OF THE HINGE COMPARED WITH NORMAL GAMMA-3 HEAVY
CC CHAINS.
CC -!- DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM OR ANOTHER GAMMA
CC CHAIN SUBCLASS.
CC -!- THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG
CC AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15-RESIDUE
CC SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE SEGMENT (12-28).
CC -!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
CC INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
CC NORMALLY PRESENT IN THE HINGE REGION.
DR EMBL; J00231;
DR PIR; A02149; G3HWT.

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DR HSP; P01857; IFC1.
DR MM; 147120; 11TH EDITION.
DR PROSITE; PS00290; IG MHC.
KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN.
FT DOMAIN 12 73 HINGE.
FT DOMAIN 74 183 CH2.
FT DOMAIN 184 289 CH3.
FT REPEAT 29 43
FT REPEAT 44 58
FT REPEAT 59 73
FT MOD RES 1 1
FT CARBOHYD 6 6
FT DISULFID 7 7
FT DISULFID 24 24
FT DISULFID 27 27
FT DISULFID 33 33
FT DISULFID 39 39
FT DISULFID 42 42
FT DISULFID 48 48
FT DISULFID 54 54
FT DISULFID 57 57
FT DISULFID 63 63
FT DISULFID 69 69
FT DISULFID 72 72
FT CARBOHYD 140 140
FT MOD RES 290 290
FT VARIANT 126 127
FT VARIANT 134 134
FT VARIANT 139 139
FT VARIANT 182 182
FT VARIANT 227 227
FT VARIANT 227 227
FT VARIANT 279 279
SQ SEQUENCE 290 AA; 32331 MW; 485009 CN;

Query Match 45.9%; Score 1590; DB 3; Length 290;
Best Local Similarity 90.1%; Pred. No. 0.00e+00;
Matches 210; Conservative 17; Mismatches 6; Indels 0; Gaps 0;

Db 58 pepkscdtpcpccpapellgspvflfpkpkdtlmisrtpevtcvvvdshedpevq 117
:||||| || |||||
Qy 246 AEPKSDKTHTCPCPCAPPELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 305
:||||| || |||||
Db 118 fkyvdgqvhnaktkpreqqfnetfrvsvltvlnqwdlqgkckvsnkalpapiak 177
:||||| || |||||
Qy 306 FNWYDGVGVHNKTPREQYNSTRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEK 365
:||||| || |||||
Db 178 tiaktkgpqpvytlpsteemtknqslctclvkfypsdiavewessgppnnyntt 237
:||||| || |||||
Qy 366 TISKAKGQRPQVYTLPSRDELTNRQVSLTCLVKGFYPSDIAVWESNGQPENNYKT 425
:||||| || |||||
Db 238 ppmldedgfflyekltvdkerwqgnifescvmealnhrftqklsapok 290
:||||| || |||||
Qy 426 PPVLDSDGSEFFLYSKLTVDKRWQGNVFCVMEALHNHYTQKLSLSPGK 478
:||||| || |||||

RESULT 7
ID GC3 MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (REL. 19, CREATED)
DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT 01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)
DE IG GAMMA-3 CHAIN C REGION, SECRETED FORM.
OS MUS MUSCULUS (MOUSE).

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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE; 85027161.
RA WELS J.A., WORD C.J., RIMM D., DER-BALAN G.P., MARTINEZ H.M.,
RA TUCKER P.W., BLATTNER F.R.;
RL EMBO J. 3:2041-2046(1984).
DR EMBL; J00451; J00451.
DR PIR; B02156; G3MSC.
DR HSP; P01857; IFC1.
DR PROSITE; PS00290; IG MHC.
KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN; TRANSMEMBRANE;
KW ALTERNATIVE SPLICING.
FT NON TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; 617081 CN;

Query Match 45.7%; Score 1584; DB 3; Length 329;
Best Local Similarity 63.6%; Pred. No. 0.00e+00;
Matches 210; Conservative 61; Mismatches 57; Indels 2; Gaps 2;

Db 1 ttapsvplvpqsdtsqssvltlqclvkqfpeptvkwnygalssgvtvsvlge-g 59
:||||| || |||||
Qy 150 STKGSPVFLPAPSKSTSGCTAALGCLVKDYPPEVTVSNWNGALTSVHTPPAVLQSSG 209
:||||| || |||||
Db 60 fyeiseltvpsstwsqtvicnvahpaektelkriepktpstpgsscpnng 119
:||||| || |||||
Qy 210 LYSLSWVTPVSSSLGTQYICNVNHNKPSNTKVDKAEKPSCD-KTHTCPCPAPPELLIG 268
:||||| || |||||
Db 120 psvfifpkpkdalmisltkptcvvvdsheddphvafvdkhkvhtawtqpreaqyn 179
:||||| || |||||
Qy 269 FSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNKTPREQYN 328
:||||| || |||||
Db 180 aftrvsvlqghdwmrgkfkckvsnkalpapiertiskpkradtqvytlpppreq 239
:||||| || |||||
Qy 329 STRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGPREQVYTLPPSRDE 388
:||||| || |||||
Db 240 mskkkvaltclvtntffseaisvewerngeledqykntppildsdqtyflyekltvtdsw 299
:||||| || |||||
Qy 389 LTRNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSEFFLYSKLTVDKSRW 448
:||||| || |||||
Db 300 lqgeiftcsvhealnhrhtqklsrapok 329
:||||| || |||||
Qy 449 QQGNVFCVMEALHNHYTQKLSLSPGK 478
:||||| || |||||

RESULT 8
ID GC1 RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE IG GAMMA-1 CHAIN C REGION.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE; 89232738.
RA BRUEGGEMANN M.;

	RL	GENE 74:473-482(1988).	
	DR	PIR; PS0017; PS0017.	
	DR	HSP; P01857; IFC1.	
	DR	PROSITE; PS00290; IG_MHC.	
	KW	IMMUNOGLOBULIN C REGION; GLYCOPROTEIN.	
	FT	NON TER 1 J	
	FT	DOMAIN 1 97 CH1.	
	FT	DOMAIN 98 112 HINGE.	
	FT	DOMAIN 113 219 CH2.	
	FT	DOMAIN 220 326 CH3.	
	FT	DISULFID 27 82	
	FT	DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN) .	
	FT	DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN) .	
	FT	DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN) .	
	FT	DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN) .	
	FT	DISULFID 140 200	
	FT	DISULFID 246 304	
	FT	CARBOHYD 176 176 POTENTIAL.	
	SQ	SEQUENCE 326 AA; 35946 MW; 630958 CN;	
		Query Match 45.6%; Score 1582; DB 3; Length 326;	
		Best Local Similarity 63.3%; Pred. No. 0.00e+00;	
		Matches 209; Conservative 60; Mismatches 57; Indels 4; Gaps	
Db	1	aettapsvyplagtaalkensmvtlgclvkgyfpepvttwnsgalssgwhtfavllqg-	59
	: : : : : : : : : : : : : : : :		
Qy	149	ASTKGSEVFPLAPSSKSTSGGTALGCLVKDYFEPTVTVSNNSGALTGFPAVLQS	208
Db	60	glyltsevtvpastwpagtvtnvahpasatkvdkkivprncg-gd-ckpiactgs-ev	116
	: : : : : : : : : : : : : : : :		
Qy	209	GLYSLSVVTPVSSSLGTQTYICNVNHPKTSNKVDKAEPKSCDKTHTCPPCPAPEL	268
Db	117	asvfifppkpdvltitlpkrtcvvvdlsqddpvhfewfdvdevehvaqtprppeeqfn	176
	: : : : : : : : : : : : : : : :		
Qy	269	PSWFLEPPKKDTLMISRPEVTVCVVDSHEDPENKEWNYDVGVHNNAKTREEQYN	328
Db	177	stfrswelpllhqdmglngrtfcckttaaafspiektiskpegirtgvphvytmptkee	236
	: : : : : : : : : : : : : : : :		
Qy	329	STRVRVSVLTLQHDLWGNGEKYCKVSKNALPADIEKTIISKAKCQPREQVITLP	388
Db	237	mtegneaitcmvkgfyypdiivyewgmngqpennykntpptmdtgdyflysklrvtkkw	296
	: : : : : : : : : : : : : : : :		
Qy	389	LTRKNQVSLTCILNRKFYPSDIATVESNGSQPNNTTKTPPDLSDSGSFFLYSKLT	448
Db	297	qqgnftscavlheglhnbbhtekslshapgk	326
	: : : : : : : : : : : : : :		
Qy	449	QQGNVFSGSVHWHEALHHNIYTOKSLSPGK	478

RESULT	9	ID	GC3M MOUSE	STANDARD;	PRT;	398 AA.
AC		AC	P03987;			
DT		DT	23-OCT-1986 (REL. 02, CREATED)			
DT		DT	01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)			
DT		DT	01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)			
DE		DE	IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.			
OS		OS	MUS MUSCULUS (MOUSE).			
OC		OC	EUKARYOTA; METAZOA;			CHORDATA; VERTEBRATA; MAMMALIA;
OC		OC	EUTHERIA; RODENTIA.			
RN		RN	{1}			
RP		RP	SEQUENCE FROM N.A.			
RX		RX	MDLINE; 85027161.			
RA		RA	WELS J.A., WORD C.J.J.,			IMM D., MARTINEZ H.M.,
RA		RA	TUCKER P.M., BLATTNER E.R.;			

RL	EMBO J. 3:2041-2046(1984).
[2]	
RN	SEQUENCE OF 328-398 FROM N.A.
RP	MEDLINE; 84041483.
RX	KOMAROMY M., CLAYTON L., ROGERS J., ROBERTSON S., KETTMAN J.,
RA	WALL R.;
RA	NUCLEIC ACIDS RES. 11:6775-6785(1983).
DR	EMBL; J00451; J00451.
DR	EMBL; V01526; V01526.
DR	PIR; A02155; G3MSM.
DR	HSSP; P01857; IFC1.
DR	PROSITE; PS00290; IG_MHC.
KW	IMMUGLOBULIN C REGION; GLYCOPROTEIN; TRANSMEMBRANE;
KW	ALTERNATIVE SPLICING.
FT	NON_TER 1 1
FT	DOMAIN 1 97 CH1.
FT	DOMAIN 98 113 HINGE.
FT	DOMAIN 114 223 CH2.
FT	DOMAIN 224 327 CH3.
FT	TRANSMEM 346 362 POTENTIAL.
FT	DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT	CONFLICT 333 333 E -> G (IN REF. 2).
FT	CONFLICT 342 342 E -> Q (IN REF. 2).
FT	CONFLICT 388 388 P -> F (IN REF. 2).
SQ	SEQUENCE 398 AA; 43929 MW; 896835 CN;

Query Match	45.3%;	Score 1570;	DB 3;	Length 398;
Best Local Similarity	63.4%;	Pred. No. 0.00e+00;		
Matches	208;	Conservative	61;	Mismatches 57; Indels 2; Gaps
Db	1	tttapsvylpvgsdsgtsavllcgvkyfpeptvkwnygalsgvtvssvlqs-g	59	
	:	: : :	:	: :
	:	: : :	:	: :
	:	: : :	:	: :
Qy	150	STKGSVPFLAPSKSCTGGTALGLCKVDFFPEPTVSNMNSGALTSGVHTFPAPVLQS	209	
Db	60	fyslsalvtvpstwpstvicnvahpasktelikriepktpstppgsacppgnlilg	119	
	:	: : :	:	: : :
	:	: : :	:	: : :
Qy	210	LYSLSWTVPESSLGQTOTYONNHHKSNTKKDAEPKCD-KTHTPCPAPELLGG	268	
Db	120	pswfifpbpkdalmisltpkvtcvrvdseddvdhvsvfdnkhvtawtqraeqyn	179	
	:	: : :	:	: : :
	:	: : :	:	: : :
Qy	269	PSVFLEPPKPDTLMSITRTEPVTGVVVDSHEDPEVKFNMYVDGEVHNNAKTGPREQYN	328	
Db	180	stfrvvsalplqhgdwmrgkefkckvnkalpalpiertiskpgraqtppvytlppreq	239	
	:	: : :	:	: : :
	:	: : :	:	: : :
Qy	329	STRVVSVLTVLHQDWINGKEKCVKNALPALPIEKTSKAKQPREEQVYTLPFSRDE	388	
Db	240	makkksaitcltvntffseaisawerengeleqdykntppildsdgttyflyekltvdtaw	299	
	:	: : :	:	: : :
	:	: : :	:	: : :
Qy	389	LTKNQVSUTLVKRGFYPSDIAVENESNGOPENNYKTPPVLDSDGSFFFLYSKLTVDKSRH	448	
Db	300	laqeiftcsvhhealhmbhtcknlrsrp	327	
	:	: : :	:	: : :
	:	: : :	:	: : :
Ov	449	OOGNFVSCSVNHMALHNIYTOKSLSLSP	476	

RESULT	10
ID	GCL MOUSE STANDARD; PRT; 324 AA.
AC	P01869;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE	IG GAMMA-1 CHAIN C REGION.
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; VERTEBRATA; TETRAPODA; MAMMALIA;

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OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 80045036.
RA HONJO T., OBATA M., YAMAWAKI-KATAOKA Y., KATAOKA T., KAWAKAMI T.,
RA TAKAHASHI N., MANO Y.;
RL CELL 18:559-568 (1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE; 80202559.
RA OBATA M., YAMAWAKI-KATAOKA Y., TAKAHASHI N., KATAOKA T., SHIMIZU A.,
RA MANO Y., SEIDMAN J.G., PETERLIN B.M., LEDER P., HONJO T.;
RL GENE 9:87-97 (1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE; 80012837.
RA ROGERS J., CLARKE P., SALSER W.;
RL NUCLEIC ACIDS RES. 6:3305-3321 (1979).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX MEDLINE; 78242288.
RA ADETUGBO K.;
RL J. BIOL. CHEM. 253:6068-6075 (1978).
RN [5]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE; 73008889.
RA SVASTI J., MILSTEIN C.;
RL BIOCHEM. J. 126:837-850 (1972).
DR EMBL; V00793; V00793.
DR EMBL; V00795; V00795.
DR PIR; A02159; GIMS.
DR HSPS; P01679; IBAF.
DR PROSITE; PS00290; IG_MHC.
KW IMMUNOGLOBULIN C REGION; ALTERNATIVE SPLICING; GLYCOPROTEIN.
FT NON TER 1 1
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198 INTERCHAIN (WITH A HEAVY CHAIN).
FT CARBOHYD 174 174
FT DISULFID 244 302
FT MOD RES 324 324 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 324 AA; 35704 MW; 601902 CN;

Query Match 45.2%; Score 1566; DB 3; Length 324;
Best Local Similarity 62.1%; Pred. No. 0.00e+00;
Matches 205; Conservative 63; Mismatches 56; Indels 6; Gaps 4;

Db 1 aktppsyyplagsgaaqtnsmvtlgclvkgyfpepytvtwnsgalsgsvhtfpavlgqd 60
| | |||||:| : : : ||||| |||||:|||||:|:|||||:|:|||||
Qy 149 ASTKGSVFPLAPSSKSTSGGTAALGCLVKRDVPEPVTVMNSGALTSGVHTFPVLQSS 208
| | |||||:| : : : ||||| |||||:|||||:|:|||||:|:|||||

Db 61 -lytleasvtypesrpsretvtcnvapaeatkvdkiiprdcg-ckpci-ctyprev--- 114
||||| ||||| : : ||| :|:||||| |:| | | | |
Qy 209 GLYSLSVVTPWSSLGTOTVCYNWNHKSNTKVDKAEPKSCDKTHTCTPPCPAPELGG 268
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 115 ssvfiappkdvltltpkvrtcvvdiiskddbevqsfwfdvdevhtactqpreefn 174
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY	269	PSVFLEPPRPKADTLMISRTPEVTCVVVDVSHEDPEVKFNWYDVGVEVHNAKTKPREEQYN	328
Db	175	stfrsvslpimhqdwlngskfkrvnsaaafapietktsktgrkapqvytipppkeq	234
QY	329	STRVVSVLTVLHQDWLNGKEYCKYSNKAALPAPIETKSIAKGAKQREPOVTLTPSRDE	388
Db	235	makdkvseltcmidtfpeditvwqngqpaaenykntcpimntngsfyysklqvqknw	294
QY	389	LTRNQVSLTCLVKGFPYSDIAVESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW	448
Db	295	eagntftscvlheglhhhtekslshspgk	324
QY	449	QQGNWFSCVMHEALHNHYTKSLSLSPGK	478
RESULT	11		
ID	GCC RAT	STANDARD;	PRT; 329 AA.
AC	P20762;		
DT	01-FEB-1991 (REL. 17, CREATED)		
DT	01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)		
DT	01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)		
DE	IG GAMMA-2C CHAIN C REGION.		
OS	RATTUS NORVEGICUS (RAT).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
NC	EUTHERIA; RODENTIA.		
RC	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE; 88166903.		
RX	BREDGEWMANN M., DELMASTRO-GALFRE P., WALDMANN H., CALABI F.;		
RL	EUR. J. IMMUNOL. 18:317-319(1988).		
DR	EMBL; X07189; X07189.		
DR	PIR; S00847; S00847.		
DR	HSSP; P01857; IFC1.		
DR	PROSITE; PS00290; IG.MHC.		
KW	IMMUNOGLOBULIN C REGION.		
FT	NON TER 1 1		
FT	D0MAIN 1 97		CHI.
FT	D0MAIN 98 113		HINGE.
FT	D0MAIN 114 222		CH2.
FT	D0MAIN 223 329		CH3.
FT	DISULFID 15 15		INTERCHAIN (WITH A LIGHT CHAIN).
FT	DISULFID 27 82		
FT	DISULFID 111 111		INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 113 113		INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 143 203		
FT	DISULFID 249 307		
SQ	SEQUENCE 329 AA; 36571 MW; 626020 CN;		
Query Match	45.0%;	Score 1559; DB 3; Length 329;	
Best Local Similarity	61.8%;	Pred. No. 0.00e+00;	
Matches	204; Conservative 61; Mismatches 64; Indels 1; Gaps 1;		
Db	1	arttapsvylpqpcsqgtsglvtlgclvkgyfpvptvkwneagsvgvhtfpavlgse- 59	
QY	149	ASTKGFVFPPLAPSSKTSGGTAAGCLWKDYFPFPVTWSNSGALTSGVHTFPVAVLGSS 208	
Db	60	glytlasvtpastwsqvtcavahpatkenlikiepricpkprptdicescdnlgrr 119	
QY	209	GLYSLSVVTPVSSSIGTGTYICNVNHKPSNTKYDKRAEPKSCDKTHTCPCPAPELLGG 268	
Db	120	psvfifppkpdklimitltpkvtcvvduseepdvqfwfdnvrvftaqtcphgeqln 179	
QY	269	PSVFLEPPRPKADTLMISRTPEVTCVVVDVSHEDPEVKFNWYDVGVEVHNAKTKPREEQYN 328	

SEQUENCE OF 1-44 FROM N.A.	
MDLINE; 8222190.	
RA. YAMAWAKI-KATOAKA Y., NAKAI S., MIYATA T., HONJO T.;	
PROC. NATL. ACAD. SCI. U.S.A. 79:2623-2627(1982).	
-1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MENA	
SPECIES FOR IGG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED	
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-	
BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED	
IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND	
SEGMENT OF MU CHAINS.	
EMBL; V00793; V00793.	
PIR; B02159; GMSM.	
HSP; P01857; IBAF.	
PROSITE; PS00290; IGMHC.	
IMMUNOGLOBULIN C REGION; ALTERNATIVE SPLICING; TRANSMEMBRANE;	
GLYCOPROTEIN.	
NON TER 1	1
DOMAIN 1	97
DOMAIN 98	110
DOMAIN 111	217
DOMAIN 218	324
DISULFID 27	82
DISULFID 102	102
INTERCHAIN (WITH A LIGHT CHAIN).	

RESULT	13
ID	GCAA MOUSE STANDARD; PRT; 330 AA.
AC	P01863;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE	IG GAMMA-2A CHAIN C REGION, A ALLELE.
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 81076554.
RA	SIKORAV J.-L., AUFRAY C., ROUGEON F.;
RL	NUCLEIC ACIDS RES. 8:3143-3155(1980).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 81198976.
RA	YAMAWAKI-KATAOKA Y., MIYATA T., HONJO T.;
RL	NUCLEIC ACIDS RES. 9:1365-1381(1981).
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 81223894.
RA	OLIO R., AUFRAY C., MORCHAMPS C., ROUGEON F.;
RL	PROC. NATL. ACAD. SCI. U.S.A. 78:2442-2446(1981).

Search completed: Tue Dec 17 15:30:47 1996
Job time : 14 secs.

(TM)

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MPsrch pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 15:28:18 1996; MasPar time 10.37 Seconds
438,998 Million cell updates/sec

Tabular output not generated.

Title: >US-08-487-550-8

Description: (1-478) from US08487550.ppt

Perfect Score: 3466

Sequence: 1 MGWSLILFLVAVATRVQCE.....MHEALHNHYTQKSLSLSPGK 478

Scoring table: PAM 150

Gap 11

Searched: 81589 seqs, 9523651 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-geneseq24

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16

Statistics: Mean 35.472; Variance 183.928; scale 0.193

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			ID	Description	Pred. No.
		Match	Length	DB			
1	2931	84.6	461	8	R42162	Anti-HIV-1 recombinan	5.92e-228
2	2931	84.6	475	3	R20057	Heavy chain of 3D6 an	5.92e-228
3	2880	83.1	481	5	R24442	Sequence of antibody	9.99e-224
4	2877	83.0	470	4	R22757	Reshaped CAMPATH-1 an	1.77e-223
5	2871	82.8	477	8	R42053	ch194.12 H3 heavy ch	5.56e-223
6	2824	81.5	459	8	R24066	Human anti-HBs heavy	4.37e-219
7	2813	81.2	453	6	R33311	Humanised MaE11 Versi	3.56e-218
8	2806	81.0	466	5	R24812	Sequence encoded by t	1.35e-217
9	2771	79.9	476	6	R31023	Antibody D heavy chai	1.07e-214
10	2762	79.7	467	15	R80617	Anti-human IL-4 human	5.98e-214
11	2759	79.6	467	4	R22759	Reshaped CD4 antibody	1.06e-213
12	2757	79.5	467	4	R22758	Reshaped CD4 antibody	1.55e-213

CC tetrapeptide motif GPCR, i.e. the Principal Neutralising
 CC Determinant common to the V3 loop of different HIV isolates.
 CC A recombinant Ab was produced in which the H chain V region was
 CC derived from 447-520 and to which a signal sequence and a H chain
 CC intronic sequence are appended, fused to a fragment contg. a short
 CC intronic segment of the human gamma 1 C region and the human gamma
 CC 1 encoding domain in its genomic form.
 SQ Sequence 461 AA;

Query Match 84.6%; Score 2931; DB 8; Length 461;
 Best Local Similarity 96.3%; Pred. No. 5, 92e-228;
 Matches 417; Conservative 16; Mismatches 25; Indels 4; Gaps 4;
 Db 1 evqlvesggllvkgqslrltcvasgftsdvlnwvraqpdkglewvqrikartdgtt 60
 Qy 20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYFRQAPKGPEWVGFINRKGSGTT 79
 Db 61 dyaaavkgrfisiardskntlylqmsalktedavyscttdgfim-irgvsedyvyyymd 119
 Qy 80 EYAAAVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTT-SYISHCRG-GVYGGYF-E 136
 Db 120 vwgkgtvtvsaatkgspsvflapssketaggtaalglcvkdyfpepvtvsmnegalts 179
 Qy 137 FMGGGALVTVSSASTKGPSVFPPLAPSSKSTSGTAAAGLGLVKDYFPEPVTVSMNEGALTS 196
 Db 180 gvhtfpavlgasglyslasvvtvpssslgtqtyicnvnhkpsntkvdskvpeksckdtht 239
 Qy 197 GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKAEKPSCKDTHT 256
 Db 240 cpcpapelggpsvflfpkpdkdtlmsirtpevtcvvmdvshedpevknfyvdygvevh 299
 Qy 257 CPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNFYVDGVEVH 316
 Db 300 naktkpreeqynstyrsvvltvldwngkeyckvknkalpapietkiskagqpre 359
 Qy 317 NAKTKPREEQYNSTYRWVSVLTVLHQDLNGLNGKEYCKVKNKALPAPIETKISKAGQPRE 376
 Db 360 ppyvtlpprdeltknqvslcvtkvgyfypsdiaveesngqpennyktptpvldeagdf 419
 Qy 377 PPYVTLPSPRDELTKNQVSLTCLVKGYFSDIAVEWESNGQPENNYKTPTPVLDSGSEFF 436
 Db 420 lyskitvdksrwqggnvfscsvmhcalhnhytqkslelepqk 461
 Qy 437 LYSKLTVDKSRWQQGNVFCSVMHREALHNYHTQKSLSLSPGK 478

RESULT 2
 ID R20057 standard; Protein; 475 AA.
 AC R20057;
 DT 25-MAR-1992 (first entry)
 DE Heavy chain of 306 anti-HIV antibody.
 KW Plasmid pUC3D6HC; human immunodeficiency virus; AIDS;
 KW complementarity determining region.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= signal
 FT Region 20..49
 FT /label= Framework_1
 FT Region 50..54
 FT /label= CDR-1
 FT Region 55..68
 FT /label= Framework_2
 FT Region 69..85

FT /label= CDR_2 86..117
 FT Region
 FT /label= Framework_3 118..134
 FT Region
 FT /label= CDR_3 135..145
 FT Region
 FT /label= Framework_4 146..475
 FT Region
 FT /label= Constant_region
 PN W09118983-A.
 PD 12-DEC-1991.
 PF 28-MAY-1991; 100067.
 PR 29-MAY-1990; AT-001178.
 PA (JUNG/) JUNGBAUER A.
 PI Felgenhauer M, Himmeler G, Kohl J, Steindl F;
 DR WPI; 92-007468/01.
 DR N-PSDB; Q20066.
 PT Recombinant protein which binds to complex viral antigen and
 PT HIV-1 - contains variable region of antibody derived from 306
 PT cell line, used for detecting HIV-1 antigen
 PS Claim 2; Page 24; 52pp; German.
 CC The variable region of the heavy chain is used in a recombinant
 CC protein with the variable region from the kappa light chain of 306,
 CC the two V regions being joined by a linker. The recombinant protein
 CC binds to HIV gp160.
 CC See also Q20067 and Q20068.
 SQ Sequence 475 AA;

Query Match 84.6%; Score 2931; DB 3; Length 475;
 Best Local Similarity 86.4%; Pred. No. 5, 92e-228;
 Matches 413; Conservative 25; Mismatches 37; Indels 3; Gaps 3;
 Db 1 melglewifllailkvqceqlvesggllvqpqrallrcacaagftfndyamhwvraq 60
 Qy 1 MGWSLILFLVAVATRVQCEQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYFRQAP 60
 Db 61 kglewvsi-sw-dassigvadavkgrftsiardnknaknalylqmslraedmalyyevkg 118
 Qy 61 KGKPEWVGFINRKGSGTTEYAAASVKDRFTISRDDSKSIAYLQMSLKIEDTAVYYCTTS 120
 Db 119 -rdydsdgyftvafdlwgqgtmtvssastkpsvflapssketaggtaalglcvkdy 177
 Qy 121 YISHCRGGVYGGYFEFGQCALVTVSSASTKGPSVFPPLAPSSKSTSGGTAAAGLGLVKDY 180
 Db 178 fpeptvsvnsgaltsegvhtfpavlgasglyslasvvtvpssslgtqtyicnvnhkpsnt 237
 Qy 181 FPEPTVTVSNNGALTSGVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNT 240
 Db 238 kvdkkvepkscdkthlcpccapelggpsvflfpkpdkdtlmsirtpevtcvvvdvsh 297
 Qy 241 KYDKKAEKPSCKDTHTCPPCAPELGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 300
 Db 298 dpevknfyvdygvevhnaktkpreeqynstyrsvvltvldwngkeyckvknkalp 357
 Qy 301 DPEVKFNFYVDGVEVHNKTPREEQYNSTYRWVSVLTVLHQDLNGLNGKEYCKVKNKALP 360
 Db 358 apiektiskagqpreppvytlppsrdeitknqvslcvtkvgyfypsdiaveesngqpen 417
 Qy 361 APIEKTISKAGQPREPPQYVTLPPSRDELTKNQVSLTCLVKGYFSDIAVEWESNGQPEN 420
 Db 418 nykttppvldeagdflyskitvdksrwqggnvfscsvmhcalhnhytqkslelepqk 475
 Qy 421 NYKTTTPVLDSGSEFFLYSKLTVDKSRWQQGNVFCSVMHREALHNYHTQKSLSLSPGK 478

CC also be achieved. See also R22754-R22763.
SQ Sequence 470 AA;

Query Match 83.0%; Score 2877; DB 4; Length 470;
Best Local Similarity 86.0%; Pred. No. 1.77e-223;
Matches 411; Conservative 29; Mismatches 30; Indels 8; Gaps 4;

[illegible]

RESULT	5	
ID	R47453	standard; Protein; 477 AA.
AC	R47453;	
DT	24-JUN-1994	(first entry)
DE	ch1784.12 H3 heavy chain.	
KW	Chimeric; carcinoembryonic antigen; CCA; murine; mouse; constant; region; transform; myeloma cell; light chain; tumour.	
KW	Synthetic.	
OS	WO9325237-A.	
PD	23-DEC-1993.	
PF	15-JUN-1993; WO5709.	
PR	15-JUN-1992; US-904074.	
PA	(CITY) CITY OF HOPE.	
PA	(YANG/) YANG Y.	
PI	Fischer R, Paxton R, Shively JE, Wu A, Yang YHJ;	
PI	Yang YH;	
DR	WPI; 94-007204/01.	
DR	N-PSDB; 054655.	
PPT	New chimeric T84.12 antibody active against carcinoembryonic antigen - has murine variable and human constant regions, also	
PPT	DNA encoding it and transformed myeloma cells	
PPT	Claim 1; Page 22-23; 2/pp; English.	
PS	The sequences (Q54651-52) show the light and heavy chain cDNAs	
CC	of murine T84.12. The T84.12 antibody is directed against the	

CC tumour marker carcinoma embryonic antigen, and is useful for
CC tumour imaging and immunotherapy.
CC The amino acid sequence given in the specification has been
CC incorrectly identified as a nucleic acid sequence, therefore
CC unacceptable characters have been represented as an 'N'.
CC The amino acid sequence given below has been derived from the
CC cDNA, by the indexer.
SQ Sequence 477 AA;

Query Match 82.8%; Score 2871; DB 8; Length 477;
Best Local Similarity 86.2%; Pred. No. 5.56e-223;
Matches 412; Conservative 22; Mismatches 34; Indels 10; Gaps 8;

Db	10	mnfgsllflvlkvqdcvklvegggfvkpggslkscasagfftsasyamewrqt p	69
Qy	1	MGWSLILFLIWAIVATRVCEVQLVSGGSLVQPGGSLRVSCAVSGFTSDHYWYWFRAQ	60
Db	70	eklewasl-s-sdg-itfyvdsvkgftvrdharnllylqmslairedtamyca-r	125
Qy	61	GKGPENVGFIIRNKPNGTTEYAASVKDRETIISRDDSKSTAYILQMSLKIETD	120
Db	126	-idy-gg---gg-fgywgqgtlatvsaastkpsvflapasesketseggtaalglcvkdy	179
Qy	121	YISHCGGVCGYGFYFEGQCALVTVSSNSATKGPVFPANPSKSTSGGTAAAGCLWKDY	180
Db	180	fpeptvswmsgaltsqgvhtfpavlgseglyslasvvvtvpasslgtgtvcinvhkpst	239
Qy	181	FPPEVTVSWNSGALTSQVHTEPAVLQSGCLYLSLSSVTVSSLGTTQTCYNVHKPSNT	240
Db	240	kvdskvepscdkthccppcapellqgpsvflfpkpkdtilmstertpvcvvdashe	299
Qy	241	KVDKAEKPSCDKTHTCPPCPAPELIGGSEVFLFPKPKDILMISRTPEVTCVVDVSH	300
Db	300	dpsvktfmyvdgvevhnaktkpreegynstvrvsvltvlhqdwlngkyckvsnkalp	359
Qy	301	DPEKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALP	360
Db	360	apiettkakgprepqvtylppsrdeltknqvsltclvkqfypediaveangpen	419
Qy	361	APIETKISKAGQPREPQVYTIPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGPEN	420
Db	420	nykttppvldsdgfflyskltdvdkrqqgnvfscsvmhealhnhytqkslsapok	477
Qy	421	NYKTTPPVLDSDGFFLYSKLTDKSRMQQGNVFGSGVSMHEALHNHYTKSLSPQK	478

RESULT	6	
ID	R42066	standard; Protein; 459 AA.
AC	R42066;	
DT	29-APR-1994	(first entry)
DE	Human anti-HBs heavy chain.	
KW	Antibody; Ab; light; heavy;	chain; hepatitis B;
KW	HB; surface antigen.	
OS	Homo sapiens.	
FS	Key	Location/Qualifiers
FT	Peptide	1..9
FT	/label= sig_peptide	
FT	Protein	10..459
FT	/label= mat_protein	
PN	W09320205-A.	
PD	14-OCT-1993.	
PF	30-MAR-1993;	J00396.
PR	30-MAR-1992;	JP-074678.
PA	(SUNR)	SUNTORY LTD.

PR 07-MAY-1992; US-879495.
PA (GETH) GENENTECH INC.
PI Jardieu PM, Presta LG;

FT	Peptide	
FT	/label= Leader	13..19
FT	Region	20..134

FI	Region	20..134
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
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59	59	59
60	60	60
61	61	61
62	62	62
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72	72	72
73	73	73
74	74	74
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76	76	76
77	77	77
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79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

Region	135..232	
/label= CH1		
Region	233..247	
/label= hinge		
Region	248..357	
/label= CH2		
Region	358..464	
/label= CH3		
Misc difference 465		
/note= "translated stop codon"		
EP-491351-A.		
PD	24-JUN-1992.	
PF	17-DEC-1991; 121591.	
PR	18-DEC-1990; JP-413829.	
PR	11-NOV-1991; JP-294464.	
PA	(TAKE) TAKEDA CHEM IND LTD.	
PI	Iwasa S, Taka H, Watanabe T, Tada H;	
DR	WPI; 92-209528/26.	
DR	N-PSDB; Q25692.	
PT	Chimeric monoclonal antibodies - contain anti-human fibrin	
PT	antibody light and heavy chain variable and constant for treating	
PT	thrombotic conditions e.g. myocardial infarction	
PS	Example; Figure 11; 87pp; English.	
CC	Plasmid pFB1373 contains the whole length of a mouse-human	
CC	chimeric anti-human fibrin heavy chain cDNA open reading	
CC	frame. It was prepd. using Poly(A)+ RNA from the anti-fibrin	
CC	chimeric Ab-producing transformant FIB1-H01/X63 as a template	
CC	to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as	
CC	a primer for first strand cDNA synthesis and the 5'C2H and 3'EH	
CC	primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding	
CC	cDNA was amplified. Similarly a human gamma-1 chain CH1 domain	
CC	encoding cDNA and an anti-fibrin antibody VH cDNA and a leader	
CC	peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'CH	
CC	respectively as a primer for first strand cDNA synthesis and the	
CC	primer combination of 5'C1H and 3'C2H, of 5'1LH and 3'C1H and of	
CC	5'SH and 3'1H respectively as primers for PCR. The amplified gene	
CC	products were isolated and used to produce plasmids. After	
CC	confirmation of the cDNA sequence of each plasmid, the cDNA	
CC	encoding LH, VH, CH1 and CH2CH3 were joined together to give	
CC	plasmid pFB1373 contg. the whole length chimeric H chain	
CC	(LH, VH, CH1, CH2CH3), also abbreviated as IgH-FIB,	
SQ	Sequence 466 AA;	
Query Match	81.0%; Score 2806; DB 5; Length 466;	
Best Local Similarity	84.9%; Pred. No. 1.35e-217;	
Matches	406; Conservative 30; Mismatches 28; Indels 14; Gaps 5;	
Db	1 mdsrlnlvflvllkvgdcvqlvesggglvkgpgsklscasagftfsnydmswvrgtp 60	
Qy	: : : : :	
1	MGWSLILFLVAVATRVCRQVLVESGGGLVPGGSLRVSCAVSGFTFSDRHYMFRQAP 60	
Db	61 errlewaasi---svagttyrpdemkqrftierdnarnilyqlslrsedtamycg-n 116	
Qy	: : : : : : : : : : :	
61	GKGFENWGVIRNKPNGGTTTAAASVKQDRFTIRDDSKSIAYLQMSLKIEDTAVYYCTTS 120	
Db	117 f-ad---am-----dywqgglrtvessaatkpvgfplapsesktogtaalgclvkdy 166	
Qy	: :	
121	YISHCRGGVCYGGYFEFWQGLVALTVSSASTKGPVFLAPSSKTSKTSGGTAALGCLWKDY 180	
Db	167 fpepvtvwmegaltegrhtfpavlqsglylalsevwtvpsseslgtqctyictvnhkpsnt 226	
Qy	181 FPEPVTVMNSGALTSG/HTTFAVLQSGGLYSSVTVTPSSSLGTQTYICNVNHHKPSNT 240	
Db	227 kvdkrivepkscdkthtccpapeellqgssvflfppkpkdklmiertbvtcvwdvse 286	

QY	241	KVDKAEPEKSCDKTHTCPPEAPELLGGFVSFLFPKPKDPTLMISRTPEVTCVVVDVSH	300
Db	287	dpevkfnwydgvevhnaktkpreegynstyrvsvltvlhqdwlngkeyckvsnkalp	346
QY	301	DPEKFNWYDGVGEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALP	360
Db	347	apiektiekakgprepqvvtlppsreémtnknvslctclvkgfypsdiaveesngqpen	406
QY	361	APIETKTSKAKGPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPEN	420
Db	407	nykttppvldsdgsfflyskltvdkerwqgmvfscsvmhlealnhhvtqkalelepqk	464
QY	421	NYKTTTPVLDSDGSFFLYSKLTVDKSRWQGMVFSCSVMHLEALNHHTOKSLSLSPCK	478
RESULT 9			
ID	R31023	standard; Protein; 476 AA.	
AC	R31023;		
DT	19-MAY-1993	(first entry)	
DE	Antibody D heavy chain.		
KW	Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;		
KW	lymphocyte; hepatitis A virus; HAV; sero; positive; patient;		
KW	murine; BSB3; polyadenylated; cDNA library; human; kappa; L; H.		
OS	Synthetic.		
PH	Key	Location/Qualifiers	
FT	Peptide	1..19	
FT	/note= "Signal peptide"	20..49	
FT	Region		
FT	/label= FR1	50..54	
FT	Region		
FT	/label= CDR1	55..68	
FT	Region		
FT	/label= FR2	69..84	
FT	Region		
FT	/label= CDR2	85..113	
FT	Region		
FT	/label= FR3	114..121	
FT	Region		
FT	/label= CDR3	122..132	
FT	Region		
FT	/label= FR4	133..241	
FT	Domain		
FT	/label= CH1	242..262	
FT	Region		
FT	/label= HINGE	263..379	
FT	Domain		
FT	/label= CH2	380..497	
FT	Domain		
FT	/label= CH3		
FT	Domain		
PN	EP-523949-A.		
PD	20-JAN-1993.		
PF	14-JUL-1992; 306420.		
PR	15-JUL-1991; GB-015284.		
PR	01-AUG-1991; GB-016594.		
PR	23-MAR-1992; GB-006284.		
PA	(WELL) WELLCOME FOUND LTD.		
PI	Crowe JS, Lewis AP;		
DR	WPI; 93-019951/03.		
DR	N-PSDB; Q35099.		
PT	Prodn. of recombinant primate antibodies - useful for treating		
PT	infections caused by hepatitis A, B and C, herpes,		
PT	cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,		
PT	arthritis etc.		

RESULT	10
ID	R80617 standard; Protein; 467 AA.
AC	R80617;
DT	19-APR-1996 (first entry)
DE	Anti-human IL-4 humanised WAB h25D2-9 mature heavy chain.
KW	Anti-human interleukin-4; IL-4; humanisation; purification; treatment; IL-4 diseases; immunoassay; heavy chain; h25D2-9; antibody.
OS	Homo sapiens.
FH	Key Location/Qualifiers
FT	Peptide 1..19
FT	/label= leader sequence
FT	Peptide _ 20..467
FT	/label= mat_peptide
PN	W09524481-A2.

RESULT	11
ID	R22759 standard; Protein; 467 AA.
AC	R22759;
DT	20-OCT-1992 (first entry)
DE	Reshaped CD4 antibody heavy chain CD4VHNEW-Ser30.
NW	Antigen; CDR; complementarity determining region; graft rejection;
KW	autoimmune diseases; rheumatoid arthritis; allergy.
OS	Rattus rattus.

EH	Key	Location/Qualifiers
FT	Peptide	1..19
FT	/note= "signal peptide"	
FT	Peptide	20..467
FT	/note= "mature peptide"	
FT	Region	50..54
FT	/note= "Complementarity determining region 1"	
FT	Region	69..85
FT	/note= "Complementarity determining region 2"	
FT	Region	118..126
FT	/note= "Complementarity determining region 3"	
PN	W09205274-A.	
PD	02-APR-1992.	
PF	16-SEP-1991; G01578.	
PR	17-SEP-1990; GB-020282.	
PI	(GORM/) GORMAN S D.	
PA	Clark M R, Cobbold S P, Gorman S D, Waldmann H.	
DR	WPI; 92-132139/16.	
DR	N-PSDB; Q23581.	
PT	Humanisation of antibodies binding to human CD4 antigen - by	
PT	mutation of framework-encoding regions of DNA encoding variable	
PT	domain of rat or mouse antibody chain	
PS	Disclosure; Fig 7; 74pp; English.	
CC	The sequence is that of the reshaped CD4 antibody heavy chain	
CC	CD4VHNEW-Ser30. Reshaped CD4 antibody can be used to induce tolerance	
CC	against an antigen. It can also be used to alleviate autoimmune diseases	
CC	such as rheumatoid arthritis, and to prevent graft rejection. Tolerance	
CC	to a graft, e.g. an organ graft or a bone marrow transplantation can	
CC	also be useful to alleviate allergies. Tolerance to allergens could	
CC	also be achieved. See also R22753-R22763.	
SQ	Sequence	467 AA;

Query Match	79.6%	Score 2759;	DB 4;	Length 467;
Best Local Similarity	84.5%;	Pred. No. 1.06e-213;		
Matches	404;	Conservative	29;	Mismatches 34; Indels 11; Gaps 5;
Db	1	mwsclllflvatatgvheqvgqlqesgplvpqsqtlsltctvsqftsfsgymawvrqp	60	
		. : : : : : : :		
Qy	1	MGSLLLTLFLVAVATRVCEQVLVESGGGLVPGGSLRVSCAVSGFTSDHYHMYFRQAP	60	
Db	61	grglewigtish--dgedtyfrdvkrgvtmlvsktnkfslrleavtaadtavyca--	116	
		: : : : : : : : :		
Qy	61	GKGPWVGCFIRNPNCGTTEYAAASVKDRFTISRDDSKSIAYLQMSIKIEDTAVYYCITS	120	
Db	117	---r-qgtl--ag-i thwgqgelvtvasaatkpavfp lapeskatsggtaalgcilvkdy	169	
		: : : : : : :		
Qy	121	YISHCRGGVCYGVEFWQGALVTVSSASTKPSVPFLAPSKSTSGCTAALGCILVKDY	180	
Db	170	fpeptvvnsgalstqvhtfpavlqsglylselvvtpsseslgtqtyicnvhnpent	229	
		: : : : :		
Qy	181	FPEPTVTVNSGALTSGVHTFPAVLQSSGLYSLSVVTPSSSLGTQTYICNVNHKPNT	240	
Db	230	kvdckvepkscdkthtcpcpapellggpvevlfpkpkpktlmiaertbevttcvvvdsha	289	
		: : : : :		
Qy	241	KVQKGAEPKSCDKTHTCPCPAPELLGGPSVLFPPPKPKDTLMISRTPEVTVCVVDVSHS	300	
Db	290	dpevktfnwydgvevhnaktkpreegynstvrvslvthgdwlngkyckvcvenkalp	349	
		: : : : :		
Qy	301	DPEVFENNYDGVCEVHNAKTKPREEQYNSTYRWSVLTJHQDWLNGEYCKVCVENKALP	360	
Db	350	apiektiskakgpqpgpyrtlpssrdeltknqvelctlvkgfypsdaavewesngqpen	409	
		: : : : :		
Qy	361	APIETISKAGQREFPYVYLTPSRDELTRKSQVSLCTLVKGYPSDLIAEWESNGQPEN	420	

Db	410	nykttppvldsdgfflyekiltvdksrwqdggnvfscvmeahlnhnytkslslspgk	467
Qy	421	nykttppvldsdgfflyskltvdksrwqdggnvfscvmeahlnhnytkslslspgk	478
RESULT	12		
ID	R22758	standard; Protein; 467 AA.	
AC	R22758;		
DC	DT 20-OCT-1992	(first entry)	
DE	Reshaped CD4 antibody heavy chain CD4VHNEW-Thr30.		
KW	Antigen; CD8; complementarity determining region; graft rejection;		
KW	autoimmune diseases; rheumatoid arthritis; allergy.		
OS	Rattus rattus.		
FH	Key	Location/Qualifiers	
FT	Peptide	1..19	
FT	/note= "signal peptide"		
FT	Peptide	20..467	
FT	/note= "mature peptide"		
FT	Region	50..54	
FT	/note= "Complementarity determining region 1"		
FT	Region	69..85	
FT	/note= "Complementarity determining region 2"		
FT	Region	118..126	
FT	/note= "Complementarity determining region 3"		
PN	W09205274-A.		
PD	02-APR-1992.		
PF	16-SEP-1991; G01578.		
PR	17-SEP-1990; GB-020282.		
PA	(GORM/) GORMAN S D.		
PI	Clark M R, Cobbold S P, Gorman S D, Waldmann H.		
DR	WPI; 92-132139/16.		
DR	N-PSDB; Q23571.		
PT	Humanisation of antibodies binding to human CD4 antigen - by		
PT	mutation of framework-encoding regions of DNA encoding variable		
PT	domain of rat or mouse antibody chain		
PS	Disclosure; Fig 6; 74pp; English.		
CC	The sequence is that of the reshaped CD4 antibody heavy chain		
CC	CD4VHNEW-Thr30. Reshaped CD4 antibody can be used to induce tolerance		
CC	against an antigen. It can also be used to alleviate autoimmune diseases		
CC	such as rheumatoid arthritis, and to prevent graft rejection. Tolerance		
CC	to a graft, e.g. an organ graft or a bone marrow transplantation can		
CC	also be useful to alleviate allergies. Tolerance to allergens could		
CC	also be achieved. See also R22753-R22763.		
SQ	Sequence 467 AA;		

	Query Match	79.5%; Score 2757; DB 4; Length 467;
	Best local Similarity	84.3%; Pred. No. 1.5e-213;
	Matches	403; Conservative 30; Mismatches 34; Indels 11; Gaps 5;
Dbb	1 mgwsciliflvatagvghesqvlgesgplvrpqetlslctcvsgeffitnmgawrrgp	60
	: : :	
	: : :	
Qy	1 MGWILLFLVAVATRVCEQLVESGGGLVPQGSLRVSICAVSGFTSDHYMYFRQP	60
Dbb	61 grglwgigtish--dgsedyfrdvkgrvtmlvdtsknfslrlesvaeadtavyca--	116
	: : : : : : : : : : : :	
Qy	61 KGKPEVGFGIRNKPNGGTVEAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYCYCTS	120
Dbb	117 ---r---agtll--agrhwqqsgltvrsasatkpevfplapasketagggtaaqlclvkdy	169
	: : : : : : : : : : : :	
Qy	121 YISHCRGVCYCCTGYFFEWGQCALVTYSASTKGPSVFPLAPSKTSKSTGGTAALGCIVRDY	180
Dbb	170 fpepptvwmsgalitgygvhtfpavlgseglylasrvtpssalqtqtcynmhkkpent	229
	:	
Qy	181 FPEPTVMWSGALTIGSVHTFPAVLQSSELYLSGSVVTPSSSGLQTGYTCNNHKNPNT	240

Db 230 kvdkvpeksedthtcpcpapellggspsvflfpkpkdtlmisrtpevtcvvvdvshe 289
|||||
Qy 241 kvdkkaepkscdkthtccpapellggspsvflfpkpkdtlmisrtpevtcvvvdvshe 300
Db 290 dpekvfnvydgvevhnaktkpreeqnetyrvsvltvlhqdwlngkeyckvsnkalp 349
|||||
Qy 301 dpekvfnvydgvevhnaktkpreeqnetyrvsvltvlhqdwlngkeyckvsnkalp 360
Db 350 apiektsakagqprepyvtlpsrdeltknqvaltcclvkfypsdiaveesngpen 409
|||||
Qy 361 apiektksakagqprepyvtlpsrdeltknqvaltcclvkfypsdiaveesngpen 420
Db 410 nykttppvldsdgsfflyskltdvksrwmqgnvfscsvmhcalhnhytqklsispk 467
|||||
Qy 421 nykttppvldsdgsfflyskltdvksrwmqgnvfscsvmhcalhnhytqklsispk 478

RESULT 13

ID P70547 standard; protein; 470 AA.
AC P70547;
DT 12-FEB-1991 (first entry)
DE Sequence of novel mouse-human chimeric antibody H chain.
KW Leukaemia lymphoma diagnosis; tumour diagnosis;
KW novel mouse-human chimeric antibody H chain.
OS Homo sapiens and Mus musculus.
FH Key Location/Qualifiers
FT Region 1..140
FT /note="Mouse V region"
FT Region 141..480
FT /note="Human C region"
PN J62201598-A.
PD 05-SEP-1987.
PF 28-FEB-1986; 041983.
PR 28-FEB-1986; JP-041983.
PA (TEIJ) TEIJIN KK.
DR WPI; 87-288384/41.
PT Mouse-human chimera antibody H chain - comprises mouse antibody H
PT chain V region amino acid sequence and human antibody C region
PT sequence, to react with leukaemia lymphoma antigen
PS Claim 8; Page 3; 21pp; Japanese.
CC A human gene library prep. from isolated human chromosomal DNA, was
CC screened for human antibody H chain gene fragment contg. human
CC C-gamma-1 gene (see N70844, N70845, N70486 and N70882). A mouse
CC NL-1 gene library prep. from isolated mouse chromosomal DNA, was
CC screened for mouse antibody H chain gene; then the DNA sequence of
CC the VDJ region of this gene was determined. Using the above human
CC and mouse genes, chimeric antibody gene expression vectors
CC pMH-1, -2, -3, -4 and -5 were prep.
SQ Sequence 470 AA;

Query Match 79.3%; Score 2748; DB 2; Length 470;
Best Local Similarity 85.6%; Pred. No. 8.64e-213;
Matches 404; Conservative 22; Mismatches 31; Indels 15; Gaps 7;

Db 1 dvqlvesggglvqpgggrklscasagftsfsgmhwvraqepkglewvayisggay--ti 58
:|||||
Qy 20 EVQLVESGGGLVQPGGSLRVSCAVSGFTSDHYMYFRQAPKGPEWVGFINRKGNGGTT 79
Db 59 yyadvtkgrftisrdpknltflqmtelsdrtamyycaasygnfwfdwgagttvtv 118
:|||||
Qy 80 EYAAVVKDRFTISRDQSKIAVLQMSLSKIDTAVYCYTTSY--ISH--CRG-G-----VC 130
Db 119 esygnfwfdwgagttvtvsaatkgpsvflapaseksteggttaalqlxlvkdyfpepvt 178

Qy 131 --YGG--YFEWGGGALVTVSSASTKGPVFPPLAPSSKTSCTGAALGCLUKDYFPEPVT 186
|||||
Db 179 vsmnsgaltsgvhtfpavllqsgllysavvtvpsaeLgtqtylxnmhkpentkvdkv 238
Qy 187 YSMNSGALTSGVHTFPVAVLQSGLLYSLSSVTVPSSSLGTQTYICNVNHRPNTKYVDKKA 246
Db 239 epkscdkthtcpcpapellggspsvflfpkpkdtlmisrtpevtcvvvdvshepdkf 298
|||||
Qy 247 EPKSCDKTHTCPCPAPELLGGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 306
Db 299 nwyvdgvevhnaktkpreeqnetyrvsvltvlhqdwlngkeyckvsnkalpalekt 358
|||||
Qy 307 NMYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQLDNLNGKEYCKVSNKALPAPTEKT 366
Db 359 Isakagqprepyvtlpsreemtknqvaltcclvkfypsdiaveesngqpenykttp 418
|||||
Qy 367 ISKAGQPREPYVTLPSPRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTP 426
Db 419 pvlstdgsfflyskltdvksrwmqgnvfscsvmhcalhnhytqklsispk 470
|||||
Qy 427 PVLSDSGSFFLYSKLTVDKSRWQGNVFCVSMHCAHNYTKQSLSLSPGK 478

RESULT 14

ID P60351 standard; protein; 470 AA.
AC P60351;
DT 01-JAN-1980 (first entry)
DE Chimeric human-mouse immunoglobulin heavy chain.
KW Chimeric protein; immunoglobulin heavy chain;
KW common acute lymphocytic leukemia antigen; cancer; tumor;
KW disease diagnosis; IgG7; ss.
OS Homo sapiens, Mus musculus.
PN EP-184187-A.
PD 11-JUN-1986.
PF 03-DEC-1985; 115311.
PR 04-DEC-1984; JP-254980.
PA (TEIJ) TEIJIN KK.
PI Akira K, Yushi N, Yataro I, Takeshi W;
DR WPI; 86-151350/24.
PT New chimeric mouse and human immunoglobulin heavy chain -
PT specific for common acute lymphocytic leukaemia antigen, and
PT corresp. DNA coding sequences
PS Claim 8; Page 26; 42pp; English.
CC Preferably the sequence of mouse Ig heavy chain variable region is
CC derived from a heavy chain reacting with the antigen specific for
CC human common acute lymphocytic leukemia and the human Ig heavy chain
CC constant region is from human IgG7. The 2 fragments are joined via
CC an Eh-fragment which contains at least a human enhancer and may
CC additionally contain a mouse enhancer or other introns derived from a
CC human or mouse. The chimeric construct is useful in the diagnosis
CC and therapy of human cALL. See also N60253, N60254-57 and N60263-64.
SQ Sequence 470 AA;

Query Match 79.3%; Score 2748; DB 3; Length 470;
Best Local Similarity 85.6%; Pred. No. 8.64e-213;
Matches 404; Conservative 22; Mismatches 31; Indels 15; Gaps 7;

Db 1 dvqlvesggglvqpgggrklscasagftsfsgmhwvraqepkglewvayisggay--ti 58
:|||||
Qy 20 EVQLVESGGGLVQPGGSLRVSCAVSGFTSDHYMYFRQAPKGPEWVGFINRKGNGGTT 79
Db 59 yyadvtkgrftisrdpknltflqmtelsdrtamyycaasygnfwfdwgagttvtv 118
:|||||

Qy	•	80	EYAASVORFETLSRDDSKSIAYLQMSLKIEDTAVYCTTSY—ISH—CRG-G-----VC	130
Db		119	seygnfwfdwvgaagtlvtvsaactkpvafplapeaketsagtaalgkvlvkdyppevvt	178
Qy		131	--YCC--YFEFWQCGALVTVSASTKGPVFP LAPSSKTSGTGTAALGCCLVKDYFPEVVT	186
Db		179	vwnegaltsgvhtfpavljqsgllysasvttvpssslgtqtylxnnvnhkpsntkvdkkv	238
Qy		187	VSNNSGALTSQVHTFPAVLQSSGLYLSSSVTVTPSSSLGTQTYICNNVHKPSNTKVDKKA	246
Db		239	epkscdtkhtcpcpcapellggpsvflfpkpkdktlmsrtbpevtcvvvdshedpevkf	298
Qy		247	EPKSCDKTHTCPCPAPPELLGGPVSFLFPKPKDKTLMISRTPEVTCVVVDVSHEDPEVKF	306
Db		299	nwyvdqvevhnaktkpreeqynstyrwvavltvlhqdwlngleykckvsnkalpapiekt	358
Qy		307	NWYVDQVEVHNAKTKPREQYNSTYRWVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT	366
Db		359	iskakgqpreqvvtlppseemtknqvaltclvkgyfypediavewesngqpennykttp	418
Qy		367	ISKAKGQPREQVYTTLPSPRELTKQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTP	426
Db		419	pvlidsdgafflyskltvdtsrkwgqgnvfacsymhealhhnhtqtqlslapggk	470
Qy		427	PVLIDSDGFFFLYSKLTVDKSRMQGNVFCSCYMHEALHHNHTQKLSLSLPGK	478

RESULT 15

ID	R43339 standard; Protein; 449 AA.
AC	R43339;
DT	29-NOV-1993 (first entry)
DE	Completely humanised C4G1 Ig heavy chain.
KW	Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIa/IIb;
KS	monoclonal antibody; platelet agglutination; humanised antibody.
OW	Synthetic.
PN	W09313133-AA.
PD	08-JUL-1993.
PF	15-DEC-1992; J01630.
PR	20-DEC-1991; US-812111.
PR	09-JUN-1992; US-895952.
PR	11-SEP-1992; US-944159.
PA	(PROT-) PROTEIN DESIGN LABS INC.
PA	(YAMA) YAMANOUCHI PHARM CO LTD.
Co MS	Teo JY;
WI	93-227275/28.
PT	Compn. contg. immunoglobulin specific for the GP-IIB and -IIIA
PT	protein - for treating disorders related to vascular thrombosis
PS	Claim 26; Fig 5C; 54pp; Japanese.
CC	This is the sequence of the humanised C4G1 immunoglobulin heavy
CC	chain fragment. See R43338 for the light chain sequence. The
CC	antibody is specific for the platelet membrane glycoprotein
CC	GPIIa/IIb and inhibits platelet agglutination. The Ig is thus
CC	useful in the treatment of thrombosis.
SQ	Sequence 449 AA;

```
Query Match      78.9%; Score 2735; DB 7; Length 449;
Best Local Similarity 85.2%; Pred. No. 1.03e-211;
Matches 391; Conservative 30; Mismatches 30; Indels 10; Gaps 6;

Db    1   qvllvgqaevkpggskvksckasgafnylllewrqrpqggilewlgvl-y-pqsagdt 58
       :|||:||: ||:||||| :|||::| :|||::| |||: | :|||: | :|||: |
Qy    20   EVQLVESGGGLVPGGSLAVSVSGFTSDHYMYWFRQAPKGKGEFWGVFIRNKPNGCTT 79

Db    59   nynekfkgvtllvdsestntaymelsalrseedtavyfca-----i-rdgn-ywfaywg 110
```

Qy	80	EYAA5VKDRFTISRDDSKSIATVQWSSLIETAVYYCTSVTSHCRGGVCYGGYFEFWG	139
Db	111	ggtlrvssaatkpavfplapsekatsgtaagclvkdvyfpepvtvwnagaltqgvh	170
Qy	140	OGALVTVSSASTKCPVFPPLAPSSKSTSGCTAALGCLUKDYEPPEPVTVSNNGALTSGVH	199
Db	171	tfpavlaqseglyslsewvtvpseelgtqtyicnvnhkpentkvdkvpekcadkthtcpp	230
Qy	200	TFPAVLQSSGLYLSLSSWTVPSLSTGTQTYICNVNHKPSNTVKDGAEPKSDKTHTCPP	259
Db	231	cpapellggpsavflfppkpkdtlmsrtptvctvwvdshedpvkfnwyvdgvevhnak	290
Qy	260	CPAPELLGCGSVFLFPKPKDTLMSRTEPVTCCVVVDVSHEDPEVKFNHWYDGVVEVHNAK	319
Db	291	tkpreeqnystyrvsvavltvhwqdlngkeyckcvankalpaiektiskakgqpreqv	350
Qy	320	TKPREQYNSTYRVSVLTVLHQDMNGKEYCKCVSNKALPAPTEKTSKAGQPREQV	379
Db	351	ytlppeardeitknqslctclvkgyfspdiaaveswngqpennyktppvldsdgdflyls	410
Qy	380	YTLPPSRDELTKNQVSLTCLVKGYFSPDIAVZWESNQCPENNYKTPPVLDSGCSFFLYLS	439
Db	411	kltvdkserwaggnvfacsymhealhnhytqkalslspgk	449
Qy	440	KLTVDKSRWQGNVFCSCSYMHEALHNHNTQKLSLSLSPGK	478

Search completed: Tue Dec 17 15:29:05 1996
Job time : 47 secs.

Result No.	Score	Query		ID	Description	Pred. No.
		Match	Length			
1	1352	82.7	235	5	S05270 Ig lambda chain prec	1.78e-124
2	1339	81.9	215	14	S29258 Ig lambda chain v re	4.23e-123
3	1333	81.5	233	11	S25752 Ig lambda chain - hu	1.83e-122
4	1326	81.1	236	11	S25746 Ig lambda chain - hu	1.01e-121
5	1322	80.9	232	11	S25742 Ig lambda chain - hu	2.67e-121
6	1323	80.9	235	11	S25750 Ig lambda chain - hu	2.09e-121
7	1318	80.6	234	11	S25757 Ig lambda chain - hu	7.07e-121
8	1291	79.0	216	5	A42193 Ig lambda chain (BJP	5.07e-118
9	1291	79.0	233	11	S25744 Ig lambda chain - hu	5.07e-118
10	1286	78.7	213	11	S21066 Ig lambda chain v re	1.71e-117
11	1284	78.5	235	11	S25754 Ig lambda chain - hu	2.79e-117
12	1279	78.2	233	5	S14675 Ig lambda chain - hu	9.42e-117

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology immunoglobulin

KEYWORDS

SUMMARY #length 226 #molecular-weight 24783 #checksum 2436

Query Match 81.1%; Score 1326; DB 11; Length 236;
Best Local Similarity 83.7%; Pred. No. 1.01e-121;
Matches 195; Conservative 23; Mismatches 14; Indels 1; Gaps 1;

Db 4 ep1llllilhtgwaqsvltppsvaapggkkticagtsnigaghhvhwyqvgpgt 63
Qy 5 AQLGLLLWLPARGCESVLTQPPSVGAPGQKVTISCTGTSNIG-CYDLHWYQLPGT 63
Db 64 apkliliydmrpgvdrigsksgeaslaigtlaedeadyyccsfdsalsgwfvgg 123
Qy 64 APKLLIYDINKRPSGISDRFSGSKSGTAASIAITGLQTEDEADYYCQSYDSSINAQVFGG 123
Db 124 atklitvgpkapavtlfppseelqankatlvcclisdfypgavtvawkadspvtgav 183
Qy 124 CTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSPVKAGV 183
Db 184 ettptqgnnkyaassyisltpqwkshrsyscqvtthegstvektvaptecs 236
Qy 184 ETTPTQSNKNKYAASSYLSLTPQWKSHRSYSQVTHEGSTVEKTVAPTECS 236

RESULT 5
ENTRY S25742 #type complete
TITLE Ig lambda chain - human
ORGANISM #formal name Homo sapiens #common name man
DATE 22-Nov-1993 #sequence_revision 26-May-1995 #text_change
ACCESSIONS S25742
REFERENCE S16439
#authors Combratio, G.; Klobbeck, H.G.
#journal Eur. J. Immunol. (1991) 21:1513-1522
#title V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.
#cross-references MUID:91257162
#accession S25742
#status preliminary
#molecule_type mRNA
#residues 1-232 ##label COM
##cross-references EMBL:X57806
##note translation of nucleotide sequence is not given
#length 232 #molecular-weight 24456 #checksum 4011

Query Match 80.9%; Score 1322; DB 11; Length 232;
Best Local Similarity 83.6%; Pred. No. 2.67e-121;
Matches 194; Conservative 19; Mismatches 19; Indels 0; Gaps 0;

Db 1 ep1llllilhtgwaqsvltppsvaapggkkticagtsnigaynywyqqlpgra 60
Qy 5 AQLGLLLWLPARGCESVLTQPPSVGAPGQKVTISCTGTSNIGCYDLHWYQLPGTA 64
Db 61 pkllifennkrpsaipdrfsgekgteatlgltgdeadycgtwdasltdivfggg 120
Qy 65 PKLLIYDINKRPSGISDRFSGSKSGTAASIAITGLQTEDEADYYCQSYDSSINAQVFGG 124
Db 121 tklitvgpkapavtlfppseelqankatlvcclisdfypgavtvawkadspvkagve 180
Qy 125 TRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSPVKAGVE 184
Db 181 ttptqgnnkyaassyisltpqwkshrsyscqvtthegstvektvaptecs 232
Qy 185 TTPTQSNKNKYAASSYLSLTPQWKSHRSYSQVTHEGSTVEKTVAPTECS 236

RESULT 6
ENTRY S25750 #type complete
TITLE Ig lambda chain - human
ORGANISM #formal name Homo sapiens #common name man
DATE 22-Nov-1993 #sequence_revision 26-May-1995 #text_change
ACCESSIONS S25750
REFERENCE S16439
#authors Combratio, G.; Klobbeck, H.G.
#journal Eur. J. Immunol. (1991) 21:1513-1522
#title V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.
#cross-references MUID:91257162
#accession S25750
#status preliminary
#molecule_type mRNA
#residues 1-235 ##label COM
##cross-references EMBL:X57815
##note translation of nucleotide sequence is not given
#length 235 #molecular-weight 24710 #checksum 4829

Query Match 80.9%; Score 1323; DB 11; Length 235;
Best Local Similarity 83.5%; Pred. No. 2.09e-121;
Matches 192; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

Db 6 lllltilthcagswaqsvltqppsagtpqgrvtiscgagasnigtndvvyqqlgtapk 65
Qy 7 LLGLLLWLPARGCESVLTQPPSVGAPGQKVTISCTGTSNIGCYDLHWYQLPGTAPK 66
Db 66 lliyrnqrpgvdrfsgekgaslaigtgdeadycaawddalqgpvfgggtk 125
Qy 67 LLTIYDINKRPSGISDRFSGSKSGTAASIAITGLQTEDEADYYCQSYDSSINAQVFGGTR 126
Db 126 ltlvgpkapavtlfppseelqankatlvcclisdfypgavtvawkadspvkagvett 185
Qy 127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSPVKAGVETT 186
Db 186 tpskqgnnkyaassyisltpqwkshrsyscqvtthegstvektvaptecs 235
Qy 187 TPSKQSNKNKYAASSYLSLTPQWKSHRSYSQVTHEGSTVEKTVAPTECS 236

RESULT 7
ENTRY S25757 #type fragment
TITLE Ig lambda chain - human (fragment)
ORGANISM #formal name Homo sapiens #common name man
DATE 22-Nov-1993 #sequence_revision 26-May-1995 #text_change
ACCESSIONS S25757
REFERENCE S16439
#authors Combratio, G.; Klobbeck, H.G.
#journal Eur. J. Immunol. (1991) 21:1513-1522
#title V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism.
#cross-references MUID:91257162
#accession S25757
#status preliminary
#molecule_type mRNA
#residues 1-234 ##label COM
##cross-references EMBL:X57822

```
##note translation of nucleotide sequence is not given
SUMMARY      #length 234 #checksum 5342

Query Match      80.6%; Score 1318; DB 11; Length 234;
Best Local Similarity 83.0%; Pred. No. 7.07e-121;
Matches 191; Conservative 25; Mismatches 14; Indels 0; Gaps 0;

Db 5 llltllthcagwaqsvltqppeasgtpqgrvtiscsgstnignsvntvwyqqlpgtapk 64
   || || :||: ||||| ||||| ||||| ||||| :||| |||||
Qy 7 LLGLLLMLPGARCESVLTQPPSVSGAPGQKVTISCTGSTNIGGYDLHWYQQLPGTAPK 66

Db 65 vlynnmrpgvdpfsgksgtsaaisglqsddeadycaawddslngrrllggstk 124
   :||: | ||||| ||||| ||||| ||||| : ||||| : ||||| : |||||
Qy 67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSINAQVFGGTR 126

Db 125 ltvlgpkkaapsvtlfppeaelqankatlvcclisdfypgavtvawkadspvkagvett 184
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186

Db 185 tpskqnmkyaasylltpeqwkshksyscqvtthegstvektvaptecs 234
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 187 TPSKQSNKYAASSYLSLTPQWKSHRYSQVTHGSGTVEKTVAPTECS 236

RESULT 8
ENTRY      A42193      #type complete
TITLE      Ig lambda chain (BJP-DIA) - human
ALTERNATE_NAMES      amyloid fibril protein AL-DIA; Bence Jones protein; Ig lambda
                      chain (I.2)
ORGANISM   #formal name Homo sapiens #common name man
DATE       03-Mar-1994 #sequence_revision 07-Apr-1994 #text_change
           30-Apr-1995
ACCESSIONS A42193; S18297
REFERENCE   #authors      Klarfki, H.W.; Kratzin, H.D.; Pick, A.I.; Eckart, K.; Karaas,
M.; Hilechmann, N.
#journal    Biochemistry (1992) 31:3265-3272
#title      Complete amino acid sequence determinations demonstrate
            identity of the urinary Bence Jones protein (BJP-DIA) and
            the amyloid fibril protein (AL-DIA) in a case of
            AL-amyloidosis.
#accession  A42193
#molecule_type protein
#residues   1-216 ##label KLA
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      pyrogutamic acid
FEATURE       1
            #modified site pyrrolidone carboxylic acid (Gln) #status
            experimental
SUMMARY      #length 216 #molecular-weight 22637 #checksum 7545

Query Match      79.0%; Score 1291; DB 5; Length 216;
Best Local Similarity 86.1%; Pred. No. 5.07e-118;
Matches 186; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

Db 1 gqvltqppeasgtpqgrvtiscsgsgenignsvntvwyqqlpgtapklllytnnqpqgvp 60'
   :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 21 ESVLTQPPSVSGAPGQKVTISCTGSTNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80

Db 61 grfsgksgtsaaislvgslqsddeadycatwddsvngwvfgggtkltvlgpkkaapsv 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 81 DRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSINAQVFGGTRTLTVLGQPKAAPSVT 140

Db 121 lfppeaelqankatlvcclisdfypgavtvawkadspvkagvetttpsksqnmkyaass 180
```

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||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 141 LFPPESEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKYAASS 200

Db 181 ylsltpeqwkshksyscqvtthegstvektvaptecs 216
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 201 YLSLTPEQWKSHRYSQVTHGSGTVEKTVAPTECS 236

RESULT 9
ENTRY      S25744      #type complete
TITLE      Ig lambda chain - human
ORGANISM   #formal name Homo sapiens #common name man
DATE       22-Nov-1993 #sequence_revision 26-May-1995 #text_change
           26-May-1995
ACCESSIONS S25744
REFERENCE   S16439
#authors    Combrato, G.; Klobeck, H.G.
#journal     Eur. J. Immunol. (1991) 21:1513-1522
#title      V(lambda) and J(lambda)-C(lambda) gene segments of the human
            immunoglobulin lambda light chain locus are separated by 14
            kb and rearrange by a deletion mechanism.
#cross-references MUID:91257162
#accession  S25744
#status      preliminary
#molecule_type mRNA
#residues     1-233 ##label COM
#cross-references EMBL:X57809
#note         translation of nucleotide sequence is not given
SUMMARY      #length 233 #molecular-weight 24548 #checksum 5114

Query Match      79.0%; Score 1291; DB 11; Length 233;
Best Local Similarity 83.0%; Pred. No. 5.07e-118;
Matches 191; Conservative 19; Mismatches 18; Indels 2; Gaps 2;

Db 6 llltllthcagwaqsvltqppeasgtpqgrvtiscsgsrnvgmnmvwyqqlpgtapk 65
   || || :||: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 7 LLGLLLMLPGARCESVLTQPPSVSGAPGQKVTISCTGSTNIGGYDLHWYQQLPGTAPK 66

Db 66 lliysnnqrpgvdpfsgksgtsaaisglqsddeadycatwdds-tv-vfgggtk 123
   |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSINAQVFGGTR 126

Db 124 ltvpgpkkaapsvtlfppeaelqankatlvcclisdfypgavtvawkadspvkagvett 183
   || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186

Db 184 tpskqnmkyaasylltpeqwkshksyscqvtthegstvektvaptecs 233
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 187 TPSKQSNKYAASSYLSLTPQWKSHRYSQVTHGSGTVEKTVAPTECS 236

RESULT 10
ENTRY      S21066      #type complete
TITLE      Ig lambda chain V region - human
ORGANISM   #formal name Homo sapiens #common name man
DATE       22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change
           17-Nov-1995
ACCESSIONS S21066
REFERENCE   S21066
#authors    Diouha, A.; Lecroisey, A.; Henschen, A.; Ruttyn, Y.; Rouger,
P.; Keil, B.
#journal     Protein Seq. Data Anal. (1991) 4:319-324
#title      Partial amino acid sequence of the light chain of human
            anti-Rh(D) monoclonal antibody H2D5D2F5.
```

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```
#accession S21066
#status preliminary
#molecule_type protein
#residues 1-213 ##label D10
#note the sequence from Fig. 4 is inconsistent with that from
Fig. 1 in having 74-Thr and lacking amino acid 111-213
SUMMARY
#length 213 #molecular-weight 22540 #checksum 4993

Query Match 78.7%; Score 1286; DB 11; Length 213;
Best Local Similarity 88.5%; Pred. No. 1.71e-117;
Matches 192; Conservative 13; Mismatches 7; Indels 5; Gaps 3;

Db 1 qsvltgppesvgaqgqvlticstgsenlgarydnwylqglptgkplliygntirpsv 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 21 ESULTQPSVSGAPGQKVITSGTSTNIGG-YDLHWYQLPCTAPKLLIYDINKRPSGI 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 pdrfsgskgtasaelaitqlaedegdyctwd---yv-vfgggtklvlgppkaapsv 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 80 SDRFSGSKGTAAASLAITGLATDEADYYCQSYDSSINAQVFGGSTRLTVLGQPKAAPSV 139
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 117 tlfpssseelqankatlvciliedfypgavtvawkadspvkagvetttkpskgnkyaas 176
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 140 TLPPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKYAAS 199
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 177 sylvltpgkshrsycqvthegstvektvaptacs 213
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 200 SYLSLTPQWKSHRSYSCQVTHEGSTVEKTVPAPTECS 236
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
ENTRY S25754 #type fragment
TITLE Ig lambda chain - human (fragment)
ORGANISM #formal name Homo sapiens #common name man
DATE 22-Nov-1993 #sequence_revision 26-May-1995 #text_change
30-Jun-1995
ACCESSIONS S25754
REFERENCE S16439
#authors Combriato, G.; Klobbeck, H.G.
#journal Eur. J. Immunol. (1991) 21:1513-1522
#title V(lambda) and J(lambda)-C(lambda) gene segments of the human
immunoglobulin lambda light chain locus are separated by 14
kb and rearrange by a deletion mechanism.
#cross-references MUID:91257162
#accession S25754
#status preliminary
#molecule_type mRNA
#residues 1-235 ##label COM
#cross-references EMBL:X57819
#note translation of nucleotide sequence is not given
SUMMARY
#length 235 #checksum 5196

Query Match 78.5%; Score 1284; DB 11; Length 235;
Best Local Similarity 81.0%; Pred. No. 2.79e-117;
Matches 187; Conservative 22; Mismatches 21; Indels 1; Gaps 1;

Db 5 llltlllthcagwagvqlcpssasgtpqgrvliiscgssnigntvmwylqpgprapx 64
||| || :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 7 LLGLLLLPARGCESVLTQPPSVSGAPGQKVITSGTSTNIGGYDLHWYQLPCTAPK 66
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65 lllhnnrpgvdpvdfsgskgtasaelaisqlsedeadeadycaawddlngryvfgt 124
||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 67 LLIIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEADYYCQSYDSSINAQ-VFCGGT 125
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 125 kvtlvgppkaptvtlfpssseelqankatlvciliedfypgavtvawkadspvkagvet 184
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 126 RLTVLGQPKAAPSVTLFPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 185 tkpskgnkyaasvylaltpeqwkshrsycqvthegstvektvaptacs 235
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 186 TTPSKQSNKYAASVSLTPEQWKSHRSYSCQVTHEGSTVEKTVPAPTECS 236
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
ENTRY S14675 #type complete
TITLE Ig lambda chain - human
ORGANISM #formal name Homo sapiens #common name man
DATE 19-May-1994 #sequence_revision 19-May-1994 #text_change
12-Apr-1995
ACCESSIONS S14675; S12445
REFERENCE S14675
#authors Vasicek, T.J.
#submission submitted to the EMBL Data Library, February 1990
#accession S14675
#molecule_type DNA
#residues 1-235 ##label VAS1
#cross-references EMBL:X51754
REFERENCE S12440
#authors Vasicek, T.J.; Leder, P.
#journal J. Exp. Med. (1990) 172:609-620
#title Structure and expression of the human immunoglobulin lambda
genes.
#cross-references MUID:90324881
#accession S12445
#molecule_type DNA
#residues 1-129 ##label VAS2
#cross-references EMBL:X51754
GENETICS
#introns 16/1; 130/1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 235 #molecular-weight 24859 #checksum 7937

Query Match 78.2%; Score 1279; DB 5; Length 235;
Best Local Similarity 79.3%; Pred. No. 9.42e-117;
Matches 184; Conservative 26; Mismatches 19; Indels 3; Gaps 3;

Db 5 llltlllthcagwagvqlcpssasgtgqvtfscgtssedignvnyvwyrbpoka 64
||| || :||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 7 LLGLLLLPARGCESVLTQPPSVSGAPGQKVITSGTSTNIGGYDLHWYQLPCTA 64
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65 pklmivytkrpsvgnrpfsgskgtasaltvsglqadeadeadyccsyags-nalifgg 123
||| ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 65 PKLLIYDINKRPSGISDRFSGSKGTAAASLAITGLQTEADYYCQSYDSSINAQVFCGG 124
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 124 trltvlgppkaapsvtlfpssseelqankatlvciliedfypgavtvawkadspvkaev 183
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 125 RLTVLGQPKAAPSVTLFPSSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 184
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 184 ttpskgnkyaasvylaltpeqwkshrsycqvthegstvektvaptacs 235
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 185 TTPSKQSNKYAASVSLTPEQWKSHRSYSCQVTHEGSTVEKTVPAPTECS 236
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13
ENTRY S03401 #type complete
TITLE Ig lambda chain (Kol) - human
ORGANISM #formal name Homo sapiens #common name man
DATE 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
12-Apr-1995
```

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ACCESSIONS      S03401
REFERENCE       S03401
#authors        Kratzin, H.D.; Palm, W.; Stangel, M.; Schmidt, W.E.;
#journal         Friedrich, J.; Hilechmann, N.
#title          Biol. Chem. Hoppe-Seyler (1989) 370:263-272
#title          The primary structure of the crystallizable monoclonal
#title          immunoglobulin IgG1 Kol. II. Amino-acid sequence of the
#title          l-chain, lambda-type, subgroup I.
#cross-references MUID:89228564
#accession      S03401
#molecule_type protein
#residues       1-216 #label KRA
#note           article in German with English abstract
#note           #superfamily immunoglobulin V region; immunoglobulin homology
#note           pyroglutamic acid
CLASSIFICATION  #modified_site pyrrolidone carboxylic acid (Gln) #status
KEYWORDS        experimental
FEATURE         #length 216 #molecular-weight 22798 #checksum 5181
SUMMARY

```

Query Match	77.5%;	Score 1267;	DB 5;	Length 216;	
Best Local Similarity	83.3%;	Pred. No. 1.75e-115;			
Matches 180;	Conservative 21;	Mismatches 15;	Indels 0;	Gaps 0;	
Db	1	qsvltqpsasgtpgqrvrticsgtsnigastvnmvqqldpmapklllyrdamrpsvp	60		
QY	21	ESVLTQPPSVSGAPGQKVTISCTGTSNIGGYQLHWYQQLPCTAPKILLIYDINKRPSGIS	80		
Db	61	drfsagsgasasaiaiglgaeedetdycaawdvainayfgtqkvtylgqpkamptvt	120		
QY	81	DRFSGSGSTAAALITGLQTEDEADYYCQSYDSSLNAGVFGGTRTLTYLGQRAAPSVT	140		
Db	121	lfpssaelqankatlvcldisdfypgavrtvawkadgspvkagvettkpsqennkyaas	180		
QY	141	LFPFSSEELQANKATLVCLISDFYPGAVTVAWKADSPVKAGVETTPSKQSNKNKYAAS	200		
Db	181	yalslpcqwkshrsyscqvtthegstvektvaptcs	216		
QY	201	YLSLTPEQWKSHRSYSCQVTHGSGTVEKTVAPTCS	236		

```

RESULT      14
ENTRY       S25759      #type complete
TITLE       Iq lambda chain - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE        22-Nov-1993 #sequence_revision 26-May-1995 #text_change
              26-May-1995
ACCESSIONS S25759
REFERENCE   S16439
            Combiato, G.; Klobeck, H.G.
            Eur. J. Immunol. (1991) 21:1513-1522
            V(lambda) and J(lambda)-C(lambda) gene segments of the human
            immunoglobulin lambda light chain locus are separated by 14
            kb and rearrange by a deletion mechanism.
            #cross-references M01D:91257162
            #accession S25759
            #status preliminary
            #molecule_type mRNA
            #residues 1-235 #label COM
            #cross-references EMBL:X57824
            #note translation of nucleotide sequence is not given
            #length 235 #molecular-weight 24748 #checksum 5527
SUMMARY

```

Query Match 77.1%; Score 1261; DB 11; Length 235;

[illegible]

```

RESULT      15
ENTRY
TITLE      Ig lambda chain - human
ORGANISM
DATE       22-Nov-1993 #sequence_revision 26-May-1995 #text_change
          26-May-1995

ACCESSIONS S25758 #type complete
REFERENCE   S16439
AUTHORS    Combiato, G.; Klobeck, H.G.
JOURNAL    Eur. J. Immunol. (1991) 21:1513-1522
TITLE      V(lambda) and J(lambda)-C(lambda) gene segments of the human
          immunoglobulin lambda light chain locus are separated by 14
          kb and rearrange by a deletion mechanism.
CROSS-REFERENCES
MUID:91257162
accession  S25758
status     preliminary
molecule_type  mRNA
residues   1-235 ##label COM
cross-references EMBL:X57823
length 235 #molecular-weight 24913 #checksum 9784
note       translation of nucleotide sequence is not given
SUMMARY

```

Query Match	76.0%;	Score 1242;	DB 11;	Length 235;
Best Local Similarity	78.0%;	Pred. No. 7.65e-113;		
Matches	181;	Conservative 26;	Mismatches 22;	Indels 3; Gaps 3;
Db	5	llfltlclqgtgwaqsaltpaasevgpgqsltiectgsasdvgyynyvwyqqhpgka	64	
		: : : : : : : : : : : :		
Qy	7	llglalllml~pgarcesvltqppsvsgapqkvttisctgststnigyD~lhwYQQLPGTA	64	
Db	65	pklmlydvtrpsgvnfrfsgskgnatlaclsglcpedeadehycte~ktassfyvfqg	123	
		: : : : : : : :		
Qy	65	PKLLIYDINKRPSCGISDRFSGSKSGTAASLAITGLQTEADYYCQSYDSINAQVFGG	124	
Db	124	tksvulgqpkantvtllfpssseelqankatlvcllisdfyggavrtvawkdqgspvkagve	183	
		: : : : : : : :		
Qy	125	TRLTVLGQKAAASVTLFPSSSEELQANKATLVCLISDFYGPATVWAMKADSSPVKAGVE	184	
Db	184	tkpkqanmkyaasyisltpqwkshrsyscqvtchegstvektvaptcs	235	
		: : : : : : : :		
Qy	185	TTTTQKSNKNKYAASYSLSLTPQWKSHRSYSQVTHGSTEKTVAPTECS	236	

Search completed: Tue Dec 17 15:36:06 1996

Dec 17 15:21

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Job time : 37 secs.

Result	No.	Score	Query		DB	ID	Description	Pred. No.
			Match	%				
1	713	43.6	213	4	I141_HUMAN	IMMUNOGLOBULIN-RELATE	1.08e-136	
2	706	43.2	105	5	LAC_HUMAN	IG LAMBDA CHAIN C REG	5.05e-135	
3	623	38.1	130	5	LV1G_HUMAN	IG LAMBDA CHAIN PRECU	2.47e-115	
4	604	36.9	111	5	LV1Z_HUMAN	IG LAMBDA CHAIN V-I R	7.51e-111	
5	587	35.9	112	5	LV2K_HUMAN	IG LAMBDA CHAIN V-I I	7.54e-107	
6	579	35.4	105	5	LAC_FIG	IG LAMBDA CHAIN C REG	5.72e-105	
7	579	35.4	111	5	LV1C_HUMAN	IG LAMBDA CHAIN V-I R	5.72e-105	
8	563	34.4	112	5	LV1H_HUMAN	IG LAMBDA CHAIN V-I R	3.25e-101	
9	560	34.3	111	5	LV2B_HUMAN	IG LAMBDA CHAIN V-I I	1.64e-100	
10	559	34.2	109	5	LV1F_HUMAN	IG LAMBDA CHAIN V-I R	2.81e-100	
11	557	34.1	105	5	LAC1_MOUSE	IG LAMBDA-1 CHAIN C R	8.26e-100	
12	554	33.9	112	5	LV2I_HUMAN	IG LAMBDA CHAIN V-I I	4.16e-99	
13	555	33.9	111	5	LV1B_HUMAN	IG LAMBDA CHAIN V-I R	2.43e-99	

ALIGNMENTS

[illegible]

RL. PROC. NATL. ACAD. SCI. U.S.A. 86:5552-5556(1989).
 CC -I- TISSUE SPECIFICITY: EXPRESSED ONLY IN PRE-B-CELLS AND A SPECIAL
 CC B-CELL LINE (WHICH IS SURFACE IG NEGATIVE).
 CC -I- THIS LAMBDA LIGHT-CHAIN-RELATED PROTEIN MAY BE THE IMMUN-
 CC GLOBULIN OMEGA LIGHT-CHAIN.
 CC -I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY
 CC AND SHOWS SIMILARITY TO LAMBDA LIGHT CHAIN IN C-TERMINAL HALF
 CC (J AND C REGIONS).
 CC ENBL; M27749; M27749.
 DR PIR; A33911; A33911.
 DR HSSP; P01842; 8FAB.
 DR PROSITE; PS00290; IG MHC.
 KW IMMUNOGLOBULIN FOLD; B-CELL; SIGNAL.

	1	?	
FT SIGNAL	?		IMMUNOGLOBULIN-RELATED 14.1 PROTEIN.
FT CHAIN		213	J REGION (BY SIMILARITY TO LAMBDA
FT DOMAIN	97	108	LIGHT-CHAIN).
FT			C REGION (BY SIMILARITY TO LAMBDA
FT DOMAIN	109	213	LIGHT-CHAIN).
FT			
SQ SEQUENCE	213 AA;	22963 MW;	259318 CN;
SQ			

Query Match 43.6%; Score 713; DB 4; Length 213;
Best Local Similarity 82.4%; Pred. No. 1.08e-136;
Matches 98; Conservative 16; Mismatches 5; Indels

95	thwfgsgtcltvlsqpkatpvtlfpssseelqankatlvcvlmndfpygiltvtwkadgt	154
Db		
118	AAQFEGGTRTVLIGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTAAKADSS	177
QY		
155	pitqgvemtptskqnnkyasyaltpqwrwrrtyscqmhgestvektvapaecs	213
Db		
178	PKRAQGVETTPSKQSNKYAASSYLSLTPQDWKSHRSYSCVTHEGGTVKTVAPTECS	236
QY		

RESULT	2	STANDARD;	PRT;	105 AA.
ID	LAC HUMAN			
AC	P01842; P80423;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)			
DE	IG LAMBDA CHAIN C REGIONS.			
OS	IGLC1 AND IGLC2 AND IGLC3.			
OC	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE (BENCE-JONES PROTEIN SH).			
EX	MEDLINE; 70166723.			
RL	TITANI K., WIKLER M., SHINODA T., PUTNAM F.W.;			
RL	J. BIOL. CHEM. 245:2171-2176(1970).			

[2]	SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.
RP	
RP	
RP	
RX	MEDLINE; 69088380.
RX	
RA	MILSTEIN C., CIEGG J.B., JARVIS J.M.;
RL	BIOCHEM. J. 110:631-652(1968).
[3]	
RP	SEQUENCE (BENCE-JONES PROTEIN NIG-64).
RP	
RP	
RX	MEDLINE; 83186114.
RX	
RA	KAMETANI F., TAKAYASU T., SUZUKI S., SHINODA T., OKUYAMA T.,
RA	SHIMIZU A.;
RL	J. BIOCHEM. 93:421-429(1983).
[4]	
RP	SEQUENCE (BENCE-JONES PROTEIN KERN).
RP	
RP	
RX	MEDLINE; 71150336.
RX	
RA	PONSTINGL H., HESS M., HILSCHMANN N.;
RL	HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 352:247-266(1971).
[5]	
RP	PARTIAL SEQUENCE (MYELOMA PROTEIN NEWM).
RP	
RP	
RX	MEDLINE; 74109253.
RX	
RA	CHEN B.-L., POLJAK R.J.;
RL	BIOCHEMISTRY 13:1295-1302(1974).

RP SEQUENCE (DOT).
RX MEDLINE; 95255298.
RA STOPPINI M., BELLOTTI V., NEGRI A., MERLINI G., GARVER F., FERRI G.;
RL EUR. J. BIOCHEM. 228:886-893(1995).
RN [7]

RP	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEMO.	
RX	MEDLINE; 75046825.	
RA	POLJAK R.J., ANZEL L.M., AVEY H.P., CHEN B.L., PHIZACKERLEY R.P.,	
RA	SAUL F.;	
RN	PROC. NATL. ACAD. SCI. U.S.A. 71:3440-3444 (1974).	
RN	[8]	
RP	PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).	
RX	MEDLINE; 75013804.	
RA	FETT J.W., DEUTSCH H.F.;	
RL	BIOCHEMISTRY 13:4102-4114 (1974).	
RN	[9]	
RP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.	
RA	EDMUNDSON A.B., ELY K.R., ABOLA E.E., SCHIEFFER M.,	
RA	PANAGIOTOPOULOS N.;	
RL	BIOCHEMISTRY 14:3953-3961 (1975).	
RN	[10]	
RP	X-RAY CRYSTALLOGRAPHY OF MCG.	
RX	MEDLINE; 90133913.	
RA	ELY K.R., HERON J.N., HARKER M., EDMUNDSON A.B.;	
RL	J. MOL. BIOL. 210:601-615 (1989).	
RN	[11]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE; 82080680.	
RA	HIETER P.A., HOLLIS G.F., KORSMEYER S.J., WALDMANN T.A., LEDER P.;	
RL	NATURE 294:536-540 (1981).	
CC	-1- THE SEQUENCE SHOWN IS THE KERN-/OZ-/MCG- CHAIN FOUND IN PROTEINS	
CC	SH, X, AND NIG-64. THE KERN PROTEIN HAS THE KERN+ MARKER, THE NEMO	
CC	PROTEIN HAS THE OZ+ MARKER, THE MCG PROTEIN HAS THE KERN+ MARKER,	
CC	AND THE MCG+ MARKER.	
CC	-1- SIX TANDEM LAMBDA-TYPE GENES WERE IDENTIFIED & THE 3 MOST 5' WERE	
CC	SEQUENCED. THESE CORRESPOND TO THE MCG SEQUENCE (LAMBDA-1), THE	
CC	KERN-/OZ- SEQUENCE (LAMBDA-2) & THE KERN-/OZ+ SEQUENCE (LAMBDA-3).	
DR	PIR; A02125; LZHU.	
DR	PDB; 2MCG; 15-JUL-92.	
DR	PDB; 7FAB; 31-JAN-94.	
DR	MM; 147220; 11TH EDITION.	
DR	PROSITE; PS00290; IG MHC.	
KW	IMMUNOGLOBULIN C REGION; 3D-STRUCTURE.	
FT	NON TER 1 1	
FT	DISULFID 27 86	
FT	DISULFID 104 104	INTERCHAIN (WITH HEAVY CHAIN).
FT	VARIANT 5 5	A -> N (IN MCG+ MARKER).
FT	VARIANT 7 7	S -> T (IN MCG+ MARKER).
FT	VARIANT 45 45	S -> G (IN KERN+ MARKER).
FT	VARIANT 56 56	T -> K (IN MCG+ MARKER).
FT	VARIANT 82 82	R -> K (IN OZ+ MARKER).
FT	STRAND 4 4	
FT	STRAND 7 11	
FT	HELIX 15 19	
FT	TURN 20 21	
FT	STRAND 23 33	
FT	STRAND 38 43	
FT	TURN 44 45	
FT	STRAND 46 48	
FT	TURN 50 51	
FT	STRAND 52 54	
FT	STRAND 58 59	
FT	TURN 61 62	
FT	STRAND 65 73	
FT	HELIX 75 79	
FT	TURN 80 80	
FT	STRAND 84 90	
FT	TURN 91 92	
FT	STRAND 93 99	

FT	NON_TER	111	111
FT	NON_	111	111

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

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RN [1]
RP SEQUENCE.
RX MEDLINE; 72233223.
RA CARVER F.A., HILSCHMANN N.;
RL EUR. J. BIOCHEM. 26:10-32(1972).
CC -!- THIS IS A BENICE-JONES PROTEIN.
DR PIR; A01970; L2HUNI.
DR HSSP; P01703; 1B3L.
KW IMMUNOGLOBULIN V REGION; BENICE-JONES PROTEIN; GLYCOPROTEIN.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT CARBOHYD 96 96
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11591 MW; 70802 CN;

Query Match 34.3%; Score 560; DB 5; Length 111;
Best Local Similarity 67.9%; Pred. No. 1.64e-100;
Matches 76; Conservative 24; Mismatches 10; Indels 2; Gaps 2;

Db 1 qsaltcpaevsgpggsitactgttdvgsynfvswygnpgkapklmyeqnkrpsgv 60
Qy 21 ESVLTQPPSVSGAPGQKVTISCTGTSNIGGYDL-HWYQQLPCTAPKLLIYDINKRPSGI 79

Db 61 anfsagsgktaalslqslqvdeadyccsyagn-strvfsggttrvtls 111
Qy 80 SDRFSGSKSGTAASLAITGIATGTEADYDQSYDSSINAQVFGSGTRLTVLG 131

RESULT 10
ID LVIF HUMAN STANDARD; PRT; 109 AA.
AC P04208;
DT 20-MAR-1987 (REL. 04, CREATED)
DT 20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG LAMBDA CHAIN V-I REGION (WAH).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 83221661.
RA TAKAHASHI Y., TAKAHASHI N., TETAERT D., PUTNAM F.W.;
RL PROC. NATL. ACAD. SCI. U.S.A. 80:3686-3690(1983).
DR PIR; A01967; LIHUMA.
DR HSSP; P01703; 1B3L.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 97 V SEGMENT.
FT DOMAIN 98 109 J SEGMENT.
FT DISULFID 22 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11725 MW; 67654 CN;

Query Match 34.2%; Score 559; DB 5; Length 109;
Best Local Similarity 73.9%; Pred. No. 2.81e-100;
Matches 82; Conservative 14; Mismatches 13; Indels 2; Gaps 1;

Db 1 qevltqpaaagtpgqrvticfsgseelnigryvyvqqldpttkllykdnqrpsgv 60
Qy 21 ESVLTQPPSVSGAPGQKVTISCTGTSNIGGYDLHWYQQLPCTAPKLLIYDINKRPSGIS 80

Db 61 drfsgsksgtaaslaeqlrsdeadycaawddslw-vfsggttrltvls 109
Qy 81 DRFSGSKSGTAASLAITQLTEADYDQSYDSSINAQVFGSGTRLTVLG 131
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RESULT 11
ID LACI MOUSE STANDARD; PRT; 105 AA.
AC P01843;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-APR-1988 (REL. 07, LAST ANNOTATION UPDATE)
DE IG LAMBDA-1 CHAIN C REGION.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83014953.
RA SELSING E., MILLER J., WILSON R., STORB U.;
RL PROC. NATL. ACAD. SCI. U.S.A. 79:4681-4685(1982).
RN [2]
RP SEQUENCE FROM N.A. (MOPC 315).
RX MEDLINE; 81148806.
RA BOTHWELL A.L.M., PASKIND M., SCHWARTZ R.C., SONENSHEIN G.E.;
RA GETTER M.L., BALTIMORE D.;
RL NATURE 290:65-67(1981).
RN [3]
RP SEQUENCE FROM N.A. (S43).
RX MEDLINE; 82220143.
RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESKY K.;
RA BALTIMORE D.;
RL NATURE 298:380-382(1982).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).
RX MEDLINE; 71107854.
RA APPELLA E.;
RL PROC. NATL. ACAD. SCI. U.S.A. 68:590-594(1971).
CC -!- THE MOPC 315 CELL LINE PRODUCES 2 LIGHT CHAINS, 1 NORMAL LAMBDA-2
CC CHAIN & 1 ABNORMAL LAMBDA-1 CHAIN THAT IS MISSING A LARGE PART OF
CC THE V REGION. THE C REGION SEQUENCE (SHOWN HERE) APPEARS COMPLET-
CC ELY NORMAL.
DR PIR; A02126; LIMS.
DR HSSP; P01842; 1MFB.
DR PROSITE; PS00290; IG MHC.
KW IMMUNOGLOBULIN C REGION.
FT NON TER 1 1
FT DISULFID 27 86 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 104 104 ET -> TE (IN REF. 4).
FT CONFLICT 19 20 Q -> E (IN REF. 4).
FT CONFLICT 56 56 Q -> E (IN REF. 4).
FT CONFLICT 75 75 MISSING (IN REF. 4).
FT CONFLICT 81 82 HS -> SH (IN REF. 4).
FT CONFLICT 85 85 S -> SS (IN REF. 4).
FT CONFLICT 96 96 E -> Q (IN REF. 4).
SQ SEQUENCE 105 AA; 11575 MW; 63813 CN;

Query Match 34.1%; Score 557; DB 5; Length 105;
Best Local Similarity 71.4%; Pred. No. 8.26e-100;
Matches 75; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

Db 1 qpkspsvtlfpaseeetkhatlvtctdfypgvvtvdkvdtgtvtgmettpsqk 60
Qy 132 QPKAAASVTLFPSPSEELQANKATLVCLISDFYFGAVTVANKADSSPVKAGVETTPSK 191

Db 61 snnkymassytlrtarawerhsydcqvtcheqtkvksleradcs 105
Qy 192 SNNKYAASSYLSLTPQWQSHRSYSQVTHEGSTVETKTVAPTECS 236
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;; RESULT 12
ID LV21 HUMAN STANDARD; PRT; 111 AA.
AC P01702;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG LAMBDA CHAIN V-II REGION (MIN).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79062503.
RA CHEN B.L., CHIU Y.-Y.H., HUMPHREY R.L., POLJAK R.J.;
RL BIOCHIM. BIOPHYS. ACTA 537:9-21(1978).
CC -!- THIS IS A BENICE-JONES PROTEIN.
DR PIR; A01978; L2HWN.
DR HSSP; P01709; IMCB.
KW IMMUNOGLOBULIN V REGION; BENICE-JONES PROTEIN.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11694 MW; 71443 CN;

Query Match 33.9%; Score 554; DB 5; Length 111;
Best Local Similarity 66.1%; Pred. No. 4.16e-99;
Matches 74; Conservative 22; Mismatches 14; Indels 2; Gaps 2;

Db 1 qsaltpvpsvsgapqgkvtsictgsntvntgynhsvyqddgkvkmiydvdkrpsgv 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 ESVLTQPPSVSGAPGQKVTISCTGSTNIGGYD-LHWYQQLPCTAPKLLIYDINKRPSGI 79

Db 61 pdfsgeksaantaisglqaneadyycsyvgt-yelifgggtklvtlg 111
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 80 SDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSINAQVFGGTRLTVLG 131

RESULT 13
ID LV1B HUMAN STANDARD; PRT; 112 AA.
AC P01700;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG LAMBDA CHAIN V-I REGION (HA).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 71103824.
RA SHINODA T., TITANI K., PUTNAM F.W.;
RL J. BIOL. CHEM. 245:4475-4487(1970).
CC -!- THIS IS A BENICE-JONES PROTEIN.
DR PIR; A01963; LIHUHA.
DR HSSP; P01703; 1BLJ.
KW IMMUNOGLOBULIN V REGION; BENICE-JONES PROTEIN.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT NON TER 112 112
SQ SEQUENCE 112 AA; 11896 MW; 66818 CN;

Query Match 33.9%; Score 555; DB 5; Length 112;
Best Local Similarity 71.2%; Pred. No. 2.43e-99;

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Matches 79; Conservative 18; Mismatches 13; Indels 1; Gaps 1;

Db 1 qsvltcpvpsvsgapqgkvtsictgsngtgmnyvyqqipgtapkllyrddkrpsgv 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 ESVLTQPPSVSGAPGQKVTISCTGSTNIGGYD-LHWYQQLPCTAPKLLIYDINKRPSGI 79

Db 61 pdfsgeksaantaisglqaneadyycsyvgt-yelifgggtklvtlg 111
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 80 SDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSINAQVFGGTRLTVLG 130

RESULT 14
ID LV1A HUMAN STANDARD; PRT; 111 AA.
AC P01699;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG LAMBDA CHAIN V-I REGION (VOR).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 76023790.
RA ENGELHARD M., HILSCHMANN N.;
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 356:1413-1444(1975).
CC -!- THE C REGION OF THIS CHAIN HAS THE OZ+ MARKER.
CC -!- THIS IS A BENICE-JONES PROTEIN.
DR PIR; A01962; LIHUVO.
DR HSSP; P01703; 1BLJ.
KW IMMUNOGLOBULIN V REGION; BENICE-JONES PROTEIN.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 89 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11514 MW; 68247 CN;

Query Match 33.6%; Score 550; DB 5; Length 111;
Best Local Similarity 65.8%; Pred. No. 3.59e-98;
Matches 73; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

Db 1 qsvltcpvpsvsgapqgkvtsictgsngfdgrnsvnyvqhpgtprlllysedqrsegv 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 ESVLTQPPSVSGAPGQKVTISCTGSTNIGGYD-LHWYQQLPCTAPKLLIYDINKRPSGIS 80

Db 61 drfsgeksaantaisglqaneadyycatwddslqdpvfgggtklvtlg 111
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 DRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSINAQVFGGTRLTVLG 131

RESULT 15
ID LV2F HUMAN STANDARD; PRT; 111 AA.
AC P01709;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE IG LAMBDA CHAIN V-II REGION (MGC).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 75013804.
RA FETT J.W., DEUTSCH H.F.;
RL BIOCHEMISTRY 13:4102-4114(1974).

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RN * [2]
RP LAMBDA CHAIN GENES.
RX MEDLINE; 76093781.
RA FETT J.W., DEUTSCH H.F.;
RL IMMUNOCHEMISTRY 12:643-652(1975).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA EDMUNDSON A.B., ELY K.R., ABOLA E.E., SCHIFFER M.,
RA PANAGIOTOPOULOS N.;
RL BIOCHEMISTRY 14:3953-3961(1975).
RN [4]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE; 90133913.
RA ELY K.R., HERRON J.N., HARKER M., EDMUNDSON A.B.;
RL J. MOL. BIOL. 210:601-615(1989).
CC -!- THIS IS A BENICE-JONES PROTEIN.
CC -!- THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH A VERY
CC UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY, SUGGESTING
CC THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.
CC -!- THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+ MARKERS.
DR PIR; A01975; L2HUMC.
DR PDB; 2MCG; 15-JUL-92.
KW IMMUNOGLOBULIN V REGION; BENICE-JONES PROTEIN; 3D-STRUCTURE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 111 111
FT STRAND 5 5
FT STRAND 10 12
FT STRAND 18 23
FT TURN 26 32
FT STRAND 36 40
FT TURN 42 43
FT STRAND 50 51
FT TURN 52 54
FT STRAND 55 55
FT TURN 62 63
FT STRAND 66 68
FT STRAND 72 77
FT HELIX 82 84
FT STRAND 86 93
FT STRAND 99 101
FT STRAND 105 109
SQ SEQUENCE 111 AA; 11558 MW; 72461 CN;

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Query Match 33.5%; Score 547; DB 5; Length 111;
Best Local Similarity 65.2%; Pred.No.1.81e-97;
Matches 73; Conservative 25; Mismatches 12; Indels 2; Gaps 2;

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Db 1 qsaltqpsaagelqgsvtisctgtsedvggnyvswyqqhagkpkviivmtrpsgv 60
Qy 21 ESLVLTQPPSVSGAPGQKVTISCTGTSNIGGYD-LHWYQQLFCTAPKLLIYDINKRPSGI 79
Db 61 pdrfsgskgntaaltvsglqsedeadycssyegs-dmfvfgtkvtvlg 111
Qy 80 SDRFSGSKGTAASLAITGLQTEDEADYQCQSYDSSINAQVEGGTRLTVLG 131

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Search completed: Tue Dec 17 15:36:43 1996
Job time : 19 secs.

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WAVES RELEASE

(TW)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 15:34:42 1996; MasPar time 5.56 Seconds
Tabular output not generated. 404.084 Million cell updates/sec

Title: >US-08-487-550-10

Description: (1-236) from US08487550.pep

Perfect Score: -1635

Sequence: 1 MRVPAQLLGLLLMLPARGC.....CQVTHEGSTVETKVAETCS 236

Scoring table: PAM 150
Gap 11

Searched: 81589 seqs, 9523651 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneeq24

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16

Statistics: Mean 32.219; Variance 178.167; scale 0.181

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	1302	79.6	217	8 R42163	Anti-HIV-1 recombinan	1.45e-88
2	1288	78.8	235	6 R31024	Antibody D light chal	1.74e-87
3	1140	69.7	233	1 P81260	VDJC regions of human	4.06e-76
4	766	46.9	234	7 R38162	Sequence of the kappa	1.42e-47
5	763	46.7	234	3 R13050	CD4-specific CDR-graf	2.40e-47
6	758	46.4	236	15 R77614	Humanised 5G1.1 VL +	5.74e-47
7	740	45.3	234	3 R20058	Light chain of 3D6 an	1.33e-45
8	735	45.0	236	8 R42065	Human anti-HBs light	3.17e-45
9	722	44.2	241	5 R28809	Vector pMDR1007.	3.05e-44
10	706	43.2	234	10 R52951	Human anti-IGE Mab li	4.95e-43
11	696	42.6	106	12 R69093	Anti-HIV Fab rev16/20	2.82e-42
12	696	42.6	133	12 R69088	Anti-HIV Fab tat16/20	2.82e-42

13	672	41.1	238	16 R93554	Monoclonal antibody D	1.83e-40
14	664	40.6	215	8 R43674	Mouse anti-bovine gro	7.34e-40
15	657	40.2	239	13 R76087	MAB 55.1 light chain.	2.48e-39
16	656	40.1	223	4 P40031	Kappa anti-carcinomb	2.94e-39
17	644	39.4	235	3 R13060	Monoclonal antibody O	2.36e-38
18	640	39.1	349	2 R12128	IB1 IgG aberrant ligh	4.72e-38
19	640	39.1	414	2 R13018	IB1 IgG aberrant ligh	4.72e-38
20	640	39.1	414	2 R13111	IB1 IgG aberrant ligh	4.72e-38
21	621	38.0	233	6 R30777	pH52-9.0 humanised mu	1.27e-36
22	621	38.0	235	8 R47451	T84.12 L4-12-1 light	1.27e-36
23	621	38.0	235	8 R47449	T84.12 light chain.	1.27e-36
24	618	37.8	105	2 R11366	Immunoglobulin lambda	2.14e-36
25	613	37.5	236	4 R22565	Vlllys-HuKappa region	5.07e-36
26	612	37.4	111	2 R12263	Anti-human RbD FOG-B	6.03e-36
27	612	37.4	233	4 R22754	Reshaped CAMPATH-1 an	6.03e-36
28	608	37.2	220	10 R53802	FAB light chain for 1	1.20e-35
29	609	37.2	234	8 R47452	chiT84.12 L6 light ch	1.01e-35
30	607	37.1	213	1 P93035	Chimeric antibody lig	1.43e-35
31	605	37.0	233	4 R22755	Reshaped CD4 antibody	2.02e-35
32	605	37.0	236	1 P93910	Y22 light chain of an	2.02e-35
33	605	37.0	239	12 R66757	Anti-tobacco mosaic v	2.02e-35
34	604	36.9	272	15 R80392	Anti-HIV-1 MAb 447 sc	2.41e-35
35	604	36.9	272	15 R80405	Anti-HIV-1 MAb 447 sc	2.41e-35
36	604	36.9	272	15 R80406	Anti-HIV-1 MAb 447 sc	2.41e-35
37	604	36.9	272	15 R80390	Anti-HIV-1 MAb 447 sc	2.41e-35
38	604	36.9	272	15 R80393	Anti-HIV-1 MAb 447 sc	2.41e-35
39	604	36.9	272	15 R80398	Anti-HIV-1 MAb 447 sc	2.41e-35
40	604	36.9	272	15 R80391	Anti-HIV-1 MAb 447 sc	2.41e-35
41	604	36.9	272	15 R80396	Anti-HIV-1 MAb 447 sc	2.41e-35
42	604	36.9	272	15 R80395	Anti-HIV-1 MAb 447 sc	2.41e-35
43	604	36.9	272	15 R80394	Anti-HIV-1 MAb 447 sc	2.41e-35
44	604	36.9	272	15 R80409	Anti-HIV-1 MAb 447 sc	2.41e-35
45	604	36.9	272	15 R80411	Anti-HIV-1 MAb 447 sc	2.41e-35

ALIGNMENTS

RESULT 1
ID R42163 standard; Protein; 217 AA.
AC R42163;
DT 27-APR-1994 (first entry)
DE Anti-HIV-1 recombinant antibody 447-52D light chain.
KW Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;
KW HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
KW acquired immune deficiency syndrome; chimeric antibody;
KW surface glycoprotein gp120; V3 loop.
OS Homo sapiens.
PN W09319785-A.
PD 14-OCT-1993.
PF 23-MAR-1993; U02629.
PR 01-APR-1992; US-861701.
PA (MERI) MERCK & CO INC.
PA (JOHN) JOHNSON L S.
PA (PFAR) PFARR D S.
PI Conley AD, Enami EA, Johnson LS, Mark GE, Pfarr DS;
WPI; 93-336600/42.
DR N-PSDB; Q49835.
PT New recombinant human antibody - with HIV neutralising activity
PT against at least two isolates, useful for preventing or treating
PT infection in diagnosis, etc.
PS Example 9; Fig 2B; 154pp; English.
CC EBV-transformed cell lines and mouse-human heterohybridomas
CC producing human MAbs specific for the gp120 V3 loop of HIV-1 MN
CC isolate were obtained. MAb 447-52D was found to recognise the

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CC tetrapeptide motif GPCR, i.e. the Principal Neutralising
 CC Determinant common to the V3 loop of different HIV isolates.
 CC A recombinant AB was produced in which the L chain V region was
 CC derived from 447-520 and to which a signal sequence and a L chain
 CC intronic sequence are appended, fused to a fragment contg. a short
 CC intronic segment of the human lambda 2 C region and the human
 CC lambda 2 constant encoding domain.
 SQ Sequence 217 AA;

Query Match 79.6%; Score 1302; DB 8; Length 217;

Best Local Similarity 88.1%; Pred. No. 1.45e-88;
 Matches 192; Conservative 16; Mismatches 7; Indels 3; Gaps 3;

Db 1 qvltppsvaapqkvrticagssnignmyl-wyqdfgtapkllygnkrtpsgi 59
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 21 ESVLTQPPSVSGAPGQKVTISCTGSTNTGG-YDLHWYQQLFGTAPKLLIYDINKRPSGI 79
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 60 pdfskskgsatqlgtlgtgdeadyfcatsdwdglsadwfgggtklvtlsgpkaps 119
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 80 SDRFSKSGTAAALATLGLQTEDEADYYCQSYDSSINAG-VFGGGRTLVLGQPKAAPS 138
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 120 vtlfpssseelqankatlvcclisdfypgavtvawkadsepvkagvettptskqsmkyaa 179
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 139 VTLFPSSSEELQANKATLVCCLISDFYPGAVTVAMKADSPVKAGVETTPSKQSNKYAA 198
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 180 ssvlsitpeqwkhrayscqthegstvektvaptacs 217
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 199 SSVLSITPEQWKHRSYSCQVTHEGSTVEKTVAPTACS 236

RESULT 2

ID R31024 standard; Protein; 235 AA.

AC R31024;

DT 19-MAY-1993 (first entry)

DE Antibody D light chain.

KW Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;

KW lymphocyte; hepatitis A virus; HAV; sero; positive; patient;

KW murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H.

OS Synthetic.

FH Key Location/Qualifiers

FT Peptide 1..19

FT /note= "Signal peptide"

FT Region 20..42

FT /label= FR1

FT Region 43..53

FT /label= CDR1

FT Region 54..68

FT /label= FR2

FT Region 69..75

FT /label= CDR2

FT Region 76..107

FT /label= FR3

FT Region 108..116

FT /label= CDR3

FT Region 117..126

FT /label= FR4

FT Domain 127..234

FT /label= C lambda

PN EP-523949-A.

PD 20-JAN-1993.

PF 14-JUL-1992; 306420.

PR 15-JUL-1991; GB-015284.

PR 01-AUG-1991; GB-016594.

PR 23-MAR-1992; GB-006284.

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4

PA (WELL) WELLCOME FOUND LTD.

PI Crowe JS, Lewis AP;

DR WPI; 93-019951/03.

DR N-PSDB; Q35100.

PT Prodn. of recombinant primate antibodies - useful for treating

PT infections caused by hepatitis A, B and C, herpes,

PT cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,

PT arthritis etc.

PS Disclosure; Fig 3; 35pp; English.

CC The sequences given in R31023-24 represent the heavy and light chains

CC of Antibody D respectively. Antibody D is a monoclonal antibody which

CC was derived from peripheral blood lymphocytes from a hepatitis A virus

CC (HAV) sero positive patient. Antibody D is closely related in nature

CC to murine antibody B5B3. Total RNA was isolated from antibody D

CC expressing cells and polyadenylated RNA was extracted. These polyA

CC RNA's were used to prepare a cDNA library which was screened for human

CC kappa light (L) chains and two positive clones were detected.

CC Further heavy (H) chain clones were also isolated.

SQ Sequence 235 AA;

Query Match 78.8%; Score 1288; DB 6; Length 235;

Best Local Similarity 80.2%; Pred. No. 1.74e-87;

Matches 186; Conservative 25; Mismatches 18; Indels 3; Gaps 3;

Db 5 lllltlltqdgswagsaltqpasvsgpsgqetiscgtntndvgsynlvswyqghpka 64
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 7 LLGLLLLLWL-FGARCESVLTQPPSVSGAPGQKVTISCTGSTNTGGYDL-HWYQQLPCTA 64
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 65 pkimlyevskrpsqvenrfsgskagntaeltslglqadeadyccsyagstv-vfggg 123
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 65 PKLLIYDINKRPSGISDRFSKSGTAAALATLGLQTEDEADYYCQSYDSSINAGVFGGG 124
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 124 tkltvlqgkkaapsvtlfpssseelqankatlvcclisdfypgavtvawkadspvkagve 183
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 125 TRLTVLGQPKAAPSVTLPFPSSSEELQANKATLVCCLISDFYPGAVTVAMKADSPVKAGVE 184
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 184 ttptskqsmkyaaasyvlstpeqwkhrayscqthegstvektvaptacs 235
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 185 TTTPSKQSNKYAAASYLSITPEQWKHRSYSCQVTHEGSTVEKTVAPTACS 236

RESULT 3

ID P81260 standard; protein; 233 AA.

AC P81260;

DT 09-NOV-1990 (first entry)

DE VDJC regions of human sperm-immobilising monoclonal antibody.

KW Anti-human sperm-immobilising monoclonal antibody; leader region;

KW variable region; joining region; constant region; sterility;

KW vaccine; contraceptive.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 21..115

FT /label=variable_region

FT Region 116..127

FT /label=joining_region

FT Region 128..233

FT /label=constant_region

PN J63126482-A.

PD 30-MAY-1988.

PF 15-NOV-1986; 272412.

PR 15-NOV-1986; JP-272412.

PA (TOFU) TOA NENRYO KOGYO KK.

DR WPI; 88-187839/27.

DR N-PSDB; N81655.

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PT Cell strain producing human sperm-immobilising monoclonal antibody -
 PT has at least V-gene in H chain coding genetic family and V gene in L
 PT chain of DNA originating from antibody of sterile woman.
 PS Disclosure; ; 14pp; Japanese.
 CC A VDJC DNA segment is inserted into pC4lambda5 together with a
 CC leader region. A cell strain, pref. a myeloma cell, can
 CC produce the Ab with immobilising value (SI50) of at least 5000,
 CC sperm agglutination value at least 1:1600 dilution, specifically
 CC reacting against human ejaculated sperm. The product can be used
 CC as a vaccine and contraceptive.
 CC See also N81654-N81656.
 SQ Sequence 233 AA;

Query Match 69.7%; Score 1140; DB 1; Length 233;
 Best Local Similarity 78.6%; Pred. No. 4.06e-76;
 Matches 180; Conservative 13; Mismatches 33; Indels 3; Gaps 3;

Db 8 ltlftlci-gevvaseltqdpvvealgtvrticqgd-s-lrtyhaswyqkprqapvl 64
 ||: ||: | : ||| ||| ||| ||| ||: | : ||| ||| |||
 Qy 8 LGLLLMLPGARCESVLTPQPSVSGAPGQKVTISCTGTSNIGGYDLHWYQLPCTAPKL 67
 ||: ||: | : ||| ||| ||| ||| ||: | : ||| ||| |||
 Db 65 viydennrpigldrfegstgntaelititgaqaedeaddyenrdsngnrlvfggqkl 124
 ||: ||: | : ||| ||| ||| ||| ||: | : ||| ||| |||
 Qy 68 LYIDINWRPSGIDRSFGSKGTASLTGLQTEDEADYQCYSDSLNAQVFGGTRL 127
 ||: ||: | : ||| ||| ||| ||| ||: | : ||| ||| |||
 Db 125 tvlgqpkaapvltlfpssseelqankatlvlclisdfypgavtvawkdaspvkagvett 184
 ||: ||: | : ||| ||| ||| ||| ||: | : ||| ||| |||
 Qy 128 TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT 187
 ||: ||: | : ||| ||| ||| ||| ||: | : ||| ||| |||
 Db 185 pstqanmyaasyeltpqewkhrsyqcqthegstvektvaptacs 233
 ||: ||: | : ||| ||| ||| ||| ||: | : ||| ||| |||
 Qy 188 PSQSNKYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS 236

RESULT 4

ID R38162 standard; Protein; 234 AA.

AC R38162;

DT 01-OCT-1993 (first entry)

DE Sequence of the kappa light chain variable region (VK) of human

DE immunoglobulin G3 (IgG3) produced by transformed human B-cell line

DE 88BV59, ATCC CRL 10624.

KW B-cell; immunoglobulin g; cancer; tumour.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 1..214

FT *tag= a

FT /label= 1st AA denoted AA#1

FT Region 24..49

FT *tag= b

FT /label= CDR 1

FT Region 50..88

FT *tag= c

FT /label= CDR 2

FT Region 89..108

FT *tag= d

FT /label= CDR 3

FT Region 109..214

FT *tag= e

FT /label= CON

PN EP-546634-A.

PD 16-JUN-1993.

PF 09-DEC-1992; 203827.

PR 13-DEC-1991; US-807300.

PA (ALKU) AK20 NV.

Dec 17 15:20

US-08-487-550-10.rag

6

PI Crichton VZ, Haspel MV, Kobrin BJ;
 DR WPI; 93-190019/24.
 DR N-PSDB; Q43773.
 PT Transformed human B-cell line for monoclonal antibody prodn. for
 PT cancer diagnosis - prepd from peripheral blood B-cells of cancer
 PT patients actively immunised with autologous tumour antigen, for
 PT treating cancers
 PS Claim 9; Fig 3; 18pp; English.
 CC The 88BV59 kappa light chain sequence is indicated by the posns.
 CC of the CDRs and the constant region exon. 88BV59 utilises Vx1 and
 CC Jx5. The first NH2 terminal 22 residues were confirmed by AA
 CC sequencing.
 SQ Sequence 234 AA;

Query Match 46.9%; Score 766; DB 7; Length 234;
 Best Local Similarity 47.5%; Pred. No. 1.42e-47;
 Matches 113; Conservative 49; Mismatches 68; Indels 8; Gaps 8;

Db 1 rqpaelqllllwlpgarcdqltqpsflaavdgdrvtitcrasqg-issy-lawyqqk 58
 ||: ||: | : ||| ||| ||| ||| ||: | : ||| ||| |||
 Qy 2 RVPAQLLGLLLMLPGARCESVLTPQPS-VSGAPGQKVTISCTGTSNIGGYDLHWYQL 60
 ||: ||: | : ||| ||| ||| ||| ||: | : ||| ||| |||
 Db 59 pgkapklliyaaaelgcvpserfsgsgstetfiteelqpdedfatycyqqlngypri-t 117
 ||: ||: | : ||| ||| ||| ||| ||: | : ||| ||| |||
 Qy 61 PCTAPKLLIYDINKRPSGIDRSFGSKGTASLTGLQTEDEADYQCYSDSLNAQV 120
 ||: ||: | : ||| ||| ||| ||| ||: | : ||| ||| |||
 Db 118 fggqtrlei-krtvaapsvfippsdeqlkagtasvcllmmfypreakvqkvdnalqs 176
 ||: ||: | : ||| ||| ||| ||| ||: | : ||| ||| |||
 Qy 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
 ||: ||: | : ||| ||| ||| ||| ||: | : ||| ||| |||
 Db 177 qnsgeavteqsdskdystlsatlklakadyekhkvyacevthqglsepvtksfrgac 234
 ||: ||: | : ||| ||| ||| ||| ||: | : ||| ||| |||
 Qy 181 AGVETTPSKSQSN-N-KYAASSYLSLTPEQWKSRSYSCQVTHEG-ST-VEKTVAPTEC 235

RESULT 5

ID R13050 standard; Protein; 234 AA.

AC R13050;

DT 27-SEP-1991 (first entry)

DE CD4-specific CDR-grafted light chain.

DE variable region; antibody; OKT4A; heavy chain; CD4;

KW complementarity determining region.

OS Synthetic.

FH Key Location/Qualifiers

FT Peptide 1..20

FT /label= signal sequence

FT Region 21..45

FT /label= framework region 1

FT Region 46..52

FT /label= CDR 1

FT Region 53..69

FT /label= framework region 2

FT Region 70..76

FT /label= CDR 2

FT Region 77..110

FT /label= framework region 3

FT Region 111..116

FT /label= CDR 3

FT Region 117..132

FT /label= framework region 4

FT Region 133..234

FT /label= kappa constant domain

PN W09109966-A.

PD 11-JUL-1991.

PF 21-DEC-1990; G02015.
PR 21-DEC-1989; GB-028874.
PR 21-DEC-1990; WO-G02017.
PR 21-DEC-1990; WO-G02018.
PR (ORTH) ORTHO PHARM CORP.
PI Jolliffe LK, Zivin RA, Pulito VL, Adair JR, Athwal DS;
PFI 91-222914/30.
DR N-PSDB; Q12633.
DR New CD4 specific recombinant - complementarity determining region
PT grafted antibody for treating graft rejection and T cell
PT disorders
PT Claim 1; Fig 8; 96pp; English.
PS This is an example of a CDR-grafted light chain of the invention.
CC The constant regions are based on sequences of the human kappa
CC constant domain, the signal sequence is derived from murine Mab
CC B72.3 and the CDR sequences are based on the murine OKT4A light chain
CC CDRs. The recombinant antibody encoded by this sequence has affinity
CC for CD4 similar to that of OKT4A.
CC See also Q12627-Q12632.
CC Sequence 234 AA.
SQ

Query Match 46.7%; Score 763; DB 3; Length 234;
Best Local Similarity 45.6%; Pred. No. 2.40e-47;
Matches 109; Conservative 55; Mismatches 66; Indels 9; Gaps 8;

Db	1	mgvptvqlglllllwtldaredicamtqspeslaesvgdrvtitckas-pdinny-lmwyqq	58
Qy	1	MRVPAQLLGILLLLWLPGARCESVLTQTPS-VSGAPGQKVTICTGTSNIGGYDLHWYQQ	59
Db	59	tpgkapklllyvtstlqgvpsvfsgsgstgetyeftisslapediatyycqyqdhllft-	117
Qy	60	LPGTAPKLLIYDINKRPSGTSIDRFSKSGSTAASLAITGLQTEADRDYQCYSYSSLNAQ	119
Db	118	-fqqgqtklqi-trtvaapsvfiippsdeqlkqgtasvvelmnnfvpreakvgkvhdnql	175
Qy	120	VFGGTRTLVTLQPKAAPSVTLPFPFSEELQANKATLVLCTSDYFPAVTVAKADSPV	179
Db	176	sgnsgsvteqdekdetsytslastltsladyekhhkyacevthqqlaspytskfnrqc	234
Qy	180	KAGVETTPPKQSNV-KYFAASVSLSTPEOMKSHRSYSCVTHGCG-ST-VKTVAPTEC	235

RESULT 6
ID R77614 standard: Protein: 236 AA.

13-MAR-1996 (first entry)
Humanised 5G1.1 VL + 012.
Complement C5; haemolysis; kidney; glomerulonephritis;
monoclonal antibody; antinflammatory; antibody engineering;
humanised antibody; complementarity determining region; CDR;
ds.

OS	Key	Synthetic	Location/Qualifiers
FF	Peptide		1..23
FF	/label= sig_peptide		
FF	Peptide		23..236
FF	/label= mat_peptide		
FF	Region		47..57
FF	/label= CDR-L1		
FF	Region		73..79
FF	/label= CDR-L2		
FF	Region		112..120
FF	/label= CDR-L3		
PN	W09529697-A1.		

PD 09-NOV-1995.
PF 01-MAY-1995; U05688.
PF 02-MAY-1994; US-236208.
PA (ALEX-) ALEXION PHARM INC.
PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins SJ;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
PI WPI: 95-392923/50.
DR N-PSDB; T08486.
DR N-Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
PT Claim 40; Page 132-34; 181pp; English.
PS A humanised CDR-grafted light chain, designated 5G1.1 VL + 012
CC (R77614), includes CDRs derived from mouse anti-C5 monoclonal
CC antibody 5G1.1. DNA (T08486) coding for the light chain can be
CC subcloned together with DNA (T08484) coding for a humanised Fd
CC (R77611) into vector APEX-3P (T08476) for expression of humanised
CC antibody in human 293 EBNA cells. Such recombinant antibodies retain
CC the ability of Mab 5G1.1 to block human complement C5a generation and
CC thus to reduce glomerular inflammation and kidney dysfunction
CC associated with glomerulonephritis.
SQ Sequence 236 AA;

Query Match 46.4%; Score 758; DB 15; Length 236;
Best Local Similarity 47.1%; Pred. No. 5.74e-47;
Matches 113; Conservative 53; Mismatches 63; Indels 11; Gaps 10;

[illegible]

RESULT	7	
ID	R20058 standard; Protein; 234 AA.	
AC	R20058;	
DT	25-MAR-1992 (first entry)	
DE	Light chain of 3D6 anti-HIV antibody.	
KW	Plasmid pUC396LC; human immunodeficiency virus; AIDS;	
KW	complementarity determining region.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Peptide	1..22
FT	/label= signal	
FT	protein	23..234
FT	Region	23..45
FT	/label= Framework_1	
FT	Region	46..56
FT	/label= CDR_1	
FT	Region	57..71
FT	/label= Framework_2	
FT	Region	72..78
FT	/label= CDR 2	

FT	Region	79..110	
FT	/label= Framework_3		
FT	Region	111..117	
FT	/label= CDR_3		
FT	Region	118..127	
FT	/label= Framework_4		
FT	Region	128..234	
FT	/label= Constant_region		
PN	W09118983-A.		
PD	PD	12-DEC-1991.	
PF	28-MAY-1991;	100067.	
PR	29-MAY-1990;	AT-001178.	
PA	(JUNG/) JUNGHAUER A.		
PI	Felgenhauer M, Himmeler G, Kohl J, Steindl F;		
DR	WPI; 92-007468/01.		
DR	N-PSDB; Q20067.		
PT	Recombinant protein which binds to complex viral antigen and		
PT	HIV-1 - contains variable region of antibody derived from 3D6		
PT	cell line, used for detecting HIV-1 antigen		
PS	Claim 3; page 28; 52pp; German.		
CC	The variable region of the light chain is used in a recombinant		
CC	protein with the variable region from the heavy chain of 3D6,		
CC	the two V regions being joined by a linker. The recombinant		
CC	protein binds to HIV gp160.		
CC	See also Q20066 and Q20068.		
SQ	Sequence	234 AA;	

Query Match	45.3%	Score 740;	DB 3;	Length 234;
Best Local Similarity	46.4%;	Pred. No. 1.33e-45;		
Matches 111;	Conservative 52;	Mismatches 65;	Indels 11;	Gaps
Db	3	mrvpagllgllllwlpgakcdlqmtqgqstlaasvqgdvritcraaqe-ierrw-lawyqq	60	
Qy	1	MRVPAQLGLLLWLPGARCESVLTQPPS-VSGAPGQKVTISGTGTSNIGGYDLHWYQQ	59	
Db	61	kpgtvpklllykaaslesgvprfsagsgagteftlisslpoddfatyccyqns---ys-	117	
Qy	60	LPGTAPKLLYDINKRPSIDSRSGSKSTAAISLAITGLTQTEDEADYTCQSYDSSIAAQ	119	
Db	118	-fpggtkvd-i-krtvaapsvfifpsdeqlkgstasvvcllnnfyreakvqvkvvdnalq	175	
Qy	120	VFGGTRLTLCQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVMKADSSPV	179	
Db	176	sgnsqesvtedskdstyelsatlslskadyekkhkvacervthqqlspvtrksfngrec	234	
Qy	180	KAGVETTPPSKQNN-KYAASYSLLTPQKMSKHSRYSQCVTHEG-SY-VEKTVAPTEC	235	

RESULT	8	
ID	R42065	standard; Protein; 236 AA.
AC	R42065;	
DT	29-APR-1994	(first entry)
DE	Human anti-HBs (light chain.	
KW	Antibody; Ab; light; heavy; chain; hepatitis B;	
KW	HB; surface antigen.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Peptide	1..22
FT	/label= sig_peptide	
FT	Protein	23..236
FT	/label= mat_protein	
PN	W09320205-A.	
PD	14-OCT-1993.	
PF	30-MAR-1993;	J00396.

PR 30-MAR-1992; JP-074678.
PA (SUNR) SUNTORY LTD.
PI Arima K, Kurihara T, Mateukura S, Nishihara T, Teurouka N;
DR WPI; 93-336913/42.
DR N-PSDB; Q49943.
PT Human anti-hepatitis B surface antigen antibody gene - can be
used to produce L and H chains of the antibody in large quantity
PT Disclosure; Fig 4-5; 46pp; Japanese.
PS Polynucleotides encoding the L and H chains of human anti-HBs
CC Ab are given in Q49943-Q49944. The Ab can be easily produced in
CC large quantities for therapeutic use.
SQ Sequence 236 AA;

Query Match	45.0%	Score 735;	DB 8;	Length 236;
Best Local Similarity	45.2%;	Pred. No. 3.17e-45;		
Matches	108;	Conservative	53;	Mismatches 69; Indels 9; Gaps 8;
Db	3	mrpvaqlgllllwfgparcdlmtqpeamaasvgdvrtitcrasqg-igny-lvwfqg	60	
Qy	1	MRVPAQLGLLLLPARCESVLTQPPS-VSGAPGQKVTISGTSTNIGGYDLHWQQ	59	
Db	61	kpgkvpkrllyaaeslqsgvperfsgegegtftlslrlqpedfatyvcylhnnh---yp	118	
Qy	60	LPGTAPKLLIYDINKRPSGISDTSKSGSTAASLAITGLTQTEDEADYYCQSYDSS	119	
Db	119	efgggtkwei-krtvaapsvflfpdsedqlkgstasvvcllnnfypreakvqwkvdnalq	177	
Qy	120	VFGGTRLTVLGQKAAPSVTLFPPSEELQANKATLVCLISDFYPGAVTVAMKADSSPV	179	
Db	178	sgnasqvteqdkdslyslstlclbkadyekkvyaecvthqglsepvtkafnrcg	236	
Qy	180	KAGVEITTPSKQSN-KYAAASYLASLTPQEMKSHRSYSCVOTHEG-ST-VEKTVAPTE	235	

RESULT	9
ID	R28809 standard; Protein; 241 AA.
AC	R28809;
DT	02-APR-1993 (first entry)
DE	Vector pMDR1007.
KW	Plasmid; pMDR1006; pSAB132; vector; pMDR1007; pMDR985; AatII; EcoRV;
KW	pMDR986; BglII; pMDR1003; JAZ21(Iq); E. coli; ampicillin resistance;
KW	NotI; dephosphorylate; calf; alkaline phosphatase; low temperature;
KW	melting agarose; immunoglobulin; kappa chain; signal peptide; LC;
KW	humanised; 5A9; light chain; variable region; LV; genomic; constant
KW	antibody; homolog; CD4; gp120; cell surface; glycoprotein; CD4+;
KW	lymphocyte; helper; inducer; HIV; syncytia; formation.
OS	Synthetic.

Key	Location/Qualifiers
FT	Peptide 1..22
FT	/note= "Immunglobulin kappa chain signal peptide"
FT	Region 23..134
FT	/note= "Humanised 5A8 IV"
FT	Region 135..241
FT	/note= "Human kappa chain LC"
FT	W09209305-A.
PD	11-JUN-1992.
PF	27-NOV-1991; U08843.
PR	27-NOV-1990; U5-618542.
PA	(BIOL) BIOGEN INC.
PI	Burkly LC, Chisholm PL, Rosa JJ, Rosa MD, Thomas D
PI	WPI: 92-398399/48.
DR	N-PSDB; Q30920.
PT	New anti-CD4 antibody homologues - which bind CD4,
PT	binding of HIV gp120 to CD4 but block HIV-induced

RESULT	10	
ID	R52951	standard; Protein; 234 AA.
AC	R52951;	
DT	27-OCT-1994	(first entry)
DE	Human anti-IgE MAb light chain.	
KW	Human IgE; CH4 region; triggers mediator release;	
KW	Mast cells; Monoclonal antibody; allergy.	
OS	Homo sapiens.	
FT	Key	Location/Qualifiers
FT	Region	21..128
FT	/label=	light chain variable region
PN	EP-592230-A.	

RESULT	11
ID	R69093 standard; Protein; 106 AA.
AC	R69093;
DT	30-AUG-1995 (first entry)
DE	Anti-HIV Fab rev16/20 light chain.
KW	HIV-1; human immunodeficiency virus type 1; AIDS; Rev protein; intracellular immunization; gene therapy; single chain antibody; Fab; antibody engineering; resistance; cell immunity.
OS	Homo sapiens.
FH	Key Location/Qualifiers
FT	Misc.difference 68
FT	/note= "not known"
FT	Misc.difference 86
FT	/note= "not known"
FT	Misc.difference 101
FT	/note= "not known"
PN	W09503832-A.
PD	09-FEB-1995.
PE	28-JUL-1994; U084448.
PR	30-JUL-1993; US-099870.
PPA	(UYJE-) UNIV JEFFERSON THOMAS.
PI	Duan L, Pomerantz R;
DR	WPI; 95-082039/11.
PT	Method for conducting gene therapy - comprises using recombinant

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Search completed: Tue Dec 17 15:35:10 1996
Job time : 28 secs.

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3

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#contents      myeloma protein Eu
#accession     B90563
#molecule_type protein
##residues     1-96,'R',98-135 ##label CUN
##note         this sequence has the GIm(3) marker, 97-Arg
REFERENCE
#authors       Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg,
                W.H.; Edelman, G.M.
#journal       Biochemistry (1970) 9:3171-3181
#title         The covalent structure of a human gammaG-immunoglobulin.
                VIII. Amino acid sequence of heavy-chain cyanogen bromide
                fragments H-S-H-7.
#cross-references MUID:71064025
#contents      Eu
#accession     A90564
#molecule_type protein
##residues     136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,
                'D',199-238,'E',240,'M',242-267,'DGEPE',273-329
                ##label RUT
##note         this sequence has the GIm(non-1) markers, 239-Glu and
                241-Met
REFERENCE
#authors       Ponstingl, H.; Hilschmann, N.
#journal       Hoppe-Seyler's Z. Physiol. Chem. (1976) 357:1571-1604
#title         Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins
                (Myelomprotein Nie), III. Die chymotryptischen Peptide der
                H-Kette, Anordnung der tryptischen Peptide und Diskussion
                der vollstaendigen Primaerstruktur.
#cross-references MUID:77070269
#contents      myeloma protein Nie
#accession     B91668
#molecule_type protein
##residues     1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',
                240,'L',242-268,'E',270-271,'D',273-330 ##label PON
##note         this sequence has the GIm(17) and GIm(1) markers
REFERENCE
#authors       Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
#journal       Hoppe-Seyler's Z. Physiol. Chem. (1983) 364:713-747
#title         Die Primaerstruktur des kristallisierten monoklonalen
                Immunglobulins IgG1 KOL, I.
#cross-references MUID:83289131
#contents      myeloma protein KOL; disulfide bonds
#accession     A91723
#molecule_type protein
##residues     1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',
                268-271,'D',273-330 ##label SCH
##note         this sequence has the GIm(3) and GIm(non-1) markers
REFERENCE
#authors       Gall, W.E.; Edelman, G.M.
#journal       Biochemistry (1970) 9:3188-3196
#title         The covalent structure of a human gammaG-immunoglobulin. X.
                Intrachain disulfide bonds.
#cross-references MUID:71064027
#contents      annotation; disulfide bonds
#accession     A91667
#authors       Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
#journal       Hoppe-Seyler's Z. Physiol. Chem. (1976) 357:1515-1540
#title         Rule of antibody structure. The primary structure of
                monoclonal IgG1 immunoglobulin (myeloma protein Nie), I:
                purification and characterization of the protein, the L-
                and H-chains and the cyanogenbromide cleavage products, and the
                disulfide bridges.
#cross-references MUID:77070267
#contents      annotation; disulfide bonds

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GENETICS
#gene          GDB:ICHG1
#map_position  14q32.33
#introns       99/1; 114/1; 224/1
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
KEYWORDS       glycoprotein
FEATURE
20-85          #domain immunoglobulin homology #label ICG1\
137-206        #domain immunoglobulin homology #label ICG2\
243-310        #domain immunoglobulin homology #label ICG3\
27-83,144-204, #disulfide bonds #status experimental\
250-308        #disulfide_bonds interchain (to light chain) #status
103            #disulfide_bonds interchain (to heavy chain) #status
109,112        #disulfide_bonds interchain (to heavy chain) #status
180            #binding_site carbohydrate (Asn) (covalent) #status
                experimental
SUMMARY        #length 330 #molecular-weight 36106 #checksum 8773
Query Match    68.0%; Score 2339; DB 2; Length 330;
Best Local Similarity 99.7%; Pred. No. 0.00e+00;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 aetkpsvfplapskatsqtaalqclvkvdfpepvtvsmesqaltsgvhtfpavlges 60
|||||
Qy 147 ASTKGPVFPLAPSKSTSGCTAALGCLVKVDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
|||||
Db 61 gylsissvvtvpssalgtqtyicnvnhkpsntkvdkvpeksckthtcpcpapellgg 120
|||||
Qy 207 GLYLSVSVVTPVSSSLGTQTYICNVNHRKPSNTKVDKKAEPKSCDKTHTPCCPAPELLGG 266
|||||
Db 121 psvflfpkpkdtlmisrtpvrtcvvdvvhedpevfknwydvgevuhnaktkpreeqn 180
|||||
Qy 267 PSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGEVHNKTKPREEQYN 326
|||||
Db 181 styrsvslvthqdwlngkeykckvskenkalepalektiekakgqprepvytclppsrde 240
|||||
Qy 327 STYRSVSVLTVLHQDWLNGKEYKCKVSKNKAIPAEKTIISKAGQPREPQVYTLPPSRDE 386
|||||
Db 241 lcknqvaelcylvgfypsdiavewesngqpennykttppvlidsdgsfflyskltvdkarw 300
|||||
Qy 387 LTRKQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 446
|||||
Db 301 qggnvfcsvmhleahhhytqkalelspgk 330
|||||
Qy 447 QGGNVFCSVMHLEAHNHHTQKSLSLSPGK 476
|||||
RESULT 2
ENTRY       S36861 #type fragment
TITLE       Ig gamma-1 chain C region - human (fragment)
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change
                02-Aug-1994
ACCESSIONS  S36861; S33887
REFERENCE   S33904
#authors    Harris, L.J.
#submission submitted to the EMBL Data Library, October 1992
#accession  S36861
#molecule_type DNA
##residues 1-329 ##label HAR
##cross-references EMBL:217370
REFERENCE   S33887

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#authors      Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.;
               Honjo, T.
#journal      Cell (1982) 29:671-679
#title        Structure of human immunoglobulin gamma genes: implications
               for evolution of a gene family.
#accession    S33887
#molecule_type DNA
#residues     87-112;234-329 ##label TAK
#cross-references EMBL:Z17370

GENETICS
#introns      98/1; 113/1; 223/1
#superfamily  immunoglobulin C region; immunoglobulin homology
#length 329 #checksum 6336
SUMMARY

```

Query Match 67.8%; Score 2335; DB 5; Length 329;
Best Local Similarity 99.7%; Pred. No. 0.00e+00;
Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 stkgpsvflapsskstsggtaalgclvkdyfpepvtvswnsqaltsqvhtfpavlgssq 60

Qy 148 STKGPSVFPLAPSSKSTSGGTAALCLCLKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 207

Db 61 lyslssvvtvpssslgtqyicvnhkpstkvdkkvepscdkthtcppcpapellgpp 120

Qy 208 LYSLSVVTPSSSLGTQTYICNVNHPNTKVDKKAEPKSCDKTHTCPPAPPELLGGP 267

```

Db      121  svlfppkpktlmi stpevtcvvdvshedpevkfnwydgvvhnaktkpreeqyns 180
      |||||

```

Qy 268 SVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 327

```
Db      tyrvsvltvlhqdwlngkeyckvsnkalpapietkistakgqpprepvytllppsrdeI 240
```

Qy 328 TYRWSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTIIPPSRDEL 387

[illegible]

04 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

```

001 qgnivscsvmeatnnmytqksislsbpgk 329
|||||
448 qgnivscsvmeatnnmytqksislsbpgk 476

```

0 1 4 V D J E C T P W Y I U N U B R H A C C C L A N E X 0 1 4 F X

RESULT	3
ENTRY	S22080
TITLE	ig heavy chain precursor (B/M7.4P.17.H5.A5) - bovine
ALTERNATE_NAMES	ig gamma-1 chain C region (clone 8.10)
ORGANISM	Formal name Bos primigenius taurus #common_name cattle
DATE	06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-May-1995

```

ACCESSIONS      S22080; S06610; A31303
REFERENCE
#authors        Sanders, P.G.
#submission     submitted to the EMBL Data Library, November 1991
#accession      S22080
#status         preliminary
#molecule_type mRNA
#residues       1-470 #label SAN
#cross-references EMBL:X62916

```

REFERENCE
#authors Symons, D.B.A.; Clarkson, C.A.; Beale, D.
#journal Mol. Immunol. (1989) 26:841-850
#title Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 2 genes.

```

#cross-references MUID:90097956
#accession S06610
#molecule_type DNA
#residues 142-470 ##label SYM
#cross-references EMBL:X16701
##note the sequence was determined from the germline gene
GENETICS
#gene
#introns
CLASSIFICATION
KEYWORDS
FEATURE
318
#binding site carbohydrate (Asn) (covalent) #status

```

```
SUMMARY      #length 470  #molecular-weight 50625  #checksum 2181
              #length 470  #molecular-weight 50625  #checksum 2181

Query Match      64.1%;  Score 2208;  DB 5;  Length 470;
Best Local Similarity 63.6%;  Pred. No. 1.55e-286;
Matches 304;  Conservative 87;  Mismatches 77;  Indels 10;  Gaps 9;
```

Db 1 mnplwtllfvlsapiqvlscvqlresqpslvkpsqtlsltctvsqfslss-yaltwvrqa 59

QY 1 MKHLWFFLLVAAAPRWLSQVQLQESGPGLVKPSSETLSLTCAVSGGSISSCYGCGWIRP 60

Db 60 pgkalewvggi-tsggttyynpalksrslsitkensksqvsisvssvtptedatyycarst 118

QY 61 PGKGLWIGSFYSSGNTYYNPSLKSVQVTISTDTSKNQFSIKLNSMTAADTAVYYCVRDR 120

```
Db 119 -ygevgaia--dawggllvtvssasttapyplssccgdkssstvtlglvssymp 175
```

QY 121 LFSVVGMYNNWEDWGPGLVTIVSSASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYPF 180

Db 176 epvtvtwnsgalksgvhtfpavlqsgglyslasmvtvpqsteg-qtftcnvahpasstkv 234

Qy 181 EPVTVSNNSGALTSGVHTEPAVLQSGSLYSLSVWVTPSSSLGTQTYICNVNHPKPSNTKV 240

Db 235 dkavdp-tc-kpspcacacpppeipgpgpsvfiipkpkdtltisgtpevtcwwdvghdap 2992

DRRAEPKSCDKRTHICPPCPAPELLGGFSVFLEPPRPKDTLMISRTPEVTCVWDVDSHEDP 300

[illegible]

QY EVKE NW I VDOGEVHNNIINE REEJ INST I RA VSZ LI V LKQZH LNAGRE INCHV SNUUUE AF 300

Dh 353 | wrt jst kanarenvuv | annose | sket vs | t cmvt sfundv | avewrrnngneesd 412

[illegible]

pb 4i3 kvattpooldadssvflvysklrvdrnswaeagdtvrcvmbhealnhhvtckstksaak 470

QY 420 -YKTPPVLDSDGSEFLYKSLTVDKSRWQQGNVFCSCVMHEALHNHYTKSLSLSPGK 476

RESULT	4
ENTRY	S31459 #type fragment
TITLE	Ig gamma-1 chain - sheep (fragment)
ORGANISM	#formal name Ovis orientalis aries, Ovis ammon aries #common name domestic sheep
DATE	13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
ACCESSIONS	S31459
REFERENCE	S31459
#authors	Patrl, S.; Nau, F.
#submission	submitted to the EMBL Data Library, December 1992

```

#accession      S31459
#status         preliminary
#molecule_type mRNA
#residues       1-472 ##label PAT
#cross-references EMBL:X69797

SUMMARY
#length 472 #checksum 9485

```

Query Match	62.6%;	Score 2156;	DB 12;	Length 472;
Best Local Similarity	62.2%;	Pred. No. 4,10e-279;		
Matches	296;	Conservative 90;	Mismatches 82;	Indels 8; Gaps 8;
bb	2	lwtllfwlsaprgvlsqvrilqesgpallatlltsvtcttsqfslmnn-ygvdkwvraqpgk	60	
QY	4	lwwflllvaaprwlslsvoqlqesgplvklpsetlslstlcavsccslsgcygwgwlrqppek	63	
bb	61	alewlqgs-gydedidnpvrlkarleiktkdeksqvaltslsvtedtavyycarvdyds	119	
QY	64	glewlgfsssgntynympslksqvtlstdtsrknqfslklnsmtaadtavyycvdrflfs	123	
bb	120	shafayas-ydfwpgqlllsvlassttpkvypltsccgdassivlglclysmppepv	178	
QY	124	vvgvnnmfvdmgpcvlvtvssastkqpsvflpapsksstsgctaalgclvkdvffepv	183	
bb	179	tvtnwsqaltsgvhfpailqesglslsvvtvpastgaqctfincvnhpasteskvdkr	238	
QY	184	tvsnwsqaltsgvhtfpavllqssglslsvvtvpssslgtqtyicnnhksntkvdck	243	
bb	239	vep-gcpdpckhcr-cppelpgqpsavfipkpkdltlsatpbevtcvvdvggdpev	296	
QY	244	aspsksc-dkthtccpcaPELLGGSVFLFPPEKOTLMSRTEPVTCCVVDVSHEDEP	302	
bb	297	qsfwfdvnhvtrartkpreeqfnstfrvealpighqdwtkgkcfkckvnhnealpapiv	356	
QY	303	kennyvdcvghvhnatkpreeqnystyrwsvlthlqhdmlngkyekckvsnkalpapie	362	
bb	357	rtlsrtkqarepvyvllappqelekstlsvtclvtqfypdylavewkngqpsedky	416	
QY	363	ktlsrakgqrpqvytlppsrdeultknqslctclvkgsfypsdlavewesngqpen-n-y	420	
bb	417	gttselqldadggyflsrlrvdknswqgdtyacvnmhealhnhytksisppgk	472	
QY	421	kttppllsdsgsfflysklvtvdksrmoqgnvfscswmhealhnhytksislsjck	476	

```

5 RESULT
G2HU      #type complete
Iq gamma-2 chain C region - human
#formal_name Homo sapiens #common name man
30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change
08-Dec-1994
A93906; A92809; A90752; A93132; A07148
A93906
#authors
#journal
#title
#cross-references MUID:82197621
#accession A93906
#molecule_type DNA
1-326 #label ELL
#residues
Lys-326 is probably removed posttranslationally
A92809
#note
Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. (1980) 125:1048-1054.
#authors
#journal
#title
#cross-references
#accession
#molecule_type
#residues
#note
Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. (1980) 125:1048-1054.
#authors
#journal
#title
#cross-references
#accession
#molecule_type
#residues
#note

```

```

#title The primary structure of a human IgG2 heavy chain: genetic,
#cross-references WUID:81007873 evolutionary, and functional implications.
#contents myeloma protein Til
#accession A92809
##molecule_type protein
##residues 1-19,'Q','21-57','Z','59','A','61-193','D','195-325 ##label WAN
##note Trp-156 is at or near the complement-binding site
REFERENCE
A90752
#authors Connell, G.E.; Parr, D.M.; Hofmann, T.
#journal Can. J. Biochem. (1979) 57:758-767
#title The amino acid sequences of the three heavy chain constant
region domains of a human IgG2 myeloma protein.
#cross-references WUID:80001357
#contents myeloma protein Zie
#accession A90752
##molecule_type protein
##residues 1-24,'E','26-57','EV','60-85','132-171','222','175','B','177-193,
'D','195-196','Q','198-234','Z','236-263,'BCEPZ',269-325
##label CON
##note this sequence has since been revised
REFERENCE
A93132
#authors Hofmann, T.; Parr, D.M.
#journal Mol. Immunol. (1979) 16:923-925
#title A note on the amino acid sequence of residues 381-391 of
human immunoglobulin gamma chains.
#cross-references WUID:80114419
#contents Zie
#accession A93132
##molecule_type protein
##residues 238-275 ##label HOF
REFERENCE
A94591
#authors Hofmann, T.; Parr, D.M.
#submission submitted to the Atlas, March 1980
#contents annotation; Zie, revisions to residues 25, 59, 60, and
264-268
#note the revised sequence differs from that shown in having 60-Ala
and in the amidation states of residues 58, 194, and 197;
the amidation states of residues 172-174, 176, and 235 were
not determined
REFERENCE
A90253
#authors Milstein, C.; Frangione, B.
#journal Biochem. J. (1971) 121:217-225
#title Disulphide bridges of the heavy chain of human immunoglobulin
G2.
#cross-references WUID:72033500
#contents annotation; myeloma protein Sa, disulfide bonds
REFERENCE
A93157
#authors Frangione, B.; Milstein, C.; Pink, J.R.L.
#journal Nature (1969) 221:145-148
#title Structural studies of immunoglobulin G.
#cross-references WUID:69064124
#contents annotation; Sa, disulfide bonds
GENETICS
#gene GDB:IGHG2
#map_position 14q32.33
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
FEATURE
20-85 #domain immunoglobulin homology #label ICG1\
133-202 #domain immunoglobulin homology #label ICG2\
239-306 #domain immunoglobulin homology #label ICG3\
14 #disulfide bonds interchain (to light chain) #status
experimental\
27-83,140-200.

```

[illegible]

```

RESULT      6
ENTRY
TITLE      Ig gamma-4 chain C region - human
ORGANISM   *   #formal name Homo sapiens #common name man
DATE       02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change
                23-Mar-1995
ACCESSIONS A90933; A90249; A02150
REFERENCE
#authors   Ellison, J.; Buxbaum, J.; Hood, L.
#journal   DNA (1981) 1:11-18
#title     Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
#cross-references MUID:83157104
#accession A90933
##molecule_type DNA
##residues_ 1-327 ##label ELL
##note     the sequence was determined from the germline gene
REFERENCE   A90249
#authors   Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
#journal   Biochem. J. (1970) 117:33-47
#title     Human immunoglobulin subclasses. Partial amino acid sequences
                of the constant region of A gamma4 chain.
#cross-references MUID:70207560 .
#accession A90249
##molecule_type protein
##residues_ 1-30;81-326 ##label PIN

```

FEATURE		#domain immunoglobulin homology #label IGC1\
20-85		
99-110		#region hinge\
134-203		#domain immunoglobulin homology #label IGG2\
240-307		#domain immunoglobulin homology #label IGC3\
14		#disulfide bonds interchain (to light chain) #status experimental\
27-83,141-201,		
247-305		#disulfide bonds #status predicted\
106,109		#disulfide_bonds interchain (to heavy chain) #status experimental
SUMMARY	#length 327 #molecular-weight 35940 #checksum 907	
Query Match	62.0%; Score 2133; DB 2; Length 327;	
Best Local Similarity	90.6%; Pred. No. 7,84e-276;	
Matches	299; Conservative 17; Mismatches 11; Indels 3; Gaps 3;	
Dbb	1	astkgsvfplapcsrsteetaalgclykdypfpvptvswnsgaltsgvhfcpavlqgs 60
Qy	147	ASTKGSVFPEPLAPSSKSTSGCTAALGCLYKDYPFPVPTVSWSGALTSGVHFPAVLQSS 206
Dbb	61	qlyslsesvvtpvssigtktctcndvdhksntkvdkrvseak-yg-p-pcpscpapeflgg 117
Qy	207	GLVLSLSVVTPVSSIGTQTYICNVNHRPSNTKVDKKAEPKSCDKTHTCPPAPELILGG 266
Dbb	118	psvfllppkpdxdtlmiartpevtcvvvdsqsdpevfnywdgvghnaktkpreeqn 177
Qy	267	PSVFLEPPKPKDXTLMISRTPEVTCCVVVDVSHEDPEVKFNMYVDGVHNAKTKPREEQN 326
Dbb	178	styrsvsvltvlhqdlwlcqeykcvcenkglpnssiectiskagqppeqvylpseeqe 237
Qy	327	STRVSVSLTVLHQDLWLCGEYKCVCENKGLPNSSIETISKAGQPPEQVYTLPPESRDE 386
Dbb	238	mtknqvsltclykgfyppediaveesngcpennykttppvldsdgsfflysriltvdkarw 297
Qy	387	LTKNQVSLTCLWKGFYPDSDIAVESNGCPENNYKTTTPPVLDSDGSFFLYSKLTVDKSrw 446
Dbb	298	qgnvfscsvmhhealnhytqtclslelgk 327
Qy	447	QGNVFSCSVMHHEALNHVYTKSLSLSPGK 476

```

RESULT      7
ENTRY
TITLE      Ig gamma-2a chain - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
           06-Jan-1995
ACCESSIONS S37483
REFERENCE   S37483
            Ducancel, F.F.D.
            #submission submitted to the EMBL Data Library, February 1993
            #accession S37483
            #status preliminary
            #molecule_type mRNA
            #residues 1-469 #label DUC
            #cross-references EMBL:X70423
SUMMARY     #length 469 #molecular_weight 51549 #checksum 7833

Query Match 56.1%; Score 1932; DB 12; Length 469;
Best Local Similarity 56.8%; Pred.No. 3.45e-247;
Matches 269; Conservative 90; Mismatches 104; Indels 11; Gaps 8;

Db 5 wifflgtagvhcqdqlqsgspelvktpgasvkiscasgyftfdyil-nwvdkpqqg 63

```

Qy	5	WFFLLVAAAPRWVL	SOVLQSGPGVLKRE	SETJSLTCAVSGGSI	SGGYGMGI	RPQPKG	64
Db	64	lkwiiglypaagntk	ynenfkgkat	ltvdsesstaymq	lseltse	dvaafca-ngat	122
Qy	65	LEWISFYSSGN	YNNPLSKQVIT	STDTKNOQF	SILKUNSTAAD	TAVYVCVRDR	124
Db	123	atll--d-y--	waggtlt	tsesaktape	vplapvcgdt	tgasvlt	177
Qy	125	VGMVYNNWF	DMVCGV	LTVVTSASATK	GPSVFLAP	SKSTSGGTAAL	184
Db	178	ltwnsgel	saesqvht	fpawlqad-	lytlesv	vtstetwpsqei	236
Qy	185	VSMNSGALT	SGVHTFP	VLQVSGGLY	SSSVTVVP	SSSLGTQTY	244
Db	237	eprg-pt	lkpcpcp	ccapnll	ggpsv	ffipk	295
Qy	245	EPKSCDKTHT	CCPPC--	PAPELLG	GSVFLFP	PKPKOTL	302
Db	296	qlawfmv	nvehvta	qatqt	hredynsl	trvvaalpi	355
Qy	303	KFNWYVD	GVEVHNAK	TKPREEQ	YNNTRV	VSVLVLH	362
Db	356	rtlskpgv	rapqvvy	lpppee	entk	kkvltlcmvtd	415
Qy	363	KTISAKAQ	PREQVYV	LPPSRDEL	TKNQVSL	CLVKGQF	422
Db	416	tepvldsdg	yfmyskl	rveknwv	rnscysv	vhgelhnh	469
Qy	423	TPVLDSDG	SEFFLY	SKLTVDKS	RMQGNV	FSCSYMHEA	476

```

RESULT      8
ENTRY
TITLE      Ig gamma-2b chain precursor - mouse
ORGANISM   Mus musculus #common name house mouse
DATE       30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change
           23-Mar-1993
ACCESSIONS S01321
REFERENCE   S01320
AUTHORS    de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.;
           Fiers, W.
JOURNAL    Eur. J. Biochem. (1988) 176:287-295
#TITLE     Expression in non-lymphoid cells of mouse recombinant
           immunoglobulin directed against the tumour marker human
           placental alkaline phosphatase.
#cross-references M01D:88329081
#accession      S01321
#molecule_type mRNA
#residues       1-475 #label DEI
#cross-references EMBL:X13188
#note           this sequence was determined from the differentiated
           gene
FEATURE
1-19
20-475
SUMMARY

```

```
Query Match      54.1%; Score 1863; DB 12; Length 475;
Best Local Similarity 54.5%; Pred. No. 2.27e-237;
Matches 263; Conservative 99; Mismatches 106; Indels 15; Gaps 8;
```

Qy	1	MKHWFLLLVAAPRWLISVQVQJQSGPGLWQSETLSLTCASVSGSISGGYGMWIRQP	60
Db	60	tqgqlwlgelypgsgnpyfnefkfkatltvdkeastaylhlesltedseavyfcagpr	119
Qy	61	PKRGLEWGFSGFYSSGNTYNNPJKSQVTIISTDTKNQFSLKINSMTAADTAVYVCVRD	120
Db	120	--gv--gll--p--fgywggtlvtasaaktppsvyplagpcgdtgsevtlglvkgypfp	173
Qy	121	LFSGWGMVNNWFDVWGPCVLVTVSSASTKGPVFLAPSSKSTSGGTAALGCLVKDYFP	180
Db	174	esvvtvtnsgslessvhsfpallqz--glytmsssvtpsestwpseqvtvcsvahpaesattv	232
Qy	181	EPVTVSNWSGALTSGVHFFNAVLOSGSLYSLSVVTVPSSSLGTQTYTCNNWHKPSNWK	240
Db	233	dkklepsqptetlnpcpcckechkcpapnleggpvsfifpnikdvlmialtpkvtcvvv	292
Qy	241	DKKAEPKSCDKT--HTCPCP-----PAPELLGGPSVFLFPKPKDITMISRTPEVTCVV	293
Db	293	dvseddpcdvqswfvnnvnevltaqtqthredynstirvvsalpiqhdmagkefcvkn	352
Qy	294	DVSHEDPEWKFNNYVDGEVHNNAKTPREEQYNSTVRVSVLTVLHQDWLNGKEYKCKVCS	353
Db	353	nkdipaiertieiklgivrapqyilepppeqlsrkdsrlcslavgfespediaevetan	412
Qy	354	NKALAPATEKTSKAGQPREQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEHESN	413
Db	413	qhteenykdtapvldegdsyfiysklmnmktektdsfscnvrhheqlknylkktilers	472
Qy	414	GQPENNYKTPPVLDSGDSFFLYSKLITVDKSRMQQGNVSCSWHEALHNHYTQKSLSLS	473
Db	473	pgk	475
Qy	474	pgk	476

```

RESULT      9
ENTRY       Ig gamma-2a chain (mab735) - mouse
TITLE       Ig gamma-2a chain (mab735) - mouse
ORGANISM    Mus musculus #common name house mouse
DATE        07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
            20-Aug-1994
ACCESSIONS  S40295
REFERENCE    S40295
            #authors
            Kleibert, S.; Kratzin, H.D.; Zimmermann, B.; Vaessen, M.;
            Prosch, M.; Weisgerber, C.; Bitter-Suermann, D.;
            Hilschmann, N.
            #submission
            submitted to the EMBL Data Library, January 1993
            #description
            Primary structure of the murine monoclonal IgG2a antibody
            mab735 against '(2-8) polysialic acid. 2. Amino acid
            sequence of the heavy (H-) chain Fc' region.
            #accession
            S40295
            #molecule_type
            protein
            #residues
            1-446 #label KLE
GENETICS
            #map position 12
KEYWORDS     disulfide bond; glycoprotein; immunoglobulin; pyroglutamic
            acid
FEATURE
            1-446
            #product Ig gamma-2a chain #status experimental #label
            MATN
            1-117
            #domain V-D-J region #label VDJ\
            118-446
            #domain C region #label CHR\
            118-214
            #domain C1 region #label CH1\
            215-230
            #region hinge\

```


61 gyls₁ssvt₁vpss₁lqtq₁tytcnvn₁hkp₁sn₁t₁kvd₁kr₁vel₁ktpl₁gdt₁t₁htc₁prc₁pep₁ksc₁ 120

Db 204 pvl₁dsdgsfflyskltvdksrwqggnvfscsvmhealnhhtqskls₁spgk 255
 |||||
 Qy 425 pvl₁dsdgsfflyskltvdksrwqggnvfscsvmhealnhhtqskls₁spgk 476

* RESULT 14

```

ENTRY .
TITLE      Ig gamma chain C region - chimpanzee
ORGANISM   #formal_name Pan troglodytes #common_name chimpanzee
DATE       23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change
          12-Apr-1995
ACCESSIONS PT0207
REFERENCE   PT0207
#authors    Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
#journal     Mol. Immunol. (1991) 28:319-322
#title       Nucleotide sequence of chimpanzee Cc and hinge regions.
#cross-references MUID:91287716
#accession   PT0207
#molecule_type mRNA
##residues_ 1-234 ##label EHR
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
SUMMARY        #length 234 #molecular-weight 26330 #checksum 6128

Query Match 48.7%; Score 1677; DB 5; Length 234;
Best Local Similarity 98.3%; Pred. No. 5.93e-211;
Matches 230; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1  entkvdkvkpeksdthtcpcapellqgqsvflfppkpkdtlmierptcvrvdv 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 236  SNTKVDKKAEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDDV 295
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61  shedpevkfnyvqgvhnnaktprceqgnatyrvsvltvlhqdwlngkeykckvank 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 296  SHEDPEVKFNWYVDGVEVHNAKTRPEEQNTYRVSVLTVLHQLDWLNGKEYKCKVSNK 355
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121  alpapietkiskagqprepyvtlpsrdeltnkqvwelclvkgfypsdiavewessgq 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 356  ALPAPIEKTISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 415
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181  pennykttppvldsdgfflyskltvdksrwqqgnvfscsvmhealnhnhtqks 234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 416  PENNYKTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVSMHEALNHNHTQKS 469
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
ENTRY      GHRB
TITLE      Ig gamma chain C region - rabbit
ORGANISM   #formal_name Oryctolagus cuniculus #common_name domestic
          rabbit
DATE       #sequence_revision 15-Nov-1984 #text_change 04-Nov-1994
ACCESSIONS A91749; A90290; A93928; A90245; A94416; A02161
REFERENCE   A91749
#authors    Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
#journal     Immunogenetics (1983) 18:387-397
#title       Nucleotide sequence of a rabbit IgG heavy chain from the
          recombinant F-1 haplotype.
#cross-references MUID:84030930
#accession   A91749
#molecule_type mRNA
##residues_ 1-323 ##label BER
##note       this sequence has the d12 allotypic marker, 104-Thr, and
          the e14 marker, 185-Thr
REFERENCE   A90290
#authors    Pratt, D.M.; Mole, L.E.
#journal     Biochem. J. (1975) 151:337-349
#title       Sequence studies on the constant region of the Fd sections of
          rabbit immunoglobulin G of different allotype.
#cross-references MUID:76135469
#accession   A90290

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#molecule_type protein
##residues_ 1-47, 'E', 49-71, 'PV', 72-128 ##label PRA
REFERENCE   A93928
#authors    Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight,
          K.L.
#journal     Proc. Natl. Acad. Sci. U.S.A. (1982) 79:6018-6022
#title       Heavy chain genes of rabbit IgG; isolation of a cDNA encoding
          gamma heavy chain and identification of two genomic C-gamma
          genes.
#cross-references MUID:83299917
#accession   A93928
#molecule_type mRNA
##residues_ 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266
          ##label MAR
##note       this sequence has the d11 allotypic marker, 104-Met, and
          the e15 allotypic marker, 185-Ala
REFERENCE   A90245
#authors    Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
#journal     Biochem. J. (1970) 116:249-259
#title       Sequence studies of the Fd section of the heavy chain of
          rabbit immunoglobulin G.
#cross-references MUID:70110015
#accession   A90245
#molecule_type protein
##residues_ 132-143, 'E', 145-161 ##label FRU
REFERENCE   A94416
#authors    Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
          in Gamma Globulins, Nobel Symp. 3, Killander, J., ed.,
          pp.109-127, Almqvist and Wiksell, Stockholm, 1967
#accession   A94416
#molecule_type protein
##residues_ 129-131, 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D',
          202-217, 'E', 219-232, 'Q', 234-245, 'D', 247-255, 'G',
          257-259, 'D', 261-265, 'D', 267-279, 'W', 281-283, 'S',
          285-322 ##label HIL
##note       this has the e15 allotypic marker, 185-Ala
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
FEATURE
20-82.
130-199
236-303
SUMMARY      #length 323 #molecular-weight 35404 #checksum 1467

Query Match 48.5%; Score 1669; DB 2; Length 323;
Best Local Similarity 70.0%; Pred. No. 8.09e-210;
Matches 229; Conservative 46; Mismatches 45; Indels 7; Gaps 3;

Db 4  kapsvflapccgdtpestvtlqclvkgylpepvtvtwnsgltngvtftpsvrgesgly 63
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Qy 150  KPSVFLAPSKSTSGTAALGCLVKDIFPEPTVTVSWNSGALTSCVHTFPAVLASSGLY 209
    :||||| ||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 64  slssvsvetlssq---qpvtcnvahpatntkvdktvapstcskp-tcqp---pellqgpav 116
    ||||| :||| | ||| :||| ||||| | :| | ||||| ||||| |||||
Qy 210  SLSSVTVPSLSGLGTQTYICNVNHRKPSNTKVDKKAEPKSCDKTHTCPCPAPELLGGPSV 269
    ||||| :||| ||||| :||| :||| :||| :||| :||| :||| :|||
Db 117  flfppkpkdtlmisrptcvrvdvqddpevqftwyinneqvartarpplreqqfnati 176
    :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 270  FLFPPKPKDTLMISRPTCVTVVDVDSHEDPEVKFNWYVDGVEVHNAKTRPEEQYNSTY 329
    :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 177  rvvtlpthqdlrgkfkckvhnkalpapietkiskargqpkvkvymgpreelss 236
    ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 330  RWSVSLVTLHQDLWLNKGEYKCKVSNKALPAPIEKTISKAGQPREPQVYTLPPSRDELTK 389
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 237  rsveltcmingfypsdiavewekngkaednykttpavldedgsyflynklevptsewqrg 296

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Dec 17 15:27

US-08-487-550-12 tpr

19

Qy 390 NQVSLTCLVKGFPDIAVEESNGQPNKYTPPVLDSDGSFFLYSKLTVDKSRWQQG 449

Db 297 dvftcsymhealhnhytqksiarspgk 323

Qy 450 NVFSCSYMHEALHNHYTKSLSPGK 476

Search completed: Tue Dec 17 15:41:48 1996
Job time : 55 secs.

M P S R C H

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 17 15:42:06 1996; MasPar time 10.04 Seconds

Tabular output not generated. 824.078 Million cell updates/sec

Title: >US-08-487-550-12

Description: (1-476) from US08487550.pep

Perfect Score: 3442

Sequence: 1 MKHLWFFLLVVAAPRWLSQ.....MHEALNHHTQKSLSPCK 476

Scoring table: PAM 150

Gap 11

Searched: 49340 seqs, 17385503 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot32

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9

Statistics: Mean 48.577; Variance 85.626; scale 0.567

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	2339	68.0	330	3	GC1_HUMAN	IG GAMMA-1 CHAIN C RE	0.00e+00
2	2133	62.0	326	3	GC2_HUMAN	IG GAMMA-2 CHAIN C RE	0.00e+00
3	2133	62.0	327	3	GC4_HUMAN	IG GAMMA-4 CHAIN C RE	0.00e+00
4	1669	48.5	323	3	GC_RABIT	IG GAMMA CHAIN C REGI	0.00e+00
5	1616	46.9	329	3	GC2_CAVPO	IG GAMMA-2 CHAIN C RE	0.00e+00
6	1590	46.2	290	3	GC3_HUMAN	IG GAMMA-3 CHAIN C RE	0.00e+00
7	1582	46.0	326	3	GC1_RAT	IG GAMMA-1 CHAIN C RE	0.00e+00
8	1584	46.0	329	3	GC3_MOUSE	IG GAMMA-3 CHAIN C RE	0.00e+00
9	1570	45.6	398	3	GC3_MOUSE	IG GAMMA-3 CHAIN C RE	0.00e+00
10	1566	45.5	324	3	GC1_MOUSE	IG GAMMA-1 CHAIN C RE	0.00e+00
11	1559	45.3	329	3	GC_RAT	IG GAMMA-2C CHAIN C R	0.00e+00
12	1559	45.3	393	3	GC1_MOUSE	IG GAMMA-1 CHAIN C RE	0.00e+00
13	1549	45.0	330	3	GC4_MOUSE	IG GAMMA-2A CHAIN C R	0.00e+00

14	1546	44.9	333	3	GC_B_RAT	IG GAMMA-2B CHAIN C R	0.00e+00
15	1542	44.8	399	3	GCAB_MOUSE	IG GAMMA-2A CHAIN C R	0.00e+00
16	1518	44.1	335	3	GCAB_MOUSE	IG GAMMA-2A CHAIN C R	0.00e+00
17	1501	43.6	322	3	GC_B_RAT	IG GAMMA-2A CHAIN C R	0.00e+00
18	1478	42.9	336	3	GC_B_MOUSE	IG GAMMA-2B CHAIN C R	0.00e+00
19	1471	42.7	405	3	GC_B_MOUSE	IG GAMMA-2B CHAIN C R	0.00e+00
20	630	18.3	146	4	HV2I_HUMAN	IG HEAVY CHAIN PRECUR	8.14e-111
21	588	17.1	129	4	HV2F_HUMAN	IG HEAVY CHAIN V-II R	2.92e-101
22	539	15.7	353	1	ALC1_HUMAN	IG ALPHA-1 CHAIN C RE	3.45e-90
23	532	15.5	353	1	ALC1_GORGO	IG ALPHA-1 CHAIN C RE	1.30e-88
24	527	15.3	116	4	HV60_MOUSE	IG HEAVY CHAIN PRECUR	1.72e-87
25	527	15.3	344	1	ALC_MOUSE	IG ALPHA CHAIN C REGI	1.72e-87
26	528	15.3	455	5	MUC_MOUSE	IG MU CHAIN C REGION	1.03e-87
27	515	15.0	476	5	MUC_MOUSE	IG MU CHAIN C REGION	8.47e-85
28	503	14.6	116	4	HV61_MOUSE	IG HEAVY CHAIN PRECUR	4.11e-82
29	504	14.6	137	4	HV46_MOUSE	IG HEAVY CHAIN PRECUR	2.45e-82
30	498	14.5	391	5	MUCB_HUMAN	IG MU HEAVY CHAIN DIS	5.38e-81
31	499	14.5	454	5	MUC_HUMAN	IG MU CHAIN C REGION	3.22e-81
32	495	14.4	428	3	EPC_HUMAN	IG EPSILON CHAIN C RE	2.51e-80
33	493	14.3	458	5	MUC_RABIT	IG MU CHAIN C REGION	7.02e-80
34	488	14.2	340	1	ALC2_HUMAN	IG ALPHA-2 CHAIN C RE	9.15e-79
35	488	14.2	388	3	EPC1_MOUSE	IG EPSILON CHAIN C RE	9.15e-79
36	485	14.1	450	5	MUC_GANFA	IG MU CHAIN C REGION	4.26e-78
37	483	14.0	117	4	HV62_MOUSE	IG HEAVY CHAIN PRECUR	1.19e-77
38	477	13.9	117	4	HV2G_HUMAN	IG HEAVY CHAIN V-II R	2.57e-76
39	478	13.9	429	3	EPC_RAT	IG EPSILON CHAIN C RE	1.54e-76
40	480	13.9	479	5	MUCB_RABIT	IG MU CHAIN C REGION	5.53e-77
41	475	13.8	457	5	MUC_SUNMU	IG MU CHAIN C REGION	7.15e-76
42	470	13.7	147	4	HV2H_HUMAN	IG HEAVY CHAIN PRECUR	9.22e-75
43	465	13.5	144	4	HV43_MOUSE	IG HEAVY CHAIN PRECUR	1.18e-73
44	463	13.5	454	5	MUC_MESAU	IG MU CHAIN C REGION	3.29e-73
45	461	13.4	423	3	EPC2_MOUSE	IG EPSILON CHAIN C RE	9.12e-73

ALIGNMENTS

RESULT	ID	GC1_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;				
DT	21-JUL-1986	(REL. 01, CREATED)			
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)			
DT	01-MAR-1992	(REL. 21, LAST ANNOTATION UPDATE)			
DE	IG GAMMA-1 CHAIN C REGION.				
GN	IGHG1.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 82274238.				
RA	ELLISON J.W., BERTSON B.J., HOOD L.E.;				
RL	NUCLEIC ACIDS RES. 10:4071-4079(1982).				
RN	[2]				
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).				
RX	MEDLINE; 71064024.				
RA	CUNNINGHAM B.A., RUTISHAUSER U., GALL W.E., GOTTlieb P.D.,				
RA	WAXDAL M.J., EDELMAN G.M.;				
RL	BIOCHEMISTRY 9:3161-3170(1970).				
RN	[3]				
RP	SEQUENCE OF 136-329 (EU).				
RX	MEDLINE; 71064025.				
RA	RUTISHAUSER U., CUNNINGHAM B.A., BENNETT C., KONIGSBERG W.H.,				
RA	EDELMAN G.M.;				
RL	BIOCHEMISTRY 9:3171-3181(1970).				

RN [4]
 R2 SEQUENCE (MYELOMA PROTEIN NIE).
 RX MEDLINE; 77070269.
 RA PONTING H., HILSCHMANN N.;
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1571-1604 (1976).
 RN [5]
 RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
 RX MEDLINE; 83289131.
 RA SCHMIDT W.E., JUNG H.-D., PALM W., HILSCHMANN N.;
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 364:713-747 (1983).
 RN [6]
 RP DISULFIDE BONDS.
 RX MEDLINE; 71064027.
 RA GALL W.E., EDELMAN G.M.;
 RL BIOCHEMISTRY 9:3188-3196 (1970).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE; 77070267.
 RA DREKER L., SCHWARZ J., REICHEL W., HILSCHMANN N.;
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1515-1540 (1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE; 81208100.
 RA DEISENHOFER J.;
 RL BIOCHEMISTRY 20:2361-2370 (1981).
 CC -1- NIE HAS THE GIM(17) ALLOTYPE MARKER, 97-K, & THE GIM(1) MARKERS,
 CC 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM
 CC (NON-1) MARKERS.
 CC -1- NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.
 CC -1- EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155, 166, 177,
 CC 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.
 CC -1- KOL ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 198,267&272.
 DR EMBL; J00228; J00228.
 DR PIR; A02146; GHU.
 DR PDB; 1FC1; 15-JUL-92.
 DR PDB; 1FC2; 15-JUL-92.
 DR NIM; 147100; 11TH EDITION.
 DR PROSITE; PS00290; IG MHC.
 KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN; 3D-STRUCTURE.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISULFID 27 83
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT VARIANT 97 97 K -> R (IN GIM(3) MARKER).
 FT VARIANT 239 239 D -> E (IN GIM(NON-1) MARKER).
 FT VARIANT 241 241 L -> M (IN GIM(NON-1) MARKER).
 FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
 FT STRAND 123 126
 FT HELIX 130 134
 FT TURN 136 137
 FT STRAND 141 148
 FT STRAND 158 162
 FT TURN 163 164
 FT STRAND 165 166
 FT STRAND 175 178
 FT STRAND 183 190

FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 206
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 240
 FT TURN 241 242
 FT STRAND 245 256
 FT STRAND 260 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 312
 FT TURN 313 314
 FT TURN 316 317
 FT STRAND 320 324
 SQ SEQUENCE 330 AA; 36106 MW; 642285 CN;
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 Best Local Similarity 99.7%; Pred. No. 0.00e+00;
 Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 astkpsvflapsskatsggtaalqclvkvdyfpeptvsmnsagaltsgvhtfpavlgss 60
 QY 147 ASTKPSVFLAPSSKSTSGGTAALQCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 206
 Db 61 gylselsvvtvpssslgtqiyicnvnhkpkentkvdkvpekscdtkhtccppapellgg 120
 QY 207 GLYSLSVVTVPSSSLGTQIYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266
 Db 121 psvflfppkpkdtlmiartpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreegn 180
 QY 267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYN 326
 Db 181 styrvsvltvlhqdwlngkeykckvsnkalpapietkakiakgqgpreqvyltppsrde 240
 QY 327 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 386
 Db 241 lcknqvslclvkgyfspdlaivesngqpennykttppvldadgsfflyskltvdkerw 300
 QY 387 LTKNQVSLTCLVKGYFSPDIAVESNGQPENNYKTTTPPVLDSDGSFELYSKLTVDKGRW 446
 Db 301 qggnvfscsvmeahlnhytqkslslepgk 330
 QY 447 QGQNVFSCSVMEAHLNHYTQKSLSLSPGK 476
 RESULT 2
 ID GC2 HUMAN STANDARD; PRT; 326 AA.
 AC P01859;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE IG GAMMA-2 CHAIN C REGION.
 GN IGHG2.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.

[1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 82197621.
 RA ELLISON J.W., HOOD L.E.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 79:1984-1988 (1982).
 RN [2]
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE; 81007873.
 RA WANG A.-C., TUNG E., FUDENBERG H.H.;
 RL J. IMMUNOL. 125:1048-1054 (1980).
 RN [3]
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE; 80001357.
 RA CONNELL G.E., PARR D.M., HOFMANN T.;
 RL CAN. J. BIOCHEM. 57:758-767 (1979).
 RN [4]
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE; 80114419.
 RA HOFMANN T., PARR D.M.;
 RL MOL. IMMUNOL. 16:923-925 (1979).
 RN [5]
 RP ZIE, REVISIONS TO 25; 59; 60 AND 264-268.
 RA HOFMANN T., PARR D.M.;
 RL SUBMITTED (MAR-1980) TO THE PIR DATA BANK.
 RN [6]
 RP SEQUENCE OF 1-121 (DOT).
 RA STOPPINI M., BELLOTTI V., NEGRI A., MERLINI G., GARVER F., FERRI G.;
 RL EUR. J. BIOCHEM. 0:0-0 (1995).
 RN [7]
 RP MYELOMA PROTEIN SA, DISULFIDE BONDS.
 RX MEDLINE; 72033500.
 RA MILSTEIN C., FRANGIONE B.;
 RL BIOCHEM. J. 121:217-225 (1971).
 RN [8]
 RP SA, DISULFIDE BONDS.
 RX MEDLINE; 69064124.
 RA FRANGIONE B., MILSTEIN C., PINK J.R.L.;
 RL NATURE 221:145-148 (1969).
 DR ENBL; V00554; V00554.
 DR PIR; A02148; G2H0.
 DR HSP; P01857; 1BBJ.
 DR MIM; 147110; 11TH EDITION.
 DR PROSITE; PS00290; IG_MHC.
 RW IMMUNOGLOBULIN C REGION.
 FT NON TER 1 1
 FT DOMAIN 1 98
 FT DOMAIN 99 110
 FT DOMAIN 111 219
 FT DOMAIN 220 326
 FT DISULFID 14 14
 FT DISULFID 27 83
 FT DISULFID 102 102
 FT DISULFID 103 103
 FT DISULFID 106 106
 FT DISULFID 109 109
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT VARIANT 60 60
 FT SITE 156 156
 FT MOD_RES 326 326
 SQ SEQUENCE 326 AA; 35384 MW; 629390 CN;

Query Match 62.0%; Score 2133; DB 3; Length 326;
 Best Local Similarity 90.9%; Pred. No. 0.00e+00;

Matches 300; Conservative 15; Mismatches 11; Indels 4; Gaps 3;
 Db 1 astkqpvfplapcrtstsestaalqclvkdypcpvtvawmsgaltsqvhftfavlges 60
 QY 147 ASTKGFVFFLAPSSKSTSGTAALGCLVKDYFPEFTVSNWNSGALTSGVHTFPAVLQSS 206
 Db 61 glyelasevtvpsenfqtqcytcnvdkhpkantkvdkverkc--ve-cpcpappv-ag 116
 QY 207 GLYSLSSVWTFSSSLGTQTYICNVNHRPNTKVDKAEKPSCDKTHTCPPCPAPPELLGG 266
 Db 117 psvflfppkpkdtlmisrtpevtcvvvdvshedpevfqfnwvgdvvevhnaktkpreeqfn 176
 QY 267 PSVFLFPPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWVGVEVHNAKTKPREEQYN 326
 Db 177 stfrvsvltvvhqdwlngkeykckvsnkglpapiekiaktkggprepyvtlpsree 236
 QY 327 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
 Db 237 mtkngvaltclvkfypsdiavewesngqpennnykttppmlsdgsefflyskltvdksrw 296
 QY 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKGRW 446
 Db 297 qggnvfscvmhealhhnytcqelslspgk 326
 QY 447 QGQNVFSCVMHEALHHNYTKQKSLSLSPGK 476
 RESULT 3
 ID GC4 HUMAN STANDARD; PRT; 327 AA.
 AC P01861;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
 DE IG GAMMA-4 CHAIN C REGION.
 GN IGHG4.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 83157104.
 RA ELLISON J.W., BUxbaum J.N., HOOD L.E.;
 RL DNA 1:11-18 (1981).
 RN [2]
 RP SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE; 70207560.
 RA PINK J.R.L., BUTTERRY S.H., DE VRIES G.M., MILSTEIN C.;
 RL BIOCHEM. J. 117:33-47 (1970).
 DR PIR; A02150; G4H0.
 DR HSP; P01857; 1BBJ.
 DR MIM; 147130; 11TH EDITION.
 DR PROSITE; PS00290; IG_MHC.
 RW IMMUNOGLOBULIN C REGION.
 FT NON TER 1 1
 FT DOMAIN 1 98
 FT DOMAIN 99 110
 FT DOMAIN 111 220
 FT DOMAIN 221 327
 FT DISULFID 14 14
 FT DISULFID 27 83
 FT DISULFID 106 106
 FT DISULFID 109 109
 FT DISULFID 141 201
 FT DISULFID 247 305
 CH1.
 HINGE.
 CH2.
 CH3.
 INTERCHAIN (WITH A LIGHT CHAIN).
 INTERCHAIN (WITH A HEAVY CHAIN).
 INTERCHAIN (WITH A HEAVY CHAIN).
 INTERCHAIN (WITH A HEAVY CHAIN).

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DR HSP; P01857; 1FC1.
DR MM; 147120; 11TH EDITION.
DR PROSITE; PS00290; IG MHC.
KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN.

FT DOMAIN 12 73 HINGE.
FT DOMAIN 74 183 CH2.
FT DOMAIN 184 289 CH3.
FT REPEAT 29 43
FT REPEAT 44 58
FT REPEAT 59 73
FT MOD_RES 1 1
FT CARBOHYD 6 6
FT DISULFID 7 7
FT DISULFID 24 24 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 27 27 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 33 33 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 39 39 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 42 42 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 48 48 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 54 54 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 57 57 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 63 63 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 69 69 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 72 72 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT CARBOHYD 140 140
FT MOD_RES 290 290
FT VARIANT 126 127 REMOVED POST-TRANSLATIONALLY.
FT VARIANT 134 134 QV -> EB (IN ZUC).
FT VARIANT 139 139 P -> L (IN OMM).
FT VARIANT 182 182 F -> Y (IN OMM).
FT VARIANT 227 227 T -> A (IN OMM).
FT VARIANT 227 227 S -> N (IN OMM).
FT VARIANT 227 227 MISSING (IN ZUC).
FT VARIANT 279 279 F -> Y (IN OMM).
SQ SEQUENCE 290 AA; 32331 MW; 485009 CN;

Query Match 46.2%; Score 1590; DB 3; Length 290;

Best Local Similarity 90.1%; Pred. No. 0.00e+00;

Matches 210; Conservative 17; Mismatches 6; Indels 0; Gaps 0;

Db 58 pepkscdtpcpccpacellgppavflfpkpkdtlmisrtpevtcvvvdvshedpevq 117

Qy 244 AEPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 303

Db 118 flwydygvqhnaktkpreqdfnstfrvavltvlnqwidgkeykckvsnkalpapek 177

Qy 304 FNWYDGVGVHNAKTKPREQNSTYRWVSLVTLHQDLNGKEYKCKVSNKALPAPIEK 363

Db 178 tsktkgqprepytllpreemtknqvalcclvkgyfypsdiavewesegqennnytt 237

Qy 364 TTSKAKQPREPYVTLPPSRDELTKNQVSLTCLVKGYFSPYDIAVWESNGQPENNYKT 423

Db 238 pmlidsgafflysklvtksrqgnifacsymhealhnrfckslslspgk 290

Qy 424 PPVLDSGFFLYSKLVDKSRHQQGVFSCVMHEALHNHYTKSLSPGK 476

RESULT 7

ID GC1 RAT STANDARD; PRT; 326 AA.

AC P20759;

DT 01-FEB-1991 (REL. 17, CREATED)

DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)

DE IG GAMMA-1 CHAIN C REGION, LAST ANNOTATION UPDATE)

OS RATTUS NORVEGICUS (RAT).

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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 89232738.

RA BRUEGGEMANN M.;

RL GENE 74:473-482(1988).

DR PIR; PS0017; PS0017.

DR HSP; P01857; 1FC1.

DR PROSITE; PS00290; IG MHC.

KW IMMUNOGLOBULIN C REGION; GLYCOPROTEIN.

FT NON_TER 1 1

FT DOMAIN 1 97 CH1.

FT DOMAIN 98 112 HINGE.

FT DOMAIN 113 219 CH2.

FT DOMAIN 220 326 CH3.

FT DISULFID 27 82

FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 140 200

FT DISULFID 246 304

FT CARBOHYD 176 176 POTENTIAL.

SQ SEQUENCE 326 AA; 35946 MW; 630958 CN;

Query Match 46.0%; Score 1582; DB 3; Length 326;

Best Local Similarity 63.3%; Pred. No. 0.00e+00;

Matches 209; Conservative 60; Mismatches 57; Indels 4; Gaps 4;

Db 1 aettapvypplagtalknsmtvlglclvkgyfpeptvtwsgalseghvhtfpavlg- 59

Qy 147 ASTRGPSVFPLAPSSKSTSGGTAALGLCKVDFPEPTVSMNSGALTSGVHTFPAVLQSS 206

Db 60 glyltlesvtvpswtvscnvahpaestkvdklvprncg-gd-ckpcictgs-ev 116

Qy 207 GLYSLSVTVTVSSSLGTQTYICNVNHPNNTKVDKKAEPKSCDKTHTCPPAPPELLGG 266

Db 117 ssvflfppkpkdvltitltpkvtcvvvdvshedpevfewfvdvdevhtaqtrppegfn 176

Qy 267 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVFENWYDGVGVHNAKTKPREQYN 326

Db 177 stfsvselplhqdwlngtrfrckvtasaafspektsiekpgrtqvphvymtptkee 236

Qy 327 STYRWVSLVTLHQDLNGKEYKCKVSNKALPAPIEKTSKAGQPREPQVYTLPPSRDE 386

Db 237 mtqneveitcmvkgfyppdiyevqmgqgqenykntpctmdtdsgyflysklnvkkew 296

Qy 387 LTKQVSLTCLVKGYFSPYDIAVWESNGQPENNYKTTPPVLDSDGSFELYSKLVTKSRW 446

Db 297 qgngtftcsavlheglhnhhtekslshspgk 326

Qy 447 QQGVFSCVMHEALHNHYTKSLSPGK 476

RESULT 8

ID GC3 MOUSE STANDARD; PRT; 329 AA.

AC P22436;

DT 01-AUG-1991 (REL. 19, CREATED)

DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)

DT 01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)

DE IG GAMMA-3 CHAIN C REGION, SECRETED FORM.

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC	EUTHERIA; RODENTIA.
RP	[1]
RN	SEQUENCE FROM N.A.
RR	MEDLINE; 85027161.
RA	WELS J.A., WORD C.J., RIMM D., DER-BALAN G.P., MARTINEZ H.M.,
RX	TUCKER P.W., BLATTNER F.R.;
RA	EMBO J. 3:2041-2046(1984).
RL	DR EMBL; J00451; J00451.
DR	DR EMBL; J00451; J00451.
DR	DR PIR; B02156; G3MSC.
DR	HSSP; P01857; 1FC1.
DR	PROSITE; PS00290; IG MHC.
DR	IMMUNOGLOBULIN C REGION; GLYCOPROTEIN; TRANSMEMBRANE;
KW	ALTERNATIVE SPLICING.
KW	NON TER 1
FT	DOMAIN 1 97
FT	DOMAIN 98 113
FT	DOMAIN 114 223
FT	DOMAIN 224 327
FT	DOMAIN 329 AA; 362228 MW; 617081 CN;
SQ	SEQUENCE 329 AA; 362228 MW; 617081 CN;

Query Match 46.0%; Score 1584; DB 3; Length 329;
Best Local Similarity 63.6%; Pred. No. 0.00e+00;
Matches 210; Conservative 61; Mismatches 57; Indels 2; Gaps 2;

Db	1	t	t	t	a	p	s	v	p	l	p	g	c	d	t	a	g	s	e	v	l	g	c	i	v	k	y	f	p	e	p	t	v	k	w	y	g	a	l	s	e	g	v	r	t	s	v	l	g	s	g	59				
Qy	148	S	T	K	G	S	V	F	L	P	L	A	P	S	K	S	T	S	G	T	A	L	G	L	V	K	D	Y	F	P	E	P	V	T	S	M	S	G	A	L	T	S	G	V	H	T	P	A	V	L	G	S	G	207		
Db	60	f	y	e	a	s	l	v	p	s	e	t	w	p	s	e	t	v	a	h	a	p	a	e	l	i	k	r	i	e	p	k	i	p	k	s	t	p	p	s	c	p	p	g	n	i	l	g	119							
Qy	208	L	Y	S	L	S	V	V	T	P	S	S	L	G	T	Q	T	Y	T	C	N	N	H	K	P	S	N	T	K	D	K	A	E	P	K	S	C	-	K	T	H	T	C	P	C	P	A	E	L	L	G	266				
Db	120	p	s	v	i	f	p	p	k	d	a	l	m	i	s	t	p	k	t	c	v	v	d	s	e	d	p	d	v	h	s	f	v	d	n	k	e	v	h	t	a	w	t	q	p	r	e	a	q	n	179					
Qy	267	P	S	V	F	P	P	K	P	K	D	L	M	I	S	R	T	P	E	V	T	C	V	V	D	S	E	D	E	V	K	F	N	Y	D	G	V	E	V	H	N	A	K	T	R	E	Q	Y	N	326						
Db	180	a	t	r	v	s	a	l	p	i	q	d	w	m	g	k	e	f	k	c	v	n	n	k	a	i	p	a	p	i	e	r	t	k	p	k	r	a	c	t	p	q	v	t	i	p	p	r	e	q	239					
Qy	327	S	T	R	V	S	V	L	T	L	Q	D	M	A	G	K	E	Y	C	K	V	S	N	K	A	P	A	P	I	E	K	T	S	K	A	K	G	Q	P	R	E	V	T	T	P	P	S	R	D	E	386					
Db	240	m	a	k	k	v	a	l	t	c	i	v	n	t	f	f	s	a	e	i	s	e	w	e	r	n	g	e	l	e	q	y	k	n	t	p	p	i	d	s	d	g	t	y	f	y	s	k	t	v	d	t	d	s	w	299
Qy	387	L	T	N	K	Q	S	V	T	C	L	V	R	G	F	P	S	D	I	A	V	E	S	N	G	O	P	E	N	N	Y	K	T	P	P	V	L	D	S	D	S	F	F	L	Y	S	K	L	T	V	D	K	S	R	446	
Db	300	l	q	e	a	f	t	c	s	v	h	e	a	l	m	h	n	t	h	t	k	n	s	r	p	k	329																													
Qy	447	Q	O	G	N	F	S	C	S	V	H	E	A	L	N	I	J	T	O	K	S	L	S	P	G	476																														

RESULT	9				
ID	GC3M MOUSE	STANDARD;	PRT;	398 AA.	
AC	P03987;				
DT	23-OCT-1986	(REL. 02, CREATED)			
DT	01-AUG-1991	(REL. 19, LAST SEQUENCE UPDATE)			
DT	01-AUG-1991	(REL. 19, LAST ANNOTATION UPDATE)			
DE	IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.				
OS	MUS MUSCULUS (MOUSE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; RODENTIA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RP					
RX	MEDLINE; 85027161.				
RA	WELS J.A., WORD C.J., RIMM D., DER-BALAN G.P., MARTINEZ H.M.,				
RA	TUCKER P.W., BLATTNER F.R.;				

RL	EMBO J. 3:2041-2046(1984).
RN	[2]
RP	SEQUENCE OF 328-398 FROM N.A.
RX	MEDLINE; 84041483.
RA	KOMAROMY M., CLAYTON L., ROGERS J., ROBERTSON S., KETTMAN J.,
RA	WALL R.;
RL	NUCLEIC ACIDS RES. 11:6775-6785(1983).
DR	EMBL; J00451; J00451.
DR	EMBL; V01526; V01526.
DR	PIR; A02155; G3MSM.
DR	HSP; P01857; IFC1.
DR	PROSITE; PS00290; IG_MHC.
KW	IMMUNOGLOBULIN C REGION; GLYCOPROTEIN; TRANSMEMBRANE;
KW	ALTERNATIVE SPLICING.
FT	NON_TER 1 1
FT	D0MAIN 1 FT CH1.
FT	D0MAIN 98 113 HINGE.
FT	D0MAIN 114 223 CH2.
FT	D0MAIN 224 327 CH3.
FT	TRANSEM 346 362 POTENTIAL.
FT	D0MAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT	CONFLICT 333 333 E -> G (IN REF. 2).
FT	CONFLICT 342 342 E -> Q (IN REF. 2).
FT	CONFLICT 388 388 P -> F (IN REF. 2).
SQ	SEQUENCE 398 AA; 43929 MW; 896835 CN;

Query Match 45.6%; Score 1570; DB 3; Length 398;
Best Local Similarity 63.4%; Pred. No. 0.00e+00;
Matches 208; Conservative 61; Mismatches 57; Indels 2; Gaps 2;

Db	1	tttapsvplvpqscdsqsvtlglcvkyfpepvtvkwnygalsegvrtvsevlqg-g	59
Qy	148	STKPSVTFPLAPSSKTSQGTAAALGLVKDFPEPVTVMWSNGALTSVGHTEPVAVLQSSG	207
Db	60	fysalseltvpsstwpstqvicnvahpaektellkrieipktpspgsscpgnllg	119
Qy	208	LYSLSLWTVPSSSLGTQTYICNVNHPKSNTKDKKAEPKSCD-KTHTCPPCPAPELLGG	266
Db	120	psvfiipfpkdaImIsItpkvtcvvddssddpvhvswfvdnkvhtawtqpreaqn	179
Qy	267	PSVFLFPKPKDITLMSRTPEVTCVVDVSHDEPEVKFNWYDVGVEVHNAKTKREQYN	326
Db	180	stfrvsaIplqhqdvmzqkfckcnvnnkaIpaIertIakpkractqgvvtippreq	239
Qy	327	STRVWVSLTVLHQDLNAGREYCKYSNKAIPALIEKTSKAKQGPREQVVTIPPSSRDE	386
Db	240	mskkvslvtclvntfssaaivseawerngeleqdykntppildsdgtyfysklvtvdtdaw	299
Qy	387	LTKNQVSLTCLVRGFYPSDIAVENESGCPENNYKTPPVLDSGDSFFLYSKLTVDKSRW	446
Db	300	lqgeiftcsvvhlaIhhhtqmlsrsp	327
Qy	447	OQGNFVSCVMHEALHNHYTKQSLISLSP	474

RESULT	10
ID	GCI MOUSE
AC	P01868;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE	IG GAMMA-1 CHAIN C REGION.
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;


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RN  * [4]
RP  MYELOMA PROTEIN MOPC 173.
RX  MEDLINE; 74175517.
RA  BOURGOIS A., FOUGEREAU M., ROCCA-SERRA J.;
RL  EUR. J. BIOCHEM. 43:423-435(1974).
[5]
RP  MOPC 173, DISULFIDE BONDS.
RX  MEDLINE; 73056887.
RA  DE PREVAL C., FOUGEREAU M.;
RL  EUR. J. BIOCHEM. 30:452-462(1972).
DR  EMBL; V00798; V00798.
DR  PIR; A02152; G2MSA.
DR  HSP; P01857; IFC1.
DR  PROSITE; PS00290; IG-MHC.
KW  IMMUNOGLOBULIN C REGION.
FT  NON TER      1
FT  DISULFID    15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT  DISULFID    27 82
FT  DISULFID    107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID    110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID    112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID    144 204
FT  DISULFID    250 308
FT  MOD RES     330 330 REMOVED POST-TRANSLATIONALLY.
SQ  SEQUENCE     330 AA; 36389 MW; 643174 CN;

Query Match      45.0%; Score 1549; DB 3; Length 330;
Best Local Similarity 63.6%; Pred. No. 0.00e+00;
Matches 211; Conservative 52; Mismatches 65; Indels 4; Gaps

Db 1 akttapsvylapvcgdtgssvtlglclvkgyfpepvtltwnsgslssgwhfipavlqsd 60
QY 147 ASTKGPSVFPLAPSSKSTSGGTAAALCLVKIOYFPEPTVYVWNSNALTSGVHTFPVAVLQSS 206

Db 61 -lytlasevvtastwpasgeitcnvahpasatkvdkkieprg-ptikpcpcpcapnll 118
QY 207 GLYSLSSVTPVSSSLGTQTYICNVNHRKPSNTKVDKKAEPKSCDKTTCPPC--PAPELL 264

Db 119 ggsfvifppkikdlmlslspivtcvvvdseddpgvisfvnnvvhvhtaqtghred 178
QY 265 GGSFVIFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 324

Db 179 nstlrsvsalpihqdwmsgskfckvnmkdlpapiertiskpkgsavrpavvyvlppe 238
QY 325 YNSTRRVVSVLTVHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 384

Db 239 eamtktqvtlcmvtdfmpediyevwtngktelnkntepvldsgsfymysklrvekk 298
QY 385 DELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKS 444

Db 299 nwnrnysvscvvhqelnhnhhtktsfertpgk 330
QY 445 RMOQGVEFSCGVNHEALHNHYHNTKSLSPGK 476

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[illegible]

OC	EUTHERIA; RODENTIA.
(1)	
RN	SEQUENCE FROM N.A.
RP	MEDLINE; 89232738.
RX	
RA	BROEGGEMANN M.;
RL	GENE 74:473-482(1988).
DR	PIR; PS0018; PS0018.
DR	HSP; P01857; IFCI.
DR	PROSITE; PS00290; IG MHC.
KW	IMMUNOGLOBULIN C REGION.
ET	NON TER
FT	DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN) .
FT	DISULFID 27 80 INTERCHAIN (WITH A HEAVY CHAIN) .
FT	DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN) .
FT	DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN) .
FT	DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN) .
FT	DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN) .
FT	DISULFID 147 207 INTERCHAIN (WITH A HEAVY CHAIN) .
FT	DISULFID 253 311
SQ	SEQUENCE 333 AA; 36497 MW; 642683 CN;

Query Match 44.9%; Score 1546; DB 3; Length 333;
Best Local Similarity 64.0%; Pred. No. 0.00e+00;
Matches 215; Conservative 52; Mismatches 60; Indels 9; Gaps 4;

[illegible]

RESULT	15
ID	GCAM MOUSE STANDARD; PRT; 399 AA.
AC	P01865;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT	01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)
DE	IG GAMMA-2A CHAIN C REGION, MEMBRANE-BOUND FORM.
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 8222190.
RA	YAMAOKI-KATAOKA Y., NAKAI S., MIYATA T., HONGO T.;

Search completed: Tue Dec 17 15:42:46 1996
Job time : 40 secs.

Result No.	Score	Query		ID	Description	Pred. No.
		Match	Length			
1	3095	89.9	475	R3353	Monoclonal antibody D	4.71e-243
2	2850	82.8	467	R22759	Reshaped CD4 antibody	1.28e-222
3	2848	82.7	467	R32758	Reshaped CD4 antibody	1.88e-222
4	2819	81.9	470	R22757	Reshaped CAMPATH-1 an	4.90e-220
5	2791	81.1	481	S R2442	Reshaped of antibody	1.06e-217
6	2781	80.8	453	R33311	Humanised MaEl1 Versel	7.20e-217
7	2771	80.5	475	R20057	Heavy chain of 3D6 an	4.91e-216
8	2755	80.0	476	R31023	Antibody D heavy chai	1.06e-214
9	2719	79.0	459	R42066	Human anti-HBs heavy	1.06e-211
10	2716	78.9	461	R42162	Anti-HIV-1 recombinan	1.88e-211
11	2698	78.4	449	R74339	Completely humanised	5.94e-210
12	2678	77.8	477	R47453	chIT94.12 H3 heavy ch	2.75e-208

ALIGNMENTS

RESULT	1
ID	R93553 standard; Protein; 475 AA.
AC	R93553;
DE	20-AUG-1996 (first entry)
DD	Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.
DT	Polymerase chain reaction; primer; amplif;
KW	65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.
OS	KW
KS	Synthetic.

Key	Location/Qualifiers
FT	1..19
FT	/note= "Signal peptide"
FT	Protein 20..475
FT	/note= "Mature heavy chain"
FT	J08038178-A.
PN	13-FEB-1996.
PP	20-FEB-1995; 030742.
PR	18-FEB-1994; JP-021628.
PPA	(NIN) NISSHINO IND INC.
PPA	(TANA) TANAKA H.
PPA	WPI: 96-154852/16.
DR	N-PSDB; T18059.
DR	Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -
PT	produced by primer amplification, used in the diagnosis of HCMV
PT	infection
PT	Claim 4; Page 16-18; 22pp; Japanese.
PS	The sequences given in R93553-54 represent the heavy and light chains
CC	respectively of a monoclonal antibody against a 65 kD antigen of human
CC	

CC cyomegalovirus (hCMV). The DNA's encoding these sequences were
 CC amplified using the sequences given in T18040-58. The monoclonal
 CC antibody may be used in the diagnosis of hCMV.
 SQ Sequence 475 AA;

Query Match 89.9%; Score 3095; DB 16; Length 475;
 Best Local Similarity 91.6%; Pred. No. 4.71e-243;
 Matches 437; Conservative 16; Mismatches 21; Indels 3; Gaps 3;
 Db 1 mklhfflllvaaprwlslqldqgpglvkpseltlctvsgdsisrasygciqr 60
 Qy 1 MKHLFFLLVAAPRWLSQVQLQESGPGLVKPSSETLSLTCVAVSGSIS-GGIGWMIQ 59
 Db 61 ppkglewigtlyys-gstynpaelkervtisvdaamqfaliksavtaadtavycart 119
 Qy 60 PPKGLEWIGSFYSSGNTYTNPSIKSQVTISTDTSKNQFSIKLNSMTAADTAVYVCVRD 119
 Db 120 sp-qyydlitgsfpywgggtlvtvsaatkpgsvfplapasketaggtaalgclvkdyf 178
 Qy 120 RLFSVVGAVYNNWFDMWGPGLVTVSSASTKGPSTPLAPSSKSTSGGTAALGCLVKDYF 179
 Db 179 peptvsnegaltsgvhtfpavlqsglylsavvtvpsasltgttyicnvnkhpkantk 238
 Qy 180 PEPVTVSNAGLTSGVHTFPVAVLQSGGLYLSVSVTVPSSSLGTQTYICNVNKHPSNTK 239
 Db 239 vdkkpeksdktctpcpapellggpavflfpkpdkdtlmiertpervicvrvdshad 298
 Qy 240 VDKKAEPSCKDHTCFPCPAPELLGGPSVFLFPKPKDITLMSRTPEVTCWVDVSHED 299
 Db 299 pevkfnwydvgevnhaaktkpreeqnystyrsvvltvlhqdwlngkeyckvsnkalpa 358
 Qy 300 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDLWLNKKEYCKVSNKALPA 359
 Db 359 piektiskakgpreqvytlpssrdeltknqvelclvkgyfypsdiavewesngqpenn 418
 Qy 360 PIEKTISKAKGPREQVYTLPPSRDELTKNQVSLCLVKGYFSPSDIAVEMESNGQPENN 419
 Db 419 ykttpevlidsgsflyskltvdkswqgnvfscvmhealhnhytqkslslepgk 475
 Qy 420 YKTTPEVLIDSGSFFLYSKLTVDKSRQQGNVFSCVMHEALHNHYTQKSLSLSPCK 476

RESULT 2
 ID R22759 standard; Protein; 467 AA.

AC R22759;
 DT 20-OCT-1992 (first entry)
 DE Reshaped CD4 antibody heavy chain CD4VHNEW-Ser30.
 KW Antigen; CDR; complementarity determining region; graft rejection;
 KW autoimmune diseases; rheumatoid arthritis; allergy.
 OS Rattus rattus.

FH Key Location/Qualifiers

FT Peptide 1..19
 FT /note= "signal peptide"
 FT Peptide 20..467
 FT /note= "mature peptide"
 FT Region 50..54
 FT /note= "Complementarity determining region 1"
 FT Region 69..85
 FT /note= "Complementarity determining region 2"
 FT Region 118..126
 FT /note= "Complementarity determining region 3"
 PN W0205274-A.
 PD 02-APR-1992.
 PF 16-SEP-1991; G01578.

PR 17-SEP-1990; GB-020282.
 PA (GORMA) GORMAN S D.
 PI Clark M R, Cobbold S P, Gorman S D, Waldmann H.
 DR WPI; 92-132139/16.
 DR N-PSDB; Q23581.
 PT Humanisation of antibodies binding to human CD4 antigen - by
 PT mutation of framework-encoding regions of DNA encoding variable
 PT domain of rat or mouse antibody chain
 PS Disclosure; Fig 7; 74pp; English.
 CC The sequence is that of the reshaped CD4 antibody heavy chain
 CC CD4VHNEW-Ser30. Reshaped CD4 antibody can be used to induce tolerance
 CC against an antigen. It can also be used to alleviate autoimmune diseases
 CC such as rheumatoid arthritis, and to prevent graft rejection. Tolerance
 CC to a graft, e.g. an organ graft or a bone marrow transplantation can
 CC also be useful to alleviate allergies. Tolerance to allergens could
 CC also be achieved. See also R22753-R22763.
 SQ Sequence 467 AA;

Query Match 82.8%; Score 2850; DB 4; Length 467;
 Best Local Similarity 87.3%; Pred. No. 1.28e-222;
 Matches 411; Conservative 31; Mismatches 20; Indels 9; Gaps 6;
 Db 6 iilflvatatgshsqvqlqesgpglvpsqtlstlctvsgftfen-ygmawvrgppgrgl 64
 Qy 6 FEILLVAAPRWLSQVQLQESGPGLVKPSSETLSLTCVAVSGSISGGYGMGWIROPKGL 65
 Db 65 ewigtishdgdyfrdevkgrvtmldvtsknqfslrslavtaadtavycarg--tia 122
 Qy 66 EWIGTSFSSGNTYTNPSIKSQVTISTDTSKNQFSIKLNSMTAADTAVYVCVRDLFSV 125
 Db 123 g-i---r-h-wggslvtvsaatkpgsvfplapasketaggtaalgclvkdyfpepvtv 176
 Qy 126 GMVYNNWFDMWGPGLVTVSSASTKGPSTPLAPSSKSTSGGTAALGCLVKDYFPEPTV 185
 Db 177 swnsagaltsgvhtfpavlqsglylsavvtvpsasltgttyicnvnkhpkantkvdkke 236
 Qy 186 SWNSAGLTSGVHTFPVAVLQSGGLYLSVSVTVPSSSLGTQTYICNVNKHPSNTKVDKAE 245
 Db 237 pkscdtkhtcpapellggpavflfpkpdkdtlmiertpervicvrvdshadpevkfn 296
 Qy 246 PKSCDKTHTCPAPPELLGGPSVFLFPKPKDITLMSRTPEVTCWVDVSHEDPEYKEN 305
 Db 297 wydvgevnhaaktkpreeqnystyrsvvltvlhqdwlngkeyckvsnkalpapiecti 356
 Qy 306 WYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDLWLNKKEYCKVSNKALPAPIE 365
 Db 357 skakgpreqvytlpssrdeltknqvelclvkgyfypsdiavewesngqpennykttpp 416
 Qy 366 SKAKGPREQVYTLPPSRDELTKNQVSLCLVKGYFSPSDIAVEMESNGQPENNYKTP 425
 Db 417 vldsgsflyskltvdkswqgnvfscvmhealhnhytqkslslepgk 467
 Qy 426 VLDSGSFFLYSKLTVDKSRQQGNVFSCVMHEALHNHYTQKSLSLSPCK 476

RESULT 3

ID R22758 standard; Protein; 467 AA.
 AC R22758;
 DT 20-OCT-1992 (first entry)
 DE Reshaped CD4 antibody heavy chain CD4VHNEW-Thr30.
 KW Antigen; CDR; complementarity determining region; graft rejection;
 KW autoimmune diseases; rheumatoid arthritis; allergy.
 OS Rattus rattus.
 FH Key Location/Qualifiers

FT	Peptide	1..19	
FT	/notes= "signal peptide"		
FT	Peptide	20..467	
FT	/notes= "mature peptide"		
FT	Region	50..54	
FT	/notes= "Complementarity determining region 1"		
FT	Region	69..85	
FT	/notes= "Complementarity determining region 2"		
FT	Region	118..126	
FT	/notes= "Complementarity determining region 3"		
PN	W09205274-A.		
PD	02-APR-1992.		
PF	16-SEP-1991; G01578.		
PR	17-SEP-1990; GB-020282.		
PA	(GORM/) GORMAN S D.		
PI	Clark M R, Cobbold S P, Gorman S D, Waldmann H.		
DR	WPI; 92-132139/16.		
DR	N-PSDB; Q23571.		
PT	Humanisation of antibodies binding to human CD4 antigen - by		
PT	mutation of framework-encoding regions of DNA encoding variable		
PT	domain of rat or mouse antibody chain		
PS	Disclosure; Fig 6; 74pp; English.		
CC	The sequence is that of the reshaped C04 antibody heavy chain		
CC	CD4VHNEH-Thr30. Reshaped CD4 antibody can be used to induce tolerance		
CC	against an antigen. It can also be used to alleviate autoimmune diseases		
CC	such as rheumatoid arthritis, and to prevent graft rejection. Tolerance		
CC	to a graft, e.g. an organ graft or a bone marrow transplantation can		
CC	also be useful to alleviate allergies. Tolerance to allergens could		
CC	also be achieved. See also R22753-R22763.		
SO	Sequence	467 AA:	

Query Match	82.7%	Score 2848;	DB 4;	Length 467;	
Best Local Similarity	87.0%;	Pred. No. 1.88e-222;			
Matches	410;	Conservative 32;	Mismatches 20;	Indels 9;	Gaps 6;
Db	6	ilflvatatgvhsqvlqesgpglvrsqetlslcttcsqfftn-ygmawrvqpqrgl	64		
	::: :			::: :	
Qy	6	fflllvaaprhlvsqvqlqesgpglvksqetlslcttcsqfftn-ygmawrvqpqrgl	65		
	::: :			::: :	
Db	65	ewlgtishdgetcyfrdsvkgvmlvdtskngfslrlasvtaadtavvyrcarqg--tia	122		
	: :: :			: :: :	
Qy	66	ewlgtfysggntynpnlksqvtlstdtksngfslrlasvtaadtavvyrcdrflrfsv	125		
	: :: :			: :: :	
Db	123	g-i---r-h-wggsglvtvssaastkqsvflapasesketeggtaalglcvkdyfepv	176		
	::: :			::: :	
Qy	126	gwynnwfvdmgpcvlvtvssastkqsvflapasesketeggtaalglcvkdyfepv	185		
	::: :			::: :	
Db	177	snsgaltesgvhctfpavlgseglylesvvtvpssslgtqyicnvnhkpsntckvdkk	236		
	::: :			::: :	
Qy	186	snsgalstsgvghfpaavlqssclslslsvvtvpssslgtqyicnvnhkpsntckvdkk	245		
	::: :			::: :	
Db	237	pkacdtkhtcpccapellggpsvflfpkpkdtlmierptevtcvvdvshedspevkn	296		
	::: :			::: :	
Qy	246	pkscukthtccpccapellggpsvflfpkpkdtlmierptevtcvvdvshedspevkn	305		
	::: :			::: :	
Db	297	wyvdgvevhnaktkpreegynstyrvvslvlhqdwlngkeyckkysnkalspapietti	356		
	::: :			::: :	
Qy	306	wyvdgvevhnaktkpreegynstyrvvslvlhqdwlngkeyckkysnkalspapietti	365		
	::: :			::: :	
Db	357	akagkqrepqvtylppsrdeltknqvsclclvkqfypsdiavewesngqenmykttpp	416		
	::: :			::: :	
Qy	366	skakgqrepqvtylppsrdeltknqvsclclvkqfypsdiavewesngqenmykttpp	425		
	::: :			::: :	
Db	417	vldsdgsfflyskltdvkrwgqgnvfvcevmhealhnhytqsklslepdk	467		
	::: :			::: :	

Qy	426	VLDSDGSEFLYSKLTVDKSRWQCNVFCGVMHEALHNHYTKSLSPGK	476
RESULT	4		
ID	R22757	standard; Protein; 470 AA.	
AC	R22757;		
DT	20-OCT-1992	(first entry)	
DE	Reshaped CAMPATH-1 antibody heavy chain.		
KW	Antigen; CDR; complementarity determining region; graft rejection;		
KW	autoimmune diseases; rheumatoid arthritis; allergy.		
OS	Rattus rattus.		
FH	Key	Location/Qualifiers	
FT	Region	50..54	
FT	/note=	"Complementarity determining region 1"	
FT	Region	69..87	
FT	/note=	"Complementarity determining region 2"	
FT	Region	101..110	
FT	/note=	"Complementarity determining region 3"	
FT	Peptide	1..19	
FT	/note=	"signal peptide"	
FT	Peptide	20..470	
FT	/note=	"mature peptide"	
PN	W09205274-A.		
PD	02-APR-1992.		
PF	16-SEP-1991; G01578.		
PR	17-SEP-1990; GB-020282.		
PR	(GORM/) GORMAN S D.		
PI	Clark M R, Cobbold S P, Gorman S D, Waldmann H.		
DR	WPI: 92-132139/116.		
DR	N-PSDB; Q23570.		
PT	Humanisation of antibodies binding to human CD4 antigen - by		
PT	mutation of framework-encoding regions of DNA encoding variable		
PT	domain of rat or mouse antibody chain		
PS	Disclosure; Fig 5; 74pp; English.		
CC	The sequence is that of the reshaped CAMPATH-1 heavy chain antibody.		
CC	Reshaped CD4 antibody can be used to induce tolerance against an		
CC	antigen. It can also be used to alleviate autoimmune diseases such		
CC	as rheumatoid arthritis, and to prevent graft rejection. Tolerance		
CC	to a graft, e.g. an organ graft or a bone marrow transplantation can		
CC	also be useful to alleviate allergies. Tolerance to allergens could		
CC	also be achieved. See also R22754-R22763.		
SC	Sequence	470 AA;	

[illegible]

Db 238 vepkscdkthtccpapeallgpgsvflfppkpkdtlmisrtpevtcvrvdshdepvk 297
 QY 244 AEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHDEPEVK 303
 Db 298 fnwydvgevhnahtkpreeqnystyrsvvltvlhqdwlngkeyckvsnkalpapiiek 357
 QY 304 FNWYDVGEVHNAHTKPREEQNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEK 363
 Db 358 tiskakgqprepqvtylppsdeltknqvsitclvkfgypsdiaveangqpmnyktt 417
 QY 364 TISKAKGQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 423
 Db 418 ppyldsdgfflyskltdvkarwqgnvfscsvmhealnhytqkslslepak 470
 QY 424 PPVLDSDGFFLYSKLTVDKSRWQQNVFSCSVMHEALNHYTQKSLSLSPGK 476

RESULT 5

ID R24442 standard; Protein; 481 AA.
 AC R24442;
 DT 02-JAN-1992 (first entry)
 DE Sequence of antibody molecule IgG1.
 KW Antibody; immunoglobulin G1.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc difference 308
 FT /label= N
 FT /note= "Substn. to create glycan addition site"
 FT Misc difference 310
 FT /label= S
 FT /note= "see above"
 FT Misc difference 321
 FT /label= N
 FT /note= "see above"
 FT Misc difference 329
 FT /label= N
 FT /note= "see above"
 FT Misc difference 331
 FT /label= S
 FT /note= "see above"
 FT Misc difference 356
 FT /label= N
 FT /note= "see above"
 FT Misc difference 369
 FT /label= N
 FT /note= "see above"

PN W09209293-A.

PD 11-JUN-1992.

PF 18-NOV-1991; U08605.

PR 23-NOV-1990; US-618314.

PA (GENO) GEN HOSPITAL CORP.

PI Seed B, Walz G;

DR WPI; 92-215789/26.

DR N-PSDB; Q25443.

PT Inhibition of cell adhesion mediated through ELAM-1 mol. binding

PT - used in treating chronic inflammation, rheumatoid arthritis,

PT psoriasis, etc.

PS Disclosure; Fig 1; 46pp; English.

CC The IgG1, in its nascent form, bears no sialyl-Lex side chains. The inventors designed a molecule including several such sites for attachment of sialyl-Lex side chains (see R24442, FT). The additional N-linked glycosylation sites are introduced at locations which impair complement fixing and Fc receptor binding ability. They are preferably located in the CH2 region of the Ig molecule.

CC Antibodies bearing multiple sialyl-Lex determinants are useful for disrupting undesirable interactions between cells or proteins.
 CC Disrupting this interaction has therapeutic applications, for example, in minimising inflammation following tissue injury.
 SQ Sequence 481 AA;

Query Match 81.1%; Score 2791; DB 5; Length 481;
 Best Local Similarity 82.4%; Pred. No. 1.06e-217;
 Matches 394; Conservative 35; Mismatches 46; Indels 3; Gaps 3;

Db 5 mndwtzrlfflffvaatqyqsvqlvgagaevktpgasevkveckasgttfss-yaiswvrq 63
 QY 1 MKHLFFELLIV-AAPRWLVLSQVLQESGPGVLPKSETLSLTCAVSGSGISGGYGMWIRQ 59
 Db 64 apqgglemmgilpifgtanyaqkfgrvrtitadeatetaymelsalreadtavvyceard 123
 QY 60 PPGKGLEWIGSFYSSSGNTYYPNLSKSQVTISTDTSKNQFSLKINSMTAADTAVYCYVRD 119
 Db 124 ngaycggsgyqgfdpwgqgtlvtvsaastkgsfvfplapeekstegtaalgclvkdy 183
 QY 120 R-LFSVWGWYNNWFDWGPCVLVTYSSASTKCPSEVFLAPSSKSTSGGTALGCLVKDY 178
 Db 184 fpeptvsvmsgalteqvhftfpavlgseglyslsadvvtvpssslgtqtyicnvnhkpsnt 243
 QY 179 FPEPTVSWNSGALTSQVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNT 238
 Db 244 kvdkkvepkcdtkthtccpapeallgpgsvflfppkpkdtlmisrtpevtcvrvdshde 303
 QY 239 KVDKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHDE 298
 Db 304 dpevkfnwydvgevhnahtkpreeqnystyrsvvltvlhqdwlngkeyckvsnkalp 363
 QY 299 DPEVKFNWYDVGEVHNAHTKPREEQNSTYRVSVLTVLHQDWLNGKEYCKVSNKALP 358
 Db 364 apiektiskakgqprepqvtylppsdeltknqvsitclvkfgypsdiaveangqpm 423
 QY 359 APIEKTISKAKGQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPM 418
 Db 424 nykttppvldsdgfflyskltdvkarwqgnvfscsvmhealnhytqkslslepak 481
 QY 419 NYKTTPPVLDSDGFFLYSKLTVDKSRWQQNVFSCSVMHEALNHYTQKSLSLSPGK 476

RESULT 6

ID R33311 standard; Protein; 453 AA.

AC R33311;

DT 05-JUL-1993 (first entry)

DE Humanised MaEII Version 1 (intact IgG) heavy chain.

KW Antibody; high affinity; FCEH; low affinity; FCEL;

KW IgE receptor; histamine; mast cell; basophil; Kabat;

KW CDR; murine; MAEII; Fab; humaelivl.

OS Synthetic.

PN W03004173-A.

PD 04-MAR-1993.

PF 14-AUG-1992; U06860.

PR 14-AUG-1991; US-744768.

PR 07-MAY-1992; US-879495.

PA (GETH) GENENTECH INC.

PI Jardieu PM, Presta LG;

DR WPI; 93-094004/11.

PT Polypeptide (s) binding to specific Fc epsilon receptors - act as

PT IgE antagonists; useful for treating and preventing IgE-mediated

PT disorders e.g. allergies

PS Example 4; Fig 3; 113pp; English.

CC Residues were selected from MaE11 and inserted or substituted into
 CC a human Fab antibody background (Vh region Kabat subgroup III and VI
 CC region kappa subgroup I). A first version, humael1v1 or version 1 is
 CC given below. The affinity of version 1 was assayed and found to be
 CC ca. 100 times lower than that of the donor antibody MaE11.
 CC Therefore, further modifications in the sequence of version 1
 CC were made.
 SQ Sequence 453 AA;

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Query Match      80.8%; Score 2781; DB 6; Length 453;
Best Local Similarity 86.5%; Pred. No. 7.20e-217;
Matches 398; Conservative 23; Mismatches 29; Indels 10; Gaps 4;

Db 1 evqlveggglvpggsrlscavsgvstsqyemwrtqpgkglwvvasi-tydgstn 59
   :||| ||| ||| : : ||| ||| ||| : ||| ||| ||| ||| : ||| : |||
Qy 20 QVQLQESGPGLVKPSETLSLTCVAVSGSISGGYGMWIRQPPGKLEWIGSFYSSGNTY 79
   :||| ||| ||| : : ||| ||| ||| : ||| ||| ||| ||| : ||| : |||
Db 60 yadvskgrftlsrdskntfylvqmaltaedtavvyrcargshy-----fghwhfawwq 113
   | :||: ||| ||| ||| : ||| : ||| ||| ||| : : ||| |||
Qy 80 YNPSLKQVTTISTDTSKNQFSIKLNSMTAADTAVYTCVDRDLFSVVGWYANNW-FDWGCP 138
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 114 gtlvtvsaatkqkqpsvflapssksteggtaalgcclvkdyfpeptvsmnsgaltsgv 173
   | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 139 GVLVTVSSASTKG--PSVPEPLAPSSKTSGGTAAALGCLVKDYPEPTVSMNGLTSGV 196
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 174 htfpavlqsglyslsvvtvpssalgtqyicnvnhkpsntkdkkvepkcdkthtcp 233
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 197 HTPFAVLQSSGLYSLSVWTPSSSLGTQTYICNVNHRPSNTKVDKAEFKSCDKTHTCP 256
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 234 pcpapellgqpsvflfpkpkdtlmrltpevtcvvvdshedpevkfnwydvgevhna 293
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 257 PCPAPELLGPGSVFLFPFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDVGEVHNA 316
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 294 ktprceqynetyrvsvltvlhqdlnghgkeyckvknkalpapietkiskagqprepq 353
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 317 KTKPREEQYNSTRYRVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTSIRKAKGQPREPQ 376
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 354 vyltppsreemtnqvsitclvkgfypsdiavewesngqpennykttppvldsdgffily 413
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 377 VYTLPPSRDELTKNQVSLTCLVKGEYPSDIAVEWESNGQPENNYKTPRPVLDSDGFFILY 436
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 414 skltvdkerwqgnvfscsvmhhealnhhytqklslepqk 453
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 437 SKLTVDKSRWQQGNVFCVSWHHEALNHHTYTKLSLSPGK 476
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT
ID R20057 standard; Protein; 475 AA.
AC R20057;
DT 25-MAR-1992 (first entry)
DE Heavy chain of 3D6 anti-HIV antibody.
KW Plasmid pUC3D6HC; human immunodeficiency virus; AIDS;
KM complementarity determining region.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= signal
FT Region 20..49
FT /label= Framework 1
FT Region 50..54
FT /label= CDR-1
FT Region 55..68
FT /label= Framework 2
FT Region 69..85

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FT /label= CDR_2      86..117
FT Region            Framework 3
FT /label= Framework 3
FT Region            118..134
FT /label= CDR_3      135..145
FT Region            Framework 4
FT /label= Framework 4
FT Region            146..475
FT /label= Constant_region
PN W09118983-A.
PD 12-DEC-1991.
PF 28-MAY-1991; 100067.
PR 29-MAY-1990; AT-001178.
PA (JUNG/) JUNGAUER A.
PI Felgenhauer M, Himmeler G, Kohl J, Steindl F;
DR WPI; 92-007468/01.
DR N-PSDB; Q20066.
PT Recombinant protein which binds to complex viral antigen and
PT HIV-1 - contains variable region of antibody derived from 3D6
PT cell line, used for detecting HIV-1 antigen
PS Claim 2; Page 24; 52pp; German.
CC The variable region of the heavy chain is used in a recombinant
CC protein with the variable region from the kappa light chain of 3D6,
CC the two V regions being joined by a linker. The recombinant protein
CC binds to HIV gp160.
CC See also Q20067 and Q20068.
SQ Sequence 475 AA;

Query Match      80.5%; Score 2771; DB 3; Length 475;
Best Local Similarity 83.3%; Pred. No. 4.91e-216;
Matches 393; Conservative 31; Mismatches 45; Indels 3; Gaps 2;

Db 7 wiflailkg--vqcevqlvesggglvpggsrlscavsgftfnd-yamhwvraqpgkq 63
   ||| ||| : | :||| ||| ||| ||| : ||| ||| ||| ||| : ||| ||| |||
Qy 5 WFFLLVLAAPRWLVLSQVLQESGPGLVKRPSETLSLTCVAVSGSISGGYGMWIRQPPGK 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 64 lewvsgiswdesi:gyadvskgrftlsrdskntfylvqmalraedmalnyvcvkgdyd 123
   ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 65 LEWIGSFSSSGNTYNPISKQVTTISTDTSKNQFSIKLNSMTAADTAVYTCVDRDLFSV 124
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 eggyftvafdlwgggtmvtvasastkqpsvflapssksteggtaalgcclvkdyfpepvt 183
   | : ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 125 VGMVYNNWFDMGPGVILVTVSSASTKGPSVEPLAPSSKTSGGTAAALGCLVKDYPEPTV 184
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 vswnsgaltsgvhtfpavlqsglyslsvvtvpssalgtqyicnvnhkpsntkdkkv 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 185 VSNNSGALTSGVHTFPVLQSSGLYSLSVWTPSSSLGTQTYICNVNHRPSNTKVDKKA 244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 epkscdkthtcpcpapellgqpsvflfpkpkdtlmrltpevtcvvvdshedpevkf 303
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 245 EPKSCDKTHTCPPCPAPPELLGPGSVFLFPFPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 304 nwyvdvgevhnahtkpreeqynetyrvsvltvlhqdlnghgkeyckvknkalpapietk 363
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 305 NWYVDGVEVHNAKTPREEQYNSTRYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETK 364
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 iskagqprepqvyltppsreemtnqvsitclvkgfypsdiavewesngqpennyktt 423
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 365 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGEYPSDIAVEWESNGQPENNYKTP 424
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 424 pvlsdgffilyskltvdkerwqgnvfscsvmhhealnhhytqklslepqk 475
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 425 PVLDSDGFFILYSKLTVDKSRWQQGNVFCVSWHHEALNHHTYTKLSLSPGK 476
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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>RESULT      8
ID   R31023 standard; Protein; 476 AA.
AC   R31023;
DT   19-MAY-1993 (first entry)
DE   Antibody D heavy chain.
KW   Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;
KW   lymphocyte; hepatitis A virus; HAV; sero; positive; patient;
KW   murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H.
OS   Synthetic.
FH   Key
Key   Location/Qualifiers
FT   Peptide
     1..19
FT   /note= "Signal peptide"
FT   Region
     20..49
FT   /label= FR1
FT   Region
     50..54
FT   /label= CDR1
FT   Region
     55..68
FT   /label= FR2
FT   Region
     69..84
FT   /label= CDR2
FT   Region
     85..113
FT   /label= FR3
FT   Region
     114..121
FT   /label= CDR3
FT   Region
     122..132
FT   /label= FR4
FT   Domain
     133..241
FT   /label= CH1
FT   Region
     242..262
FT   /label= HINGE
FT   Domain
     263..379
FT   /label= CH2
FT   Domain
     380..497
FT   /label= CH3
PN   EP-523949-A.
PD   20-JAN-1993.
PF   14-JUL-1992; 306420.
PR   15-JUL-1991; GB-015284.
PR   01-AUG-1991; GB-016594.
PR   23-MAR-1992; GB-006284.
PA   (WELL ) WELLCOME FOUND LTD.
PI   Crowe JS, Lewis AP;
DR   WPI; 93-019951/03.
DR   N-PSDB; Q35099.
PT   Prodn. of recombinant primate antibodies - useful for treating
PT   infections caused by hepatitis A, B and C, herpes,
PT   cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,
PT   arthritis etc.
PS   Disclosure; Fig 2; 35pp; English.
CC   The sequences given in R31023-24 represent the heavy and light chains
CC   of Antibody D respectively. Antibody D is a monoclonal antibody which
CC   was derived from peripheral blood lymphocytes from a hepatitis A virus
CC   (HAV) sero positive patient. Antibody D is closely related in nature
CC   to murine antibody B5B3. Total RNA was isolated from antibody D
CC   expressing cells and polyadenylated RNA was extracted. These polyA
CC   RNA's were used to prepare a cDNA library which was screened for human
CC   kappa light (L) chains and two positive clones were detected.
CC   Further heavy (H) chain clones were also isolated.
SQ   Sequence 476 AA;

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Query Match 80.0%; Score 2755; DB 6; Length 476;
 Best Local Similarity 81.8%; Pred. No. 1.06e-214;
 Matches 390; Conservative 36; Mismatches 49; Indels 2; Gaps 2;

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Db   1 mdwtwrlfvaaatgvqemqvvqgaevkkgssvsvtsckasggtfan-yaiswvrqa 59
     | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   1 MKHLWFFLLVAAPRWVLSQVQLQESGPGLVKPSSETLSLTCAVSGGSIISGCGWGWIRQP 60

Db   60 pqqglewmggliplfgtptyeqnfgqvritadkatstahmeltalreedtavyvcatdr 119
     | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   61 PKGLEWIGSYSSNGTYNPSLKQVITSTIDTSKNQFSKINSMTAADTAVYCYVRDR 120

Db   120 yrqanfdtrvrgfdpvgggtltvtsasastkqpsvflapsekstsggtaalgclvkdyl 179
     | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   121 LF-SVGMVYNNMFDVWGFGVLTVTSASTKGPSPVFPFLAPSSKSTSGGTAALGCLVKDYF 179

Db   180 pepvtvsnsgaltsgvhtfpavlqseglylseavtvpsseelgtqtyicnmhkpantk 239
     | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   180 PEPVTVMNSGALTSGVHTFPVAVLQSSGLYSLSVWTVFSSSLGTQTYICNVNHPKSNTK 239

Db   240 vdkkvepkcdkthtccpcapellggsavflfppkpkdtlmsrtpevtcvvvdvshed 299
     | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   240 VDKKAEPKSCDKTHTCPCPAPELLGGPSVF LFPKPKDTLMISRTPEVTCVWVDVSHED 299

Db   300 pevknwvvdgvevhnaktkpreeqnystyrvasvltvlhgdwlngkeyckvsnkalpa 359
     | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   300 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPA 359

Db   360 plektiskakgpreqvytlppsrdektknqvalclvkgfypsdiavewesngqpenn 419
     | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   360 PIEKTISKAKGPREQVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENN 419

Db   420 ykttppvldsgsflyskltvdksrwqgnvfscvmhealhhnhytklelepgk 476
     | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy   420 YKTPPVLDSGSEFFLYSKLTVDKSRMQGNVFCVMHEALHHNHYTKSLSPGK 476

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RESULT      9
ID   R42066 standard; Protein; 459 AA.
AC   R42066;
DT   29-APR-1994 (first entry)
DE   Human anti-HBs heavy chain.
KW   Antibody; Ab; light; heavy; chain; hepatitis B;
KW   HB; surface antigen.
OS   Homo sapiens.
FH   Key
Key   Location/Qualifiers
FT   Peptide
     1..9
FT   /label= sig_peptide
FT   Protein
     10..459
FT   /label= mat.protein
PN   W09320205-A.
PD   14-OCT-1993.
PF   30-MAR-1993; J00396.
PR   30-MAR-1992; JP-074678.
PA   (SUNN ) SUNTORY LTD.
PI   Arima K, Kurihara T, Matsuura S, Nishihara T, Tsuruoka N;
DR   WPI; 93-336913/42.
DR   N-PSDB; Q49944.
PT   Human anti-hepatitis B surface antigen antibody gene - can be
PT   used to produce L and H chains of the antibody in large quantity
PS   Disclosure; Fig 6-8; 46pp; Japanese.
CC   Polynucleotides encoding the L and H chains of human anti-HBs
CC   Ab are given in Q49943-Q49944. The Ab can be easily produced in
CC   large quantities for therapeutic use.
SQ   Sequence 459 AA;

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Query Match 79.0%; Score 2719; DB 8; Length 459;

Best Local Similarity 84.6%; Pred. No. 1.06e-211;
Matches 389; Conservative 31; Mismatches 33; Indels 7; Gaps 4;

Db 7 vqcqvlesggvvgvqgslrlcaasgftfsn-amhwvraqpgkglewvavilydgn 65
Qy 17 VLSQVLQESGGLVKVETSLTSLCAVSGSGISGCGWGMIRQPPKGLWLGSPYSYG 76

Db 66 hkyfadvkgrftisrdnknkntlylevkqltdetdyvyyicirdty--g-v--hrfdaw 119
Qy 77 NTTYNESLKASQVTTSTDTSKNQFSLKLNSTAAADTAVYTCVRDLFSVWGMVNNWEDW 136

Db 120 qggltvtvssastkgsfpvlpaskestagtaalgclvkdypfpvptvsnsgalasv 179
Qy 137 GPGVLTVSSASTKGSVPFLAPSSKTSCTGTAALGCLVKDYFEPVTVSNWNSGALTSGV 196

Db 180 htfpavlqsglyelsvvtvpssslgtqtyicnvnhkpsentkvdckvepkcdkthtcp 239
Qy 197 HTFPAVLQSSGLYSLSVVTVPSLSLGTQTYICNVNHKPSNTKYDKKAEKPKSCDKTHTCP 256

Db 240 pcapaelqggsvfllfpkpkdtlmisrtpevtcvvvdshbedvknwydvgevhna 299
Qy 257 PCPAPELLGGFSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKNWYDVGEVHNA 316

Db 300 tkpreegynstyrsvvltvhlhqdwlngkeyckvknkalpapiektiekakgprep 359
Qy 317 KTKPREEQYNSTYRWVSVLTVLHQDWLNGKEYCKVKNKALPAPTEKTSKAKGQPREPQ 376

Db 360 vyltpperdeltknqslclvkgfypsdiavewesngpennkttppvldsdgsffly 419
Qy 377 VYTLFPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLY 436

Db 420 skltvdksrwqgnvfscvsmhealnhhytqkslslepgk 459
Qy 437 SKLTVDKSRWQGNVFCSCVMHEALNHHTYQKSLSLSPGK 476

RESULT 10

ID R42162 standard; Protein; 461 AA.
AC R42162;
DT 27-APR-1994 (first entry)
DE Anti-HIV-1 recombinant antibody 447-520 heavy chain.
KW Human immunodeficiency Virus; antigen; ELISA; recombinant antibody;
KW HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
KW acquired immune deficiency syndrome; chimeric antibody;
KW surface glycoprotein gp120; V3 loop.
OS Homo sapiens.
PN W09319785-A.
PF 14-OCT-1993.
PD 23-MAR-1993; U02629.
PR 01-APR-1992; US-861701.
PA (MERI) MERCK & CO INC.
PA (JOHN) JOHNSON L.S.
PA (PFAR) PFARR D.S.
PI Conley AJ, Emini EA, Johnson LS, Mark GE, Pfarr DS;
DR WPI; 93-336600/42.
DR N-PSDB; Q49834.
PT New recombinant human antibody - with HIV neutralising activity
PT against at least two isolates, useful for preventing or treating
PT infection in diagnosis, etc.
PS Example 9; Fig 2A; 154pp; English.
CC EBV-transformed cell lines and mouse-human heterohybridomas
CC producing human MabE specific for the gp120 V3 loop of HIV-1 MN
CC isolate were obtained. Mab 447-520 was found to recognise the
CC tetrapeptide motif GPGK, i.e. the Principal Neutralising

CC Determinant common to the V3 loop of different HIV isolates.
CC A recombinant Ab was produced in which the H chain V region was
CC derived from 447-520 and to which a signal sequence and a H chain
CC intronic sequence are appended, fused to a fragment contg. a short
CC intronic segment of the human gamma 1 C region and the human gamma
CC 1 encoding domain in its genomic form.
SQ Sequence 461 AA;

Query Match 78.9%; Score 2716; DB 8; Length 461;
Best Local Similarity 85.1%; Pred. No. 1.88e-211;
Matches 394; Conservative 23; Mismatches 38; Indels 8; Gaps 6;

Db 1 evqlvesggglvkpggelrltcaasgftfsdv--wlnwvraqpgkglewvrikartdgg 58
Qy 20 QVQLQESGGLVKVETSLTSLCAVSGSGISGCGWGMIRQPPKGLWLGSPYS-SSEN 77

Db 59 ttdyaasvkgftisrdnknkntlylqmslktedavyscttdgfmirgvsedyvyyym 118
Qy 78 TY-YNESLKASQVTTSTDTSKNQFSLKLNSTAAADTAVYTCVRDLFSVWGMV--YNNWF- 133

Db 119 dwkggtvtvssastkgsfpvlpaskestagtaalgclvkdypfpvptvsnsgalt 178
Qy 134 DWMGPGVLTVSSASTKGSVPFLAPSSKTSCTGTAALGCLVKDYFEPVTVSNWNSGALT 193

Db 179 egvhtfpavlqsglyelsvvtvpssslgtqtyicnvnhkpsentkvdckvepkcdkth 238
Qy 194 SGVHTFPAVLQSSGLYSLSVVTVPSLSLGTQTYICNVNHKPSNTKYDKKAEKPKSCDKTH 253

Db 239 tcpcpapaelqggsvfllfpkpkdtlmisrtpevtcvvvdshbedvknwydvgevev 298
Qy 254 TCFPCPAPELLGGFSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKNWYDVGEV 313

Db 299 hnaktkpreegynstyrsvvltvhlhqdwlngkeyckvknkalpapiektiekakgpr 358
Qy 314 HNAKTKPREEQYNSTYRWVSVLTVLHQDWLNGKEYCKVKNKALPAPTEKTSKAKGQPR 373

Db 359 eqvytlpperdeltknqslclvkgfypsdiavewesngpennkttppvldsdgsf 418
Qy 374 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSF 433

Db 419 flyakltvdksrwqgnvfscvsmhealnhhytqkslslepgk 461
Qy 434 FLYSKLTVDKSRWQGNVFCSCVMHEALNHHTYQKSLSLSPGK 476

RESULT 11

ID R43339 standard; Protein; 449 AA.
AC R43339;
DT 29-NOV-1993 (first entry)
DE Completely humanised C4G1 Ig heavy chain.
KW Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIb/IIIb;
KW monoclonal antibody; platelet agglutination; humanised antibody.
OS Synthetic.
PN W09313133-A.
PD 08-JUL-1993.
PE 15-DEC-1992; J01630.
PR 20-DEC-1991; US-812111.
PR 09-JUN-1992; US-895952.
PR 11-SEP-1992; US-944159.
PA (PROT-) PROTEIN DESIGN LABS INC.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
PI Co MS, Teo JY;
DR WPI; 93-227275/28.
PT Compens. contg. immunoglobulin specific for the GP-IIB and -IIIA

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US-08-487-550-12.rag

19

Qy 307 YVDGVEVHNKTRPEEQYNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPAIEXTIS 366
Db 355 kagqgprepyvtlppstreentknqslctlvkgfypsdiavewesngqpennkttppv 414
Qy 367 KMGQPREPYVTLPSPRDELTKQVSLCLVKGFYPSDIAVEWESNGQPNKYKTPPV 426
Db 415 lldsgfflyskltvdksrwqgnvfscvmhealhnhytqkslspgk 464
Qy 427 LDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSPGK 476

RESULT 15

ID R40750 standard; Protein; 466 AA.
AC R40750;
DT 01-OCT-1993 (first entry)
DE Sequence encoded by the heavy chain expression
DE vector pAG4235.
KW Chimeric monoclonal antibody; expression plasmid.
OS Synthetic.
PN W09311252-A.
PD 10-JUN-1993.
PF 24-NOV-1992; U10207.
PR 26-NOV-1991; US-798696.
PA (REGC) UNIV CALIFORNIA.
PI Haatings A, Morrison SL, Wims L;
DR WPI; 93-197069/24.
DR N-PSDB; Q43497.
PT Expression plasmids and derivs. - used to produce protein
PT molecules esp. chimaeric monoclonal antibodies
PS Disclosure; Fig 3; 54pp; English.
CC The expression plasmid pAG4235 (ATCC No. 75038) is claimed. It is
CC used to express chimeric monoclonal antibodies. It contains genes
CC with leader sequences and is functional. The variable region and
CC constant regions exons were sequenced, however the other sequences
CC are from published references and have not been verified for this
CC particular plasmid. Regions for which there is no sequence
CC information are indicated by N's with the length determined by sizes
CC of fragments observed on agarose gels.
SQ Sequence 466 AA;

Query Match 76.5%; Score 2632; DB 7; Length 466;
Best Local Similarity 80.1%; Pred. No. 1.87e-204;
Matches 382; Conservative 37; Mismatches 46; Indels 12; Gaps 6;
Db 1 mdwlnllfpmaaaqslqsdqlvgqpelkpggetvkiackasgyftn-ygmmwvkqa 59
Qy 1 MKHLWFFLLVAPRWVLSQVQLQESGPGLVKPSSETLSUTCAVSGSGISGGYGWIRQP 60
Db 60 qgqglkwmgwintntgeptyteefkgrfaisletsantayllimlnknedatyfcarg- 118
Qy 61 PGKLEWICGSFYSSGNTYINPILKQVITSTDTSKNQFSILKNSMTAADTAVYCVDRD 120
Db 119 ---g---hawgfaywggltvtvsaatkgpavfplapseksteggtaalgcivkdyf 171
Qy 121 LFSVWGMVYNNW-FDVWGPGLVTVSSASTKGPVFP LAPSSKSTSGGTAALGCLVKDYF 179
Db 172 pepvtvwnsgaltsgvhtfpavilqseglyslsavvtvpesslgtqtyicnvnhkpkentk 231
Qy 180 PEPVTVWNSGALTSQVHTFPAVLQSSGLYSLSSVTVFPSSSLGCTQTYICNVNHPKNTK 239
Db 232 ydkkvepkcdkthtccpcapellggsavflfppkpkdtlmisrtpevtcvvvdvshed 291
Qy 240 YDKKAEPKSCDKHTHTCCPCAPPELLGGPVSF LPPPKPKOTLMISRTPEVTCVWVDVSHED 299

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US-08-487-550-12.rag

20

Db 292 pevtfnwvdygvevhnaktkpreeqynstyrsvltvlhqdmlngkeyckvsnkalpa 351
Qy 300 PEVKFNWYVDGVEVHNKTRPEEQYNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPA 359
Db 352 piektisk--gqprepyvtlppsdeltknqvalctlvkgfypsdiavewesngqpenn 409
Qy 360 PIEKTISKAKQPREPYVTLPSPRDELTKQVSLCLVKGFYPSDIAVEWESNGQPNEN 419
Db 410 ykttppvldsdgdsfflyskltvdksrwqgnvfscvmhealhnhytqkslspgk 466
Qy 420 YKTTTPVLDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSPGK 476

Search completed: Tue Dec 17 15:40:34 1996
Job time : 51 secs.

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FILE 'WPIDS' ENTERED AT 07:40:35 ON 18 DEC 96

E ANDERSON D/AU
L1 87 S E3,E22
E BRAMS P/AU
L2 13 S E3
E HANNA N/AU
L3 20 S E3-E7
E SHESTOWSK W/AU
L4 1 S E4
L5 0 S L1 AND L2 AND L3 AND L4
L6 120 S L1-L4
L7 0 S B7 AND L6
L8 0 S (B71 OR B72) AND L6
L9 0 S B()7 AND L6
E 16C10
E 7C10
L10 1 S E3
E 20C9
L11 1 S E3
E 7B6
L12 1 S E3
L13 1 S L10-L12 AND MONOCLONAL?

FILE 'HCAPLUS' ENTERED AT 07:49:36 ON 18 DEC 96

E ANDERSON D/AU
L14 272 S E3,E33,E34,E85,E86,E88,E89
E BRAMS P/AU
L15 7 S E3,E4
E HANNA N/AU
L16 100 S E3-E12
E SHESTOWSK /AU
L17 4 S E4,E5
L18 0 S L14 AND L15 AND L16 AND L17
L19 380 S L14-L17
L20 0 S L19 AND B7
L21 0 S L19 AND B7#
L22 429 S B7() (1 OR 2)

L23 28 S 16C10 OR 7C10 OR 20C9 OR 7B6
L24 0 S L22 AND L23
L25 0 S L19 AND L23
L26 2 S B7 AND L23
L27 45 S (?16C10? OR ?7C10? OR ?20C9?)/IA
L28 1 S P7B6
L29 46 S L27,L28
L30 0 S L29 AND L19
L31 2 S L27 AND B7
L32 3 S L26,L28,L31

FILE 'BIOSIS' ENTERED AT 07:59:57 ON 18 DEC 96

E ANDERSON D/AU
L33 1087 S E3,E30
E BRAMS P/AU
L34 20 S E3
E HANNA N/AU
L35 215 S E3-E11
E SHESTOWSK /AU
L36 4 S E4,E5
L37 0 S L33 AND L34 AND L35 AND L36
L38 1321 S L33-L36
L39 0 S L38 AND B7
L40 19 S 16C10 OR 7C10 OR 20C9 OR 7B6
L41 0 S L38 AND L40
L42 2 S L40 AND B7

FILE 'USPATFULL' ENTERED AT 08:01:24 ON 18 DEC 96

E ANDERSON D/AU
L43 7 S E4,E26,E28,E31
E BRAMS P/AU
L44 3 S E4
E HANNA N/AU
L45 11 S E4,E5
E SHESTOWSK /AU
L46 1 S E4
L47 0 S L43 AND L44 AND L45 AND L46
L48 22 S L43-L46
L49 0 S L48 AND B7/BI,AB
L50 19 S (16C10 OR 7C10 OR 20C9 OR 7B6)/BI,AB
L51 0 S L50 AND L48
L52 3 S L50 AND B7/BI,AB
L53 0 S L52 AND (MONOCLONAL OR ANTIBOD? OR MAB#)/BI,AB

FILE 'MEDLINE' ENTERED AT 08:04:11 ON 18 DEC 96

E ANDERSON D/AU
L54 686 S E3,E24
E BRAMS P/AU
L55 8 S E3
E HANNA N/AU
L56 136 S E3-E10
E SHESTOWSK /AU
L57 9 S E2,E4-E7
L58 0 S L54 AND L55 AND L56 AND L57
L59 837 S L54-L57
L60 0 S L59 AND B7
L61 16 S 16C10 OR 7C10 OR 20C9 OR 7B6
L62 0 S L59 AND L61
L63 2 S L61 AND B7

FILE 'EMBASE' ENTERED AT 08:06:01 ON 18 DEC 96

E ANDERSON D/AU
L64 605 S E3,E27
E BRAMS P/AU
L65 9 S E3
E HANNA N/AU
L66 124 S E3-E8
E SHESTOWSK /AU
L67 3 S E4,E5
L68 0 S L64 AND L65 AND L66 AND L67
L69 739 S L64-L67
L70 0 S L69 AND B7
L71 11 S 16C10 OR 7C10 OR 20C9 OR 7B6
L72 2 S L71 AND B7
L73 0 S L69 AND L71
L74 2 S L71 AND B7

FILE 'WPIDS, HCAPLUS, BIOSIS, MEDLINE, EMBASE' ENTERED AT 08:08:28
ON 18 DEC 96

L75 4 DUP REM L13 L32 L42 L63 L72 (6 DUPLICATES REMOVED)

FILE 'WPIDS, HCAPLUS, BIOSIS, MEDLINE, EMBASE' ENTERED AT 08:08:45
ON 18 DEC 96

=> d bib ab 1-4

L75 ANSWER 1 OF 4 HCAPLUS COPYRIGHT 1996 ACS DUPLICATE 1
AN 1994:75033 HCAPLUS
DN 120:75033
TI Induction of B cell costimulatory function by recombinant murine
CD40 ligand
AU Kennedy, Mary K.; Mohler, Kendall M.; Shanebeck, Kurt D.; Baum,
Peter R.; Picha, Kathleen S.; Otten-Evans, Carol A.; Janeway,
Charles A., Jr.; Grabstein, Kenneth H.
CS Immunex Res. and Dev. Corp., Seattle, WA, USA
SO Eur. J. Immunol. (1994), 24(1), 116-23
CODEN: EJIMAF; ISSN: 0014-2980
DT Journal
LA English
AB T cell-dependent regulation of B cell growth and differentiation
involves an interaction between CD40, a B cell surface mol., and the
CD40 ligand (CD40L) which is expressed on activated CD4+ T cells.
Recombinant membrane-bound murine CD40L induces B cells to express
costimulatory function for the proliferation of CD4+ T cells.
CD40L- or lipopolysaccharide (LPS)-activated, but not
control-cultured B cells were strong costimulators and anti-CD3 or
alloantigen-dependent T cell responses. The mol. interactions
responsible for the increased costimulatory functions were examd. by
analyzing the activated B cells for changes in the expression of two
costimulatory mols., B7 and heat-stable antigen (HSA), as
well as by the use of antagonists of B7 and HSA (CTLA4.Fc
and 20C9, resp.). The expression of both B7 and
HSA was enhanced on B cells activated with LPS. The costimulatory
activity of the LPS-activated B cells was dependent on both
B7 and HSA and was completely inhibited in the presence of a
combination of CTLA4.Fc and 20C9. In contrast, activation
of B cells and CD40L induced the expression of B7 but did
not enhance the expression of HSA. In addn. the costimulatory

activity of the CD40L-activated B cells was partially, but not completely, inhibited by the combination of CTLA4.Fc and **20C9**. Thus, CD40L regulates costimulatory function of B cells in part by inducing the expression of **B7**, and CD40L-activated B cells may express an addnl. costimulatory activity that is not assocd. with LPS-activated B cells.

L75 ANSWER 2 OF 4 HCAPLUS COPYRIGHT 1996 ACS
 AN 1993:511509 HCAPLUS
 DN 119:111509
 TI 7B6, a ubiquitous mRNA: with significant homology to L41 human ribosomal protein RNA
 AU Francis, S. E.; Duff, G. W.
 CS Sect. Mol. Med., Univ. Sheffield, Sheffield, S10 2JF, UK
 SO Nucleic Acids Res. (1993), 21(12), 2944
 CODEN: NARHAD; ISSN: 0305-1048
 DT Journal
 LA English
 AB The nucleotide sequence of a 350 base pair cDNA clone previously designated **p7B6** is reported here. This clone has been used as an invariant control in Northern blot anal. but no DNA sequence was available. The cDNA hybridizes to a constantly expressed mRNA that appears to be abundant in human tissue and mammalian cell lines cultured in different physiol. conditions, thus providing a good control transcript that may be very useful for RNA quantification. The cDNA sequence was obtained from the original clone (**p7B6/pBR322**) using a conventional double-stranded sequencing method. FASTA searching of the EMBL database revealed that **p7B6** shared homol. (95.4% identity in a 283bp overlap) to the mRNA for the human ribosomal protein L41 which participates in amino acyl-tRNA binding ensuring fidelity in translation of mRNA. Now that the cDNA sequence for **p7B6** is available, it may also prove useful as an invariant control in quant. RT-PCR expts. with eukaryotic cells and tissues.

L75 ANSWER 3 OF 4 WPIDS COPYRIGHT 1996 DERWENT INFORMATION LTD
 AN 92-270165 [33] WPIDS
 DNN N92-206513 DNC C92-120444
 TI New **monoclonal** antibody specific for Derf 11 - useful for immunologically identifying and determining Derf 11.
 DC B04 D16 S03
 IN AKAGAWA, M; ANDOH, T; HAYASHI, Y; MORI, T; SUGIYAMA, S
 PA (ASAK) ASAHI BREWERIES LTD; (TORI) TORII & CO LTD; (ASAH) ASAHI KASEI KOGYO KK; (TORI) TORII YAKUHHN KK
 CYC 4
 PI EP 498124 A1 920812 (9233)* EN 20 pp
 AU 9187026 A 920827 (9242)
 CA 2054551 A 920807 (9243)
 JP 05207892 A 930820 (9338) 12 pp
 US 5286628 A 940215 (9407) 15 pp
 AU 654506 B 941110 (9445) ,
 CA 2054551 C 960604 (9634)
 JP 02516842 B2 960724 (9634) 10 pp
 ADT EP 498124 A1 EP 91-312058 911227; AU 9187026 A AU 91-87026 911106;
 CA 2054551 A CA 91-2054551 911030; JP 05207892 A JP 91-35018 910206;
 US 5286628 A US 91-798483 911126; AU 654506 B AU 91-87026 911106; CA 2054551 C CA 91-2054551 911030; JP 02516842 B2 JP 91-35018 910206
 FDT AU 654506 B Previous Publ. AU 9187026; JP 02516842 B2 Previous Publ. JP 05207892

PRAI JP 91-35018 910206

AB EP 498124 A UPAB: 931025

A new **monoclonal** antibody (Ab) selectively recognises Derf II (the major allergen of the house dust mite *Dermatophagoides farinae*); is of IgG or IgM class and is produced by immunising a mammal with Derf II. Also new are hybridoma cell lines which produce Ab.

Pref. Ab are designated 1B2(FERM BP-3247); **7C10** (BP-3248); 15E11 (BP-3249); 18G8(BP-3250); 13A4(BP-3251) and 24B7(BP-3252), and may be labelled with an enzyme, fluorophore or chemiluminescent cpd.

USE/ADVANTAGE - Ab are useful (1) in affinity chromatography for purification of Derf II (for use in desensitisation therapy) and (2) as immunoassay reagent for detecting and quantifying Derf II, e.g. in house dust. Derf II is a major allergen in cases of bronchial asthma, rhinitis, etc. This assay is simpler, more sensitive (down to 10ng/ml Derf II) and more specific than known methods which use antibodies raised against extracts of the mites.

1/8

Dwg.1/8

L75 ANSWER 4 OF 4 HCAPLUS COPYRIGHT 1996 ACS

DUPLICATE 2

AN 1993:57667 HCAPLUS

DN 118:57667

TI Co-stimulation of murine CD4 T cell growth: cooperation between **B7** and heat-stable antigen

AU Liu, Yang; Jones, Bryan; Brady, William; Janeway, Charles A., Jr.; Linley, Peter S.

CS Sch. Med., Yale Univ., New Haven, CT, USA

SO Eur. J. Immunol. (1992), 22(11), 2855-9

CODEN: EJIMAF; ISSN: 0014-2980

DT Journal

LA English

AB The contributions of B cell activation antigen **B7**/BB1 and heat-stable antigen (HSA) to the co-stimulatory activity of antigen-presenting cells (APC) were evaluated. Mouse **B7** provides co-stimulatory activity for murine CD4 T cells in anti-CD3-induced proliferation. Human CTLA4Ig, a chimeric mol. comprising the extracellular region of CTLA-4 fused to an Ig C.gamma. fragment, binds to murine **B7**. Therefore, human CTLA4IG and the hamster anti-HSA monoclonal antibody **20C9** were used to analyze the relative contributions of **B7** and HSA to the co-stimulatory activity of murine spleen APC. The data reveal that both murine **B7** and HSA are expressed by dendritic cells and by low-d. spleen B cells. Either CTLA4Ig alone or anti-HSA alone inhibited CD4 T proliferation to anti-CD3 by >90%, while CTLA4Ig and anti-HSA together were far more efficient in inhibiting clonal expansion of CD4 T cells. Thus, functionally defined co-stimulation involves at least **B7** and HSA; perhaps signals delivered by **B7** and HSA synergize in promoting T cell growth.